

EXHIBIT 1

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.

Defendant.

C.A. No. 21-669 (GBW)

**HIGHLY CONFIDENTIAL –
ATTORNEY’S EYES ONLY**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.

Defendant.

C.A. No. 21-1635 (GBW)

EXHIBIT 1: JOINT STATEMENT OF UNCONTESTED FACTS

In accordance with Local Rule 16.3(c)(3) of the Local Rules of Civil Practice and Procedure of the United States District Court for the District of Delaware, Plaintiff Laboratory Corporation of America Holdings (“Plaintiff” or “Labcorp”) and Defendant Natera, Inc. (“Defendant” or “Natera”) submit the following joint statement of facts that are undisputed or have been agreed or stipulated to by the parties, and for which no proof is needed at trial.

I. THE PARTIES AND NATURE OF THE CASE

A. Plaintiff

1. Plaintiff Laboratory Corporation of America Holdings is a corporation organized and existing under the laws of the State of Delaware, having a principal place of business at 1400 16th Street, San Francisco, California 94103.

B. Defendant

2. Defendant Natera, Inc. is a corporation organized and existing under the laws of Delaware, having a principal place of business at 201 Industrial Road, San Carlos, California 94070.

C. Nature of the Case

3. This is an action for alleged patent infringement arising under the Patent Laws of the United States, Title 35, United States Code, § 1, *et seq.*

4. Labcorp has alleged infringement of claims 1–13 and 15–16 of U.S. Patent No. 10,604,799 (the “’799 Patent”); claims 1, 4–9, 12, and 15–27 of U.S. Patent No. 11,149,308 (the “’308 Patent”); and claims 1–13 and 15–18 of U.S. Patent No. 11,155,863 (the “’863 Patent”) (collectively, with respect to the patents, the “Asserted Patents” or “Patents-in-Suit,” and with respect to the claims, the “Asserted Claims”) against Natera.

5. Natera has asserted defenses and affirmative defenses of non-infringement and invalidity of the Asserted Patents.

6. Subject matter jurisdiction over this action is proper pursuant to 28 U.S.C. §§ 1331 and 1338(a).

7. Venue for this action as proper in the District of Delaware pursuant to 28 U.S.C. §§ 1391(b), 1391(c), and 1400(b) is not contested.

8. This Court's personal jurisdiction over the parties is not contested.

II. THE ACCUSED PRODUCT

9. Labcorp accuses the SignateraTM test of infringing the Asserted Patents ("Accused Product" or "Signatera").

10. The software that performs the allegedly infringing method is called TNseq and is sold by Sentieon, Inc.

11. Portions of the source code for TNseq have been produced in this action bearing the Bates number SENTIEONSOURCECODE00001, which the parties agree qualifies as a business record and is admissible at trial.

12. Labcorp does not accuse any other Natera product of infringing the Asserted Patents.

III. THE ASSERTED PATENTS

A. The '799 Patent

13. The '799 Patent is titled "Sequence Assembly."

14. The application for the '799 Patent, Appl. No. 14/250,891 ("891 Application"), was filed on April 11, 2014 and is a continuation of U.S. Pat. Appl. No. 13/494,616, filed June 12, 2012, which issued as U.S. Patent No. 8,738,300 (the "'300 Patent"), which is a continuation of

U.S. Pat. Appl. No. 13/439,508, filed on April 4, 2012 and which issued as U.S. Patent No. 8,209,130 (the “’130 Patent”).

15. The inventors named on the face of the ’799 Patent are Gregory Porreca and Caleb Kennedy.

16. Gregory Porreca and Caleb Kennedy are both former employees of Good Start Genetics, Inc. (“Good Start Genetics”).

17. Gregory Porreca is the founder and CEO of Molecular Loop Biosolutions, LLC (“Molecular Loop”).

18. The ’799 Patent issued on March 31, 2020.

19. The assignee listed on the face of the ’799 Patent is Molecular Loop.

20. Molecular Loop assigned its rights in the ’799 Patent to Invitae under a Patent Assignment Agreement executed on March 13, 2021 in connection with an Asset Purchase Agreement executed on March 13, 2021.

21. Invitae was the sole owner of, and holder of, all substantial rights in the ’799 Patent at the time it filed the complaints in this case. Subsequently, Labcorp acquired all substantial rights in the ’799 Patent and now has sole ownership of the ’799 Patent.

B. The ’308 Patent

22. The ’308 Patent is titled “Sequence Assembly.”

23. The application for the ’308 Patent, U.S. Patent Appl. No. 17/322,610, was filed on May 17, 2021 and is a continuation of U.S. Patent Appl. No. 16/790,519, filed on February 13, 2020, which is a continuation of the ’891 Application, which issued as the ’799 Patent and claims priority to Appl. No. 13/494,616, filed June 12, 2012 and which issued as the ’300 Patent, and Appl. No. 13/439,508, filed on April 4, 2012 and which issued as the ’130 Patent.

24. The named inventors of the '308 Patent are Gregory Porreca and Caleb Kennedy.

25. The '308 Patent issued on October 19, 2021.

26. The assignee listed on the face of the '308 Patent is Invitae Corporation.

27. Invitae was the sole owner of, and holder of, all substantial rights in the '308 Patent at the time it filed the complaints in this case. Subsequently, Labcorp acquired all substantial rights in the '308 Patent and now has sole ownership of the '308 Patent.

C. The '863 Patent

28. The '863 Patent is titled "Sequence Assembly."

29. The application for the '863 Patent, U.S. Patent Appl. No. 17/322,587, was filed on May 17, 2021 and is a continuation of U.S. Patent Appl. No. 16/790,519, filed on February 13, 2020, which is a continuation of the '891 Application, which issued as the '799 Patent and claims priority to Appl. No. 13/494,616, filed June 12, 2012, and which issued as the '300 Patent, and Appl. No. 13/439,508, filed on April 4, 2012, and which issued as the '130 Patent.

30. The inventors named on the face of the '863 Patent are Gregory Porreca and Caleb Kennedy.

31. The '863 Patent issued on October 26, 2021.

32. The assignee listed on the face of the '863 Patent is Invitae Corporation.

33. Invitae was the sole owner of, and holder of, all substantial rights in the '863 Patent at the time it filed the complaints in this case. Subsequently, Labcorp acquired all substantial rights in the '863 Patent and now has sole ownership of the '863 Patent.

IV. CLAIM CONSTRUCTION

34. On October 18, 2022, the Court construed the terms below to have the following meanings (D.I. 84, 85)¹:

<u>Claim Term</u>	<u>Court's Construction</u>
Court's Construction	
“sequence reads”	raw reads as generated by the sequencing instrument
“a plurality of sequence reads” (’799 Patent) “the plurality of sequence reads” (’863 Patent) “the sequence reads” (’308 Patent)	“sequence reads” to be defined as above, no other construction necessary
“said plurality of sequence reads” (’799 Patent) “the plurality of sequence reads” (’799 Patent)	“sequence reads” to be defined as above, no other construction necessary
“contig:reference descriptions of mutations” (’799 Patent) “contig-to-reference descriptions of mutations” (’863 Patent)	a description of a mutation in a contig as it exists in the nucleic acid with reference to the genome
“reference alignment(s)” (’308 Patent)	placement in a reference genome
“read:contig descriptions” (’799 Patent) “read-to-contig descriptions” (’863 Patent)	a description of a sequence read with reference to a contig
“sequence read alignments” (’308 Patent)	placements of sequence reads
“read:reference descriptions” (’799 Patent) “read-to-reference descriptions” (’863 Patent)	description of a sequence read with reference to the reference genome
“combining the contig:reference descriptions with the read:contig descriptions” (’799 Patent)	No construction necessary. Plain and ordinary meaning.

¹ Unless stated otherwise, citations to docket numbers refer to Case No. 21-cv-669-GBW.

“combining the reference alignment and the sequence read alignment” (’308 Patent)	
Agreed-Upon Construction	
“genotyping” (’308 Patent)	assigning a genotype to

V. FACTS PERTAINING TO INVALIDITY

35. The following documents and materials are admissible evidence at trial and are business records and were available to the public as of the specified dates (except the public availability of the source code for version 1.8.2 of CASAVA):

- The source code for version 1.8.2 of Illumina’s CASAVA software program, produced as ILLUMINA-0008568 and ILLUMINA-0008569;
- The Complete Secondary Analysis Workflow for the Genome Analyzer Technical Note, produced as ILLUMINA-0000988 and ILLUMINA-0003413, which was publicly available no later than October 2009;
- The GenomeStudio Software DNA Sequencing Module Workflow Technical Note, produced as ILLUMINA-0000987, which was publicly available no later than January 2009;
- The CASAVA v.1.8 Changes document, produced as ILLUMINA-0001185, which was publicly available no later than September 2011;
- The CASAVA 1.8.2 Release Notes document, produced as ILLUMINA-0002642, which was publicly available no later than September 2011;
- The Genome Analyzer Pipeline Software User Guide, produced as ILLUMINA-0002650, which was publicly available no later than January 2009;

- The CASAVA 1.8.2 Quick reference Guide, produced as ILLUMINA-0004065 and ILLUMINA-0005041, which was publicly available no later than October 2011;
- The CASAVA v.1.8.2 User Guide, produced as ILLUMINA-0004093 and ILLUMINA-0003123, which was publicly available no later than December 2011;
- The Improved Accuracy for ELAND and Variant Calling document, produced as ILLUMINA-0008542, which was publicly available no later than October 2011;
- The “From reads to results: alignment and analysis of NextGen sequence data” document, produced as ILLUMINA-0008550, which was publicly available no later than October 2009; and
- The CASAVA User Guide, produced as NTRA-INVT-00000891, which was publicly available no later than May 2011.

36. The prior art reference Li_2008_samtools.pdf - Li et al., *Mapping short DNA sequencing reads and calling variants using mapping quality scores*, GENOME RESEARCH 18(11):1851–1858 (2008) (“Li, Ruan, & Durbin (2008)”) is admissible and was publicly available as of August 19, 2008, and was produced bearing the Bates number Invitae0010119541–Invitae0010119549.

37. The prior art reference Li and Durbin, *Fast and accurate short read alignment with Burrows-Wheeler transform*, BIOINFORMATICS 25:1754-1760 (2009) (“Li and Durbin”) is admissible and was publicly available as of May 18, 2009, and was produced bearing the Bates number Invitae0010122662–Invitae0010122668.

38. The prior art reference Albers et al., *Dindel: Accurate indel calls from short-read data*, GENOME RESEARCH 21:961-973 (2011) (“Albers (2011)”) is admissible and was publicly

available as of October 27, 2010, and was produced bearing the Bates number NTRA-INV-00000719–NTRA-INV-00000733.

39. The prior art reference Albers et al., *Dindel: Accurate indel calls from short-read data*, GENOME RESEARCH 21:961-973 (2011) Supplementary Information (“Albers (2011) Supplementary Information”) is admissible and was publicly available as of October 27, 2010, and was produced bearing the Bates number NTRA-INV-00000734–NTRA-INV-00000746.

40. The prior art reference Birol et al., *De novo transcriptome assembly with ABySS*, BIOINFORMATICS 25:2872–2877 (2009) (“Birol (2009)”) is admissible and was publicly available as of June 15, 2009, and was produced bearing the Bates number NTRA-INV-00000830–NTRA-INV-00000835.

41. The prior art reference Chiu et al., *Trans-AbySS v1.2.0: User Manual* (2011) (“Trans-ABYSS User Manual”) is admissible and was publicly available as of January 7, 2011, and was produced bearing the Bates number NTRA-INV-00001105–NTRA-INV-00001136.

42. The prior art reference Craig et al., *Identification of genetic variants using bar-coded multiplexed sequencing*, NATURE METHODS 5:887–893 (2008) (“Craig (2008)”) is admissible and was publicly available as of September 14, 2008, and was produced bearing the Bates number NTRA-INV-00001151–NTRA-INV-00001166.

43. The prior art reference DePristo et al., *A framework for variation discovery and genotyping using next-generation DNA sequencing data*, NATURE GENETICS 43:491-498 (2011) (“DePristo (2011)”) is admissible and was publicly available as of April 10, 2011, and was produced bearing the Bates number NTRA-INV-00001186–NTRA-INV-00001205.

44. The prior art reference DePristo et al., *A framework for variation discovery and genotyping using next generation DNA sequencing data*, NATURE GENETICS 43:491-498 (2011), Supplemental Information (“DePristo (2011) Supplemental Information”) is admissible and was publicly available as of April 10, 2011, and was produced bearing the Bates number NTRA-INVNT-00001206–NTRA-INVNT-00001223.

45. The prior art reference DePristo et al., *A framework for variation discovery and genotyping using next-generation DNA sequencing data*, NATURE GENETICS 43:491-498 (2011) Online Methods (“DePristo (2011) Online Methods”) is admissible and was publicly available as of April 10, 2011, and was produced bearing the Bates number NTRA-INVNT-00001224–NTRA-INVNT-00001233.

46. The prior art reference Etter, P. et al., *Local De Novo Assembly of RAD Paired-End Contigs Using Short Sequencing Reads*, PLoS ONE 6(4):e18561, (2011) (“Etter (2011)”) is admissible and was publicly available as of April 13, 2011, and was produced bearing the Bates number NTRA-INVNT-00001283–NTRA-INVNT-00001292.

47. The prior art reference Etter, P. et al., *Local De Novo Assembly of RAD Paired-End Contigs Using Short Sequencing Reads*, PLoS ONE 6(4):e18561, (2011) Supplemental Information (“Etter (2011)” Supplemental Information) is admissible and was publicly available as of April 13, 2011, and was produced bearing the Bates number NTRA-INVNT-00001293–NTRA-INVNT-00003907.

48. The prior art reference Etter, P. et al., *Local De Novo Assembly of RAD Paired-End Contigs Using Short Sequencing Reads*, PLoS ONE 6(4):e18561, (2011) Supplemental Information -TXT (“Etter (2011) Supplemental Information – TXT”) is admissible and was

publicly available as of April 13, 2011, and was produced bearing the Bates number NTRA-INVNT-00003908–NTRA-INVNT-00007528.

49. The prior art reference Frith et al., *Parameters for accurate genome alignment*, BMC BIOINFORMATICS 11(80):1-14 (2010) (“Frith (2010)”) is admissible and was publicly available as of February 9, 2010, and was produced bearing the Bates number NTRA-INVNT-00007959–NTRA-INVNT-00007972.

50. The prior art reference Genome Analyzer System, Illumina® Sequencing (2009) (“Illumina Genome Analyzer (2009)”) is admissible and was publicly available as of May 4, 2009, and was produced bearing the Bates number NTRA-INVNT-00007982–NTRA-INVNT-00007985.

51. The prior art reference George et al., *Trans genomic capture and sequencing of primate exomes reveals new targets of positive selection*, GENOME RESEARCH 21: 1686–1694 (2011) (“George (2011)”) is admissible and was publicly available as of July 27, 2011, and was produced bearing the Bates number NTRA-INVNT-00007993–NTRA-INVNT-00008002.

52. The prior art reference George et al., *Trans genomic capture and sequencing of primate exomes reveals new targets of positive selection*, GENOME RESEARCH 21: 1686–1694 (2011) Supplemental Information (“George (2011) Supplemental Information”) is admissible and was publicly available as of July 27, 2011, and was produced bearing the Bates number NTRA-INVNT-00008003–NTRA-INVNT-00008033.

53. The prior art reference HiSeq™ 2000 sequencing system, *Redefining the trajectory of sequencing*, Specifications Sheet: Illumina® Sequencing (2010) (“Illumina HiSeq (2010) Specification Sheet”) is admissible and was publicly available as of July 17, 2010, and was produced bearing the Bates number NTRA-INVNT-00008063–NTRA-INVNT-00008066.

54. The prior art reference Illumina, *De novo assembly using Illumina reads*, Technical Note Illumina Sequencing (2009) (“Illumina Technical Note”) is admissible and was publicly available as of October 12, 2009, and was produced bearing the Bates number NTRA-INVT-00008110–NTRA-INVT-00008118.

55. The source code file IndelRealigner.java (“IndelRealigner”) is admissible and was publicly available as of June 28, 2010, and was produced bearing the Bates number NTRA-INVT-00008163–NTRA-INVT-00008194.

56. The prior art reference LeVan et al., *ChiP-seq analysis of SOLiD™ sequence reads with NextGENe™ software*, SOFTGENETICS (2008) (“LeVan (2008)”) is admissible and was publicly available as of September 2008, and was produced bearing the Bates number NTRA-INVT-00008421–NTRA-INVT-00008424.

57. The prior art reference Li et al., *De novo assembly of human genomes with massively parallel short read sequencing*, GENOME RESEARCH 20:265-272 (2010) (“Li (2009)”) is admissible and was publicly available as of December 17, 2009, and was produced bearing the Bates number NTRA-INVT-00008457–NTRA-INVT-00008477.

58. The prior art reference Li, H. and Homer, N., *A survey of sequence alignment algorithms for next-generation sequencing*, Briefings in Bioinformatics, 11(5):473-83 (2010) (“Li & Homer (2010)”) is admissible and was publicly available as of May 11, 2010, and was produced bearing the Bates number NTRA-INVT-00008485–NTRA-INVT-00008495.

59. The prior art reference Li et al., *The sequence alignment/map format and SAMtools*, BIOINFORMATICS 25:2078-2079 (2009) (“Durbin (2009)”) is admissible and was publicly

available as of June 8, 2009, and was produced bearing the Bates number NTRA-INVT-00008516–NTRA-INVT-00008517.

60. The prior art reference Manion, M. et al., *Deep sequencing analysis and low frequency SNP/Mutation detection with NextGENe Software*, NextGENe™ by SoftGenetics (2009) (“Manion (April 2009)”) is admissible and was publicly available as of April 2009, and was produced bearing the Bates number NTRA-INVT-00008534–NTRA-INVT-00008537.

61. The prior art reference Manion, M. et al., *Sequence Analysis Using Barcode/Index Tags of Pooled Samples with NextGENe Software*, NextGENe™ by SoftGenetics (2009) (“Manion (March 2009)”) is admissible and was publicly available as of March 2009, and was produced bearing the Bates number NTRA-INVT-00008538–NTRA-INVT-00008540.

62. The prior art reference McKenna et al., *The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data*, *Genome Research* 20(9):1297-1303 (2010) (“McKenna (2010)”) is admissible and was publicly available as of July 19, 2010, and was produced bearing the Bates number NTRA-INVT-00008591–NTRA-INVT-00008598.

63. The prior art reference Metzker, *Sequencing technologies - the next generation*, *NATURE REVIEWS GENETICS* 11:31-46 (2010) (“Metzker (2010)”) is admissible and was publicly available as of December 8, 2009, and was produced bearing the Bates number NTRA-INVT-00008599–NTRA-INVT-00008614.

64. The prior art reference Miller, J., et al., *Assembly algorithms for next-generation sequencing data*, *Genomics*, 95, 315-327 (2010) (“Miller (2010)”) is admissible and was publicly

available as of March 6, 2010, and was produced bearing the Bates number NTRA-INV-00008633–NTRA-INV-00008645.

65. The prior art reference Morin, R. et al., *Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma*, Nature 476(7360):298-303 (2011) (“Morin (2011)”) is admissible and was publicly available as of July 27, 2011, and was produced bearing the Bates number NTRA-INV-00008646–NTRA-INV-00008651.

66. The prior art reference Morin, R. et al. (2011) Supplemental Information (“Morin (2011) Supplemental Information”) is admissible and was publicly available as of July 27, 2011, and was produced bearing the Bates number NTRA-INV-00008652–NTRA-INV-00008703.

67. The source code file RealignerTargetCreator.java (“RealignerTargetCreator”) is admissible and was publicly available as of June 28, 2010, and was produced bearing the Bates number NTRA-INV-00008926–NTRA-INV-00008932.

68. The prior art reference Reinhardt, J. et al., *De novo assembly using low-coverage short read sequence data from the rice pathogen Pseudomonas syringae pv. oryzae*, Genome Research 19:294-305 (2009) (“Reinhardt (2009)”) is admissible and was publicly available as of November 17, 2008, and was produced bearing the Bates number NTRA-INV-00008933–NTRA-INV-00008951.

69. The prior art reference Reinhardt et al. (2009) Supplemental Information (“Reinhardt (2009) Supplemental Information”) is admissible and was publicly available as of November 17, 2008, and was produced bearing the Bates number NTRA-INV-00008952–NTRA-INV-00008958.

70. The prior art reference Robertson, G., et al., *De novo assembly and analysis of RNA-seq data*, NATURE METHODS 7:909-912 (2010) (“Robertson (2010)”), is admissible and was publicly available as of October 10, 2010, and was produced bearing the Bates number NTRA-INVT-00008959–NTRA-INVT-00008965.

71. The prior art reference Robertson et al., *De novo assembly and analysis of RNA-seq data*, NATURE METHODS 7:909-912 (2010) Supplemental Information (“Robertson (2010) Supplemental Information”) is admissible and was publicly available as of October 10, 2010, and was produced bearing the Bates number NTRA-INVT-00008966–NTRA-INVT-00009000.

72. The prior art reference Schwartz, T., et al., *A garter snake transcriptome: pyrosequencing, de novo assembly, and sex specific differences*, BMC Genomics 11 (694) (2010) (“Schwartz (2010)”) is admissible and was publicly available as of December 7, 2010, and was produced bearing the Bates number NTRA-INVT-00009036–NTRA-INVT-00009052.

73. The prior art reference Simpson, J., et al., *ABYSS: A parallel assembler for short read sequence data*, GENOME RESEARCH 19: 1117–1123 (2009) (“Simpson (2009)”) is admissible and was publicly available as of February 27, 2009, and was produced bearing the Bates number NTRA-INVT-00009065–NTRA-INVT-00009072.

74. The prior art reference Simpson, J., et al., *ABYSS: A parallel assembler for short read sequence data*, GENOME RESEARCH 19: 1117–1123 (2009) Supplemental Materials (“Simpson (2009) Supplemental Materials”) is admissible and was publicly available as of February 27, 2009, and was produced bearing the Bates number NTRA-INVT-00009096–NTRA-INVT-00009111.

75. The prior art reference U.S. Patent No. 6,138,077 (Brenner) - Method, Apparatus and Computer Program Product for Determining a Set of Non-Hybridizing Oligonucleotides (“Brenner ’077”) is admissible and was filed June 3, 1998, and issued and was publicly available as of October 24, 2000, and was produced bearing the Bates number NTRA-INVT-00009211–NTRA-INVT-00009246.

76. The prior art reference U.S. Patent No. 8,271,206 (Liu et al.) - DNA Sequence Assembly Methods of Short Reads (“Liu (2009)”) is admissible and was filed April 21, 2009, and issued and was publicly available as of September 18, 2012, and was produced bearing the Bates number NTRA-INVT-00009318–NTRA-INVT-00009367.

77. The prior art reference Warren, R., et al., *Assembling millions of short DNA sequences using SSAKE*, Bioinformatics 23:500-501 (2007) (“Warren (2007)”) is admissible and was publicly available as of December 8, 2006, and was produced bearing the Bates number NTRA-INVT-00009934–NTRA-INVT-00009956.

78. The prior art reference Wiseman, R., et al., *Major histocompatibility complex genotyping with massively parallel pyrosequencing*, NATURE MEDICINE 15:1322-1326 (2009) (“Wiseman (2009)”), is admissible and was publicly available as of October 11, 2009, and was produced bearing the Bates number NTRA-INVT-00009951–NTRA-INVT-00009956.

79. The prior art reference WO 2011/160206 A1 (Morin, R. et al.) - Biomarkers for Non-Hodgkin Lymphomas and Uses Thereof (“WO ’206”) is admissible and was filed June 23, 2011, and was issued and was publicly available as of December 29, 2011, and was produced bearing the Bates number NTRA-INVT-00010144–NTRA-INVT-00010240.

80. The prior art reference Zerbino, D. and Birney, E., *Velvet: Algorithms for de novo short read assembly using de Bruijn graphs*, Genome Research 18:821–829 (2008) (“Zerbino (2008)”) is admissible and was publicly available as of March 18, 2008, and was produced bearing the Bates number NTRA-INVT-00010232–NTRA-INVT-00010240.

81. The source code for the GATK software package that is available as supplemental data to McKenna (2010), produced with the filename GATK_source_6_28=2010.tar.gz (“McKenna (2010) Supplemental Source Code,” or “GATK Version 1”) is admissible and was publicly available as of June 28, 2010, and was produced bearing the Bates number NTRA-INVT-00310548.

82. The source code for the first version of HaplotypeCaller (“HaplotypeCaller (2011)”), produced with the native filename gatk_privateGitArchive_08-24-2011.tar, is admissible and was produced bearing the Bates number NTRA-INVT-00358917–NTRA-INVT-00359487.

83. The prior art reference Illumina sequencing, *Multiplexed sequencing with the Illumina Genome Analyzer System* (“Illumina Multiplexed Sequencing (2008)”) is admissible and was publicly available as of December 2, 2008, and was produced bearing the Bates number NTRA-INVT-00414242–NTRA-INVT-00414245.

84. The prior art reference Schneeberger, K. et al., *Reference-guided assembly of four diverse Arabidopsis thaliana genomes*, Proceedings of the National Academy of Sciences 108(25):10249–10254 (2011) (“Schneeberger (2011)”) is admissible and was publicly available as of June 6, 2011, and was produced bearing the Bates number NTRA-INVT-00414896–NTRA-INVT-00414901.

85. The prior art reference Schneeberger, K. et al., *Reference-guided assembly of four diverse Arabidopsis thaliana genomes*, Proceedings of the National Academy of Sciences 108(25):10249–10254 (2011) Supporting Information (“Schneeberger (2011) Supporting Information”) is admissible and was publicly available as of June 6, 2011, and was produced bearing the Bates number NTRA-INVNT-00414246–NTRA-INVNT-00414254.

86. The prior art reference Albers, Dindel User Guide, version 1.0 (2010) (“Dindel User Guide”) is authentic and admissible and was publicly available as of October 26, 2010, and was produced bearing the Bates number NTRA-INVNT-00414265–NTRA-INVNT-00414280.

87. The prior art reference Mayer, *Bioinformatics for Omics Data*, Methods in Molecular Biology (2011) (“Mayer (2011)”) is admissible and was publicly available as of March 3, 2011, and was produced bearing the Bates number NTRA-INVNT-00414318– NTRA-INVNT-00414895.

88. Source code for the software program Trans-ABYSS (“Trans-ABYSS Source Code”) is admissible and was publicly available as of January 7, 2011, and was produced bearing the Bates number NTRA-INVNT-00414915–NTRA-INVNT-00415498.

89. The source code for the 2012 version of HaplotypeCaller (“HaplotypeCaller (2012)”) that was included in the GATK 2.0 software package is admissible and was publicly available as of July 24, 2012, and was produced bearing the Bates number NTRA-INVNT-00415528–NTRA-INVNT-00419832.

90. The prior art reference Altschul et al., *Basic local alignment search tool*, Journal of Molecular Biology 215(3):403-410 (1990) (“Altschul (1990)”) is admissible and was publicly

available as of October 5, 1990, and was produced bearing the Bates number NTRA-INVNT-00430298–NTRA-INVNT-00430305.

91. The prior art reference Ning et al., *SSAHA: A Fast Search Method for Large DNA Databases*, *Genome Research* 11:1725-1729 (2001) (“Ning (2001)”) is admissible and was publicly available as of October 2001 and was produced bearing the Bates number NTRA-INVNT-00432574–NTRA-INVNT-00432579.

92. The prior art reference Willing et al., *Paired-end RAD-seq for de novo assembly and marker design without available reference*, *BIOINFORMATICS* 27:2187-2193 (2011) (“Willing (2011)”) is admissible and was publicly available as of June 27, 2011, and was produced bearing the Bates number NTRA-INVNT-00433184–NTRA-INVNT-00433190.

93. The prior art reference Kurtz et al., *Versatile and open software for comparing large genomes*, *Genome Biology* 5(R12) (2004) (“Kurtz (2004)”) is admissible and was publicly available as of January 30, 2004, and was produced bearing the Bates number NTRA-INVNT-00433191–NTRA-INVNT-00433199.

94. The prior art reference Margulies et al., *Genome sequencing in microfabricated high-density picolitre reactors*, *NATURE* 437:376-380 (2005) (“Margulies (2005)”) is admissible and was publicly available as of July 31, 2005, and was produced bearing the Bates number NTRA-INVNT-00431705–NTRA-INVNT-00431710.

95. The prior art reference Johnson et al., *NCBI BLAST: a better web interface*, *Nucleic Acids Research* 36:W5-W9 (2008) (“Johnson (2008)”) is admissible and was publicly available as of April 24, 2008, and was produced bearing the Bates number NTRA-INVNT-00430315–NTRA-INVNT-00430319.

96. The prior art reference Myllykangas and Hnlee Ji, *Targeted deep resequencing of the human cancer genome using next-generation technologies*, Biotechnol. Genet. Eng'g. Rev. 27:135-158 (2010) ("Myllykangas (2010)") is admissible and was publicly available as of 2010, and was produced bearing the Bates number NTRA-INVNT-00432549–NTRA-INVNT-00432573.

97. The prior art reference Schedule for Workshop I: Next-Generation Sequencing Technology and Algorithms for Primary Data Analysis, CONFERENCE OF THE INSTITUTE FOR PURE & APPLIED MATHEMATICS (October 3–6, 2011) ("Next-Generation Sequencing Workshop") is admissible and was publicly available as of October 6, 2011, and was produced bearing the Bates number NTRA-INVNT-00432440–NTRA-INVNT-00432445.

98. The prior art reference Manske and Kwiatkowski, *LookSeq: A browser-based viewer for deep sequencing data*, Genome Research 19:2125-2032 (2009) ("Manske (2009)") is admissible and was publicly available as of August 13, 2009, and was produced bearing the Bates number NTRA-INVNT-00008541–NTRA-INVNT-00008548.

99. The prior art reference Danecek et al., *The variant call format and VCFtools*, Bioinformatics, 27(15):2156-2158 (2011) ("Danecek (2011)") is admissible and was publicly available as of June 7, 2011, and was produced bearing the Bates number NTRA-INVNT-00430320–NTRA-INVNT-00430322.

100. The prior art reference Wiesner et al., *Germline mutations in BAP1 predispose to melanocytic tumors*, Nat Genet. 43(10):1018-1021 (2011) ("Wiesner (2011)") is admissible and was publicly available as of August 28, 2011, and was produced bearing the Bates number NTRA-INVNT-00431711–NTRA-INVNT-00431715.

101. The prior art reference Li et al., *SOAP: short oligonucleotide alignment program*, BIOINFORMATICS 24:713–714 (2008) (“Li (2008)”) is admissible and was publicly available as of January 28, 2008.

102. The prior art reference Li and Durbin, *Fast and accurate long-read alignment with Burrows-Wheeler Transform*, BIOINFORMATICS 26:589-595 (2010) (“Li & Durbin (2010)”) is admissible and was publicly available as of January 15, 2010.

103. The prior art reference Lukashin, et al., *GeneMark.hmm: New solutions for gene finding*, NUCLEIC ACIDS RESEARCH 26(4):1107–1115 (1998) (“Lukashin (1998)”) is admissible and was publicly available as of February 15, 1998.

EXHIBIT 2

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-669 (GBW)
v.)	
)	
NATERA, INC.,)	
)	
Defendant.)	
<hr/>		
LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-1635 (GBW)
v.)	
)	
NATERA, INC.,)	
)	
Defendant.)	

**EXHIBIT 2: PLAINTIFF LABCORP CORPORATION'S STATEMENT OF FACTS
THAT REMAIN TO BE LITIGATED**

Pursuant to Delaware Local Rule 16.3(c)(4), Plaintiff Laboratory Corporation of America Holdings (“Labcorp”) hereby submits the following statement of issues of fact that remain to be litigated.

This statement is based on the current status of the case and Court’s rulings to date. Labcorp reserves the right to revise, amend, supplement, or modify the following statement based on any pretrial ruling by the Court and/or to address any additional issues, arguments, evidence, or other developments in the case, including edits to the draft pretrial order, any meet and confers or other negotiations between the parties, pending motions, and Defendant’s identification of issues of law and fact to be litigated or any new issues Defendant may raise, or for other good cause. Labcorp does not assume the burden of proof with regard to any of the below-listed issues of facts. Further details regarding these issues have been explained at length in Labcorp’s pleadings and discovery responses, including in its contentions, interrogatory responses, expert reports, by experts at depositions and by fact witnesses at depositions, which Labcorp incorporates by reference. Should the Court determine that any issue identified in this list is more properly considered an issue of law, it shall be so considered and Labcorp incorporates such issue into Labcorp’s Statement of Issues of Law That Remain to be Litigated (Ex. 4 to Proposed Final Pretrial Order). To the extent that Labcorp’s Statement of Issues of Law That Remain to be Litigated contains issues that the Court deems to be issues of fact, those issues are incorporated herein by reference. The following statement of issues of fact is not exhaustive and Labcorp reserves the right to prove any matters identified in the pleadings and discovery responses, including in its contentions, expert reports, by experts at depositions, and by fact witnesses at depositions. Labcorp intends to offer evidence as to the issues of fact and issues of law identified in this Pretrial Order. Labcorp further intends to offer evidence to rebut evidence offered by Defendant.

I. ISSUES ON WHICH LABCORP BEARS THE BURDEN OF PROOF

A. Infringement

1. Whether Labcorp can prove by a preponderance of the evidence that the use of the Signatera Accused Products perform each step of the '799 Patent Asserted Claims.

2. Whether Labcorp can prove by a preponderance of the evidence that Defendant directly infringes the '799 Patent Asserted Claims by using the Signatera Accused Products in an infringing manner.

3. Whether Labcorp can prove by a preponderance of the evidence that the use of the Signatera Accused Products perform each step of the '308 Patent Asserted Claims.

4. Whether Labcorp can prove by a preponderance of the evidence that Defendant directly infringes the '308 Patent Asserted Claims by using the Signatera Accused Products in an infringing manner.

5. Whether Labcorp can prove by a preponderance of the evidence that the use of the Signatera Accused Products perform each step of the '863 Patent Asserted Claims.

6. Whether Labcorp can prove by a preponderance of the evidence that Defendant directly infringes the '863 Patent Asserted Claims by using the Signatera Accused Products in an infringing manner.

B. Remedies

7. The amount of damages in lost profits that Labcorp is owed from Defendant due to Defendant's infringement of one or more of the Asserted Claims of the Patents-In-Suit through the date of the verdict.

8. The amount of damages in reasonable royalties that Labcorp is owed from Defendant due to Defendant's infringement of one or more of the Asserted Claims of the Patents-In-Suit through the date of the verdict.

9. Whether Labcorp is entitled to a permanent injunction, enjoining Defendant and its officers, directors, employees, agents, servants, affiliates, and/or all persons in active concert or participation with it from continued infringement of the Patents-In-Suit, prior to the expiration of the patents, pursuant to 35 U.S.C. § 283.

10. Whether Labcorp has established that this is an exceptional case and that it is entitled to an award of attorneys' fees and costs under 35 U.S.C. § 285, and if so, the amount.

11. Whether Labcorp is entitled to an award of prejudgment and post-judgment interest, and if so, the amounts.

II. RESPONSE TO DEFENDANT'S STATEMENT OF CONTESTED FACTS FOR ISSUES ON WHICH DEFENDANTS BEAR THE BURDEN OF PROOF

A. Validity

12. Whether Defendant can prove by clear and convincing evidence that any of the Asserted Claims of the Patents-in-Suit are invalid as patent ineligible under 35 U.S.C. § 101, including whether any of the Asserted Claims of the Patents-in-Suit are directed to an abstract idea and/or whether any of the Asserted Claims of the Patents-in-Suit contain an inventive concept or merely well-understood, routine, and/or conventional activities, steps, or elements.¹

13. Whether Defendant can prove by clear and convincing evidence that any of the Asserted Claims of the Patents-in-Suit are invalid as anticipated under 35 U.S.C. § 102, including

¹ Labcorp objects to Defendant's statement of the patentable subject matter issue as an issue that remains to be litigated at the jury trial. This issue has already been resolved by the Court, finding the claims were not directed to an abstract idea under *Alice* step one. Dkt. No. 28.

whether the prior art asserted against any of the Asserted claims of the Patents-in-Suit qualifies as prior art under pre-AIA 35 U.S.C. §§ 102(a), 102(b), 102(e), and/or 102(g) and whether the asserted prior art discloses each and every element of the claims.

14. Whether Defendants can prove by clear and convincing evidence that any of the Asserted Claims of the Patents-in-Suit are invalid as obvious under 35 U.S.C. § 103, including issues of the level of ordinary skill in the art at the time of the alleged invention of the Asserted Claims of the Patents-in-Suit, the scope and content of the asserted prior art, and the differences between the claimed invention of the Asserted Claims of the Patents-in-Suit and the asserted prior art.

15. Whether the secondary considerations of non-obviousness demonstrate that the Asserted Claims of the Patents-in-Suit would not have been obvious.

16. Whether Defendant can prove by clear and convincing evidence that any of the Asserted Claims of the Patents-in-Suit are invalid for failure to satisfy the enablement requirement under 35 U.S.C. § 112, including whether the Patents-in-Suit teach those of ordinary skill in the art how to make and use the full scope of the claimed invention without undue experimentation.

17. Whether Defendant can show by clear and convincing evidence that any of the Asserted Claims of the Patents-in-Suit are invalid for failure to satisfy the written description requirement under 35 U.S.C. § 112, including whether the Patents-in-Suit describe the full scope of the claimed invention in sufficient detail so that they reasonably convey to one of ordinary skill in the art that the named inventors had possession of the claimed subject matter as of the filing date.

18. Whether Defendant can show by clear and convincing evidence that any of the Asserted Claims of the '799 Patent are invalid for failure to satisfy the definiteness requirement

under 35 U.S.C. § 112, including whether the claims, read in light of the specification and the prosecution history, fail to inform, with reasonable certainty, a person of ordinary skill in the art about the scope of the alleged invention.²

B. Defendant's Alleged Remedies³

19. Whether this is an exceptional case justifying an award of attorneys' fees under 35 U.S.C. § 285, including interest.

20. Whether Labcorp is entitled to attorneys' fees, costs, and litigation expenses.

21. Whether Labcorp is entitled to any other relief that the Court deems just and proper.

² Labcorp objects to Defendant's statement of the definiteness issue as a contested fact that remains to be litigated at the jury trial. "A determination of claim definiteness is a question of law." *Personalized Media Commc'ns, LLC v. Int'l Trade Comm'n*, 161 F.3d 696, 705 (Fed. Cir. 1998). *See also Atmel Corp. v. Info. Storage Devices, Inc.*, 198 F.3d 1374, 1378 (Fed. Cir. 1999) ("Indefiniteness, therefore, like claim construction, is a question of law that we review *de novo*."); *Nature Simulation Sys. Inc. v. Autodesk, Inc.*, 50 F.4th 1358, 1360 (Fed. Cir. 2022).

³ Defendant bears the burden of proving it is entitled to any alleged remedies, including whether it is entitled to costs and attorneys' fees under 35 U.S.C. § 285. Labcorp, to the extent necessary, will introduce evidence to rebut Defendant's assertion that it is entitled to any remedies, including whether it is entitled to costs and attorneys' fees under 35 U.S.C. § 285.

EXHIBIT 3

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

**EXHIBIT 3: DEFENDANT'S STATEMENT OF ISSUES OF FACT
THAT REMAIN TO BE LITIGATED**

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Natera respectfully submits the following statement of issues of fact that remain to be litigated. This statement is based on Natera's claims, counterclaims, and defenses, Natera's current understanding of Plaintiff's claims and defenses, and the proceedings in this action to date. Should the Court determine that any issue identified in this list is more properly considered an issue of law, it shall be so considered and Natera incorporates such issue into Natera's Statement of Issues of Law That Remain to Be Litigated (Ex. 5 to Proposed Final Pretrial Order). To the extent that Natera's Statement of Issues of Law That Remain to Be Litigated contains issues that the Court deems to be issues of fact, those issues are incorporated herein by reference. Natera reserves the right to revise, modify, supplement, or change the issues of fact to be litigated in response to subsequent Court rulings and/or Labcorp's identification of issues of law and fact to be litigated or any new issues Labcorp may raise, or for other good cause. The following statement of issues of fact is not exhaustive and Natera reserves the right to prove any matters identified in the pleadings and discovery responses, including in its contentions, expert reports, by experts at depositions, and by fact witnesses at depositions. Natera further intends to offer evidence to rebut evidence offered by Labcorp. The following issues are identified insofar as they are issues of fact or involve underlying issues of fact. By identifying the following issues, Natera does not necessarily concede that each of these issues, in whole or in part, is a pure issue of fact. By identifying the following issues, Natera does not necessarily concede that any of these issues, in whole or in part, is a material fact as to which there is any genuine dispute. Further, insofar as the following issues, as a matter of law and precedent, themselves turn on additional or subsidiary factual issues or elements, those factual issues or elements are incorporated.

I. INVALIDITY OF THE ASSERTED PATENTS

A. Invalidity of the '799 Patent

1. Whether or not Labcorp has proven the date to which it is entitled to claim priority for the Asserted Claims of the '799 Patent.
2. Whether or not Labcorp has proven the date on which the alleged invention claimed by the Asserted Claims of the '799 Patent was conceived.
3. Whether or not Labcorp has proven that the alleged invention claimed by the Asserted Claims of the '799 Patent was reduced to practice.
4. Whether or not Labcorp has proven that the alleged inventors of the alleged invention claimed by the Asserted Claims of the '799 Patent were diligent in reducing to practice that invention.
5. Whether the Asserted Claims of the '799 Patent are directed to patent-ineligible subject matter.
6. Whether the Asserted Claims of the '799 Patent are directed to an abstract idea.
7. Whether the Asserted Claims of the '799 Patent contain an inventive concept or merely well-understood, routine, and/or conventional activities, steps, or elements.
8. Whether the Asserted Claims of the '799 Patent are anticipated by the asserted prior art under 35 U.S.C. § 102.
9. Whether the prior art asserted against the Asserted Claims of the '799 Patent qualifies as prior art under pre-AIA 35 U.S.C. §§ 102(a), 102(b), 102(e), and/or 102(g).
10. Whether the prior art discloses each element of the Asserted Claims of the '799 Patent, explicitly or inherently.
11. Whether the Asserted Claims of the '799 Patent would have been obvious to one of ordinary skill in the art at the time of the alleged invention.

12. To the extent that there is any remaining dispute between the parties, the level of ordinary skill in the art at the time of the alleged invention of the Asserted Claims of the '799 Patent.

13. The scope and content of the prior art asserted against the Asserted Claims of the '799 Patent.

14. The differences, if any, between the claimed invention of the Asserted Claims of the '799 Patent and the asserted prior art.

15. Whether or not there are secondary considerations in support of the nonobviousness of the Asserted Claims of the '799 Patent.

16. Whether the Asserted Claims of the '799 Patent, read in light of the specification and the prosecution history, fail to inform, with reasonable certainty, a person of ordinary skill in the art about the scope of the alleged invention.

17. Whether the '799 Patent teaches those of ordinary skill in the art how to make and use the full scope of the claimed invention without undue experimentation.

18. Whether the '799 Patent describes the full scope of the claimed invention in sufficient detail so that they reasonably convey to one of ordinary skill in the art that the named inventors had possession of the claimed subject matter as of the filing date.

B. Invalidity of the '308 Patent

19. Whether or not Labcorp has proven the date to which it is entitled to claim priority for the Asserted Claims of the '308 Patent.

20. Whether or not Labcorp has proven the date on which the alleged invention claimed by the Asserted Claims of the '308 Patent was conceived.

21. Whether or not Labcorp has proven that the alleged invention claimed by the Asserted Claims of the '308 Patent was reduced to practice.

22. Whether or not Labcorp has proven that the alleged inventors of the alleged invention claimed by the Asserted Claims of the '308 Patent were diligent in reducing to practice that invention.

23. Whether the Asserted Claims of the '308 Patent are directed to patent-ineligible subject matter.

24. Whether the Asserted Claims of the '308 Patent are directed to an abstract idea.

25. Whether the Asserted Claims of the '308 Patent contain an inventive concept or merely well-understood, routine, and/or conventional activities, steps, or elements.

26. Whether the Asserted Claims of the '308 Patent are anticipated by the asserted prior art under 35 U.S.C. § 102.

27. Whether the prior art asserted against the Asserted Claims of the '863 Patent qualifies as prior art under pre-AIA 35 U.S.C. §§ 102(a), 102(b), 102(e), and/or 102(g).

28. Whether the prior art discloses each element of the Asserted Claims of the '308 Patent, explicitly or inherently.

29. Whether the Asserted Claims of the '308 Patent would have been obvious to one of ordinary skill in the art at the time of the alleged invention.

30. To the extent that there is any remaining dispute between the parties, the level of ordinary skill in the art at the time of the alleged invention of the Asserted Claims of the '308 Patent.

31. The scope and content of the prior art asserted against the Asserted Claims of the '308 Patent.

32. The differences, if any, between the claimed invention of the Asserted Claims of the '308 Patent and the asserted prior art.

33. Whether or not there are secondary considerations in support of the nonobviousness of the Asserted Claims of the '308 Patent.

34. Whether the '308 Patent teaches those of ordinary skill in the art how to make and use the full scope of the claimed invention without undue experimentation.

35. Whether the '308 Patent describes the full scope of the claimed invention in sufficient detail so that they reasonably convey to one of ordinary skill in the art that the named inventors had possession of the claimed subject matter as of the filing date.

C. Invalidity of the '863 Patent

36. Whether or not Labcorp has proven the date to which it is entitled to claim priority for the Asserted Claims of the '863 Patent.

37. Whether or not Labcorp has proven the date on which the alleged invention claimed by the Asserted Claims of the '863 Patent was conceived.

38. Whether or not Labcorp has proven that the alleged invention claimed by the Asserted Claims of the '863 Patent was reduced to practice.

39. Whether or not Labcorp has proven that the alleged inventors of the alleged invention claimed by the Asserted Claims of the '863 Patent were diligent in reducing to practice that invention.

40. Whether the Asserted Claims of the '863 Patent are directed to patent-ineligible subject matter.

41. Whether the Asserted Claims of the '863 Patent are directed to an abstract idea.

42. Whether the Asserted Claims of the '863 Patent contain an inventive concept or merely well-understood, routine, and/or conventional activities, steps, or elements.

43. Whether the Asserted Claims of the '863 Patent are anticipated by the asserted prior art under 35 U.S.C. § 102.

44. Whether the prior art asserted against the Asserted Claims of the '308 Patent qualifies as prior art under 35 U.S.C. §§ 102(a), 102(b), 102(e), and/or 102(g).

45. Whether the prior art discloses each element of the Asserted Claims of the '863 Patent, explicitly or inherently.

46. Whether the Asserted Claims of the '863 Patent would have been obvious to one of ordinary skill in the art at the time of the alleged invention.

47. To the extent that there is any remaining dispute between the parties, the level of ordinary skill in the art at the time of the alleged invention of the Asserted Claims of the '863 Patent.

48. The scope and content of the prior art asserted against the Asserted Claims of the '863 Patent.

49. The differences, if any, between the claimed invention of the Asserted Claims of the '863 Patent and the asserted prior art.

50. Whether or not there are secondary considerations in support of the nonobviousness of the Asserted Claims of the '863 Patent.

51. Whether the '863 Patent teaches those of ordinary skill in the art how to make and use the full scope of the claimed invention without undue experimentation.

52. Whether the '863 Patent describes the full scope of the claimed invention in sufficient detail so that they reasonably convey to one of ordinary skill in the art that the named inventors had possession of the claimed subject matter as of the filing date.

II. REMEDIES TO LABCORP (IN THE EVENT LIABILITY IS FOUND)

53. In the event liability is found with respect to at least one of the Asserted Claims, whether or not Labcorp has proven an amount of damages in reasonable royalties, if any, to which

it is entitled, including underlying facts regarding the number of infringing acts and the appropriate reasonable royalty for such acts under 35 U.S.C. § 284.

54. In the event liability is found with respect to at least one of the Asserted Claims, whether or not Labcorp has proven that it is entitled to lost profits, including underlying facts regarding the number of infringing acts and the underlying facts regarding the factors articulated in *Panduit Corp. v. Stahl Bros. Fibre Works*, 575 F. 2d 1152, 1156 (6th Cir. 1978), *i.e.*: (1) demand for the patented product; (2) absence of non-infringing alternatives; (3) manufacturing and marketing capability to exploit the demand; and (4) the amount of profit, if any, that Labcorp would have earned but for the alleged infringement.

55. In the event liability is found with respect to at least one of the Asserted Claims, whether Labcorp has proven that it is entitled to an award of pre-judgment and post-judgment interest for alleged infringement and if so, the amount.

56. In the event liability is found with respect to at least one of the Asserted Claims, whether Labcorp has established that the type of harm it allegedly has suffered, the alleged inadequacy of available remedies at law, the balance of hardship, and public interest warrant injunctive relief.

57. In the event liability is found, whether this is an exceptional case pursuant to 35 U.S.C. § 285.

58. In the event liability is found, whether attorney fees, expenses, and/or costs are due to Labcorp, and the amount.

59. In the event liability is found, whether costs should be limited under 35 U.S.C. § 288.

EXHIBIT 4

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-669 (GBW)
v.)	
)	
NATERA, INC.,)	
)	
Defendant.)	

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-1635 (GBW)
v.)	
)	
NATERA, INC.,)	
)	
Defendant.)	

**EXHIBIT 4: PLAINTIFF LABORATORY CORPORATION OF AMERICA
HOLDINGS' STATEMENT OF ISSUES OF LAW THAT REMAIN TO BE LITIGATED**

Pursuant to Delaware Local Rule 16.3(c)(5), Plaintiff Laboratory Corporation of America Holdings (“Labcorp”) hereby submit the following statement of issues of law that remain to be litigated.

This statement is based on the current status of the case and Court’s rulings to date. Labcorp reserves the right to revise, amend, supplement, or modify the following statement based on any pretrial ruling by the Court and/or to address any additional issues, arguments, evidence, or other developments in the case, including edits to the draft pretrial order, any meet and confers or other negotiations between the parties, pending motions, and Defendant’s identification of issues of law and fact to be litigated or any new issues Defendant may raise, or for other good cause. Labcorp does not assume the burden of proof with regard to any of the below-listed issues of law. Further details regarding these issues have been explained at length in Labcorp’s pleadings and discovery responses, including in its contentions, interrogatory responses, expert reports, by experts at depositions and by fact witnesses at depositions, which Labcorp incorporates by reference. Should the Court determine that any issue identified in this list is more properly considered an issue of fact, it shall be so considered and Labcorp incorporates such issue into Labcorp’s Statement of Issues of Facts That Remain to be Litigated (Ex. 2 to Proposed Final Pretrial Order). To the extent that Labcorp’s Statement of Issues of Facts That Remain to be Litigated contains issues that the Court deems to be issues of law, those issues are incorporated herein by reference. The following statement of issues of law is not exhaustive and Labcorp reserves the right to prove any matters identified in the pleadings and discovery responses, including in its contentions, expert reports, by experts at depositions, and by fact witnesses at depositions. Labcorp intends to offer evidence as to the issues of fact and issues of law identified

in this Pretrial Order. Labcorp further intends to offer evidence to rebut evidence offered by Defendant.

I. ISSUES ON WHICH LABCORP BEARS THE BURDEN OF PROOF

A. Infringement

Direct infringement occurs when the accused infringer “without authority makes, uses, offers to sell, or sells any patented invention, within the United States or imports into the United States any patented invention during the term of the patent therefor.” 35 U.S.C. § 271(a). Infringement, whether literal or under the doctrine of equivalents, is a question of fact. *Sunovion Pharms., Inc. v. Teva Pharms. USA, Inc.*, 731 F.3d 1271, 1275 (Fed. Cir. 2013); *Hilgraeve Corp. v. Symantec Corp.*, 265 F.3d 1336, 1341 (Fed. Cir. 2001).

To prove infringement, the patentee must show by a preponderance of the evidence, *i.e.*, that it is more likely than not, that an accused product embodies or practices all limitations of the claim. *Warner-Lambert Co. v. Teva Pharms. USA, Inc.*, 418 F.3d 1326, 1341 n.15 (Fed. Cir. 2005); *Nuance Commc’ns Inc. v. Tellme Networks Inc.*, 707 F. Supp. 2d 472, 481 (D. Del. 2010). *Seal-Flex, Inc. v. Athletic Track and Court Const.*, 172 F.3d 836, 842 (Fed. Cir. 1999) “A patentee may prove infringement by any method of analysis that is probative of the fact of infringement, and circumstantial evidence may be sufficient.” *Martek BioSciences Corp. v. Nutrinova, Inc.*, 579 F.3d 1363, 1372 (Fed. Cir. 2009) (internal citations and quotations omitted); *see also Liquid Dynamics Corp. v. Vaughan Co., Inc.*, 449 F.3d 1209, 1219 (Fed. Cir. 2006) (“A patentee may prove direct infringement or inducement of infringement by either direct or circumstantial evidence.” (citation omitted)).

To prove direct infringement of a claim in a patent, a patentee must show that an accused product meets every limitation of the claim, either literally or under the doctrine of equivalents.

See Pfizer, Inc. v. Teva Pharms., USA, Inc., 429 F.3d 1364, 1376 (Fed. Cir. 2005). A two-step analysis is applied to determine infringement: first, the Court construes the asserted claims to determine their meaning and scope, and second the fact finder compares the accused product to the properly construed claims. *See Nuance Commc 'ns Inc. v. Tellme Networks Inc.*, 707 F. Supp. 2d 472, 480-481 (D. Del. 2010).

Literal infringement is shown where “the accused device contains or performs each limitation of the asserted claim.” *Moba, B.V. v. Diamond Automation, Inc.*, 325 F.3d 1306, 1313 (Fed. Cir. 2003). “The addition of unclaimed elements does not typically defeat infringement when a patent uses an open transitional phrase such as ‘comprising.’” *Free Motion Fitness, Inc. v. Cybex Int’l, Inc.*, 423 F.3d 1343, 1347 (Fed. Cir. 2005); *see also Amstar Corp. v. Envirotech Corp.*, 730 F.2d 1476, 1482 (Fed. Cir. 1984) (“An accused device cannot escape infringement by merely adding features, if it otherwise has adopted the basic features of the patent.”) (internal quotation marks omitted).

Infringement under the doctrine of equivalents may be found where an accused product performs substantially the same function in substantially the same way to obtain the same result. *See Brilliant Instruments, Inc. v. GuideTech, LLC*, 707 F.3d 1342 (Fed. Cir. 2013); *Warner-Jenkinson Co. v. Hilton Davis Chem. Co.*, 520 U.S. 17, 28 (1997). “A claim element is equivalently present in an accused device if only ‘insubstantial differences’ distinguish the missing claim element from the corresponding aspects of the accused device.” *Sage Prods Inc. v. Devon Indus.*, 126 F.3d 1420, 1423 (Fed. Cir. 1997). Whether a difference is “insubstantial” is evaluated from the perspective of the person of ordinary skill in the art and depends on the context of the patent, the prior art, and the particular circumstances of the case. *See Brilliant Instruments, Inc.*, 707 F.3d at 1347-48. “Equivalence . . . does not require complete identity for every purpose and

in every respect.” *Warner-Jenkinson Co.*, 520 U.S. at 24-25 (internal quotation marks omitted). Known interchangeability of a claim element and the proposed equivalent is a factor that can support a finding of infringement under the doctrine of equivalents. *See id.* at 36 (“The known interchangeability of substitutes for an element of a patent is one of the express objective factors ... bearing upon whether the accused device is substantially the same as the patented invention.”).

“Infringement, literal or by equivalence, is determined by comparing an accused product not with a preferred embodiment described in the specification, or with a commercialized embodiment of the patentee, but with the properly and previously construed claims in suit.” *SRI Int’l v. Matsushita Elec. Corp. of Am.*, 775 F.2d 1107, 1121 (Fed. Cir. 1985). “[I]t is error for a court to compare in its infringement analysis the accused product or process with the patentee’s commercial embodiment or other version of the product or process; the only proper comparison is with the claims of the patent.” *Zenith Labs. Inc. v. Bristol-Myers Squibb Co.*, 19 F.3d 1418, 1423 (Fed. Cir. 1994); *see also ACCO Brands, Inc. v. Micro Sec. Devices, Inc.*, 346 F.3d 1075, 1081-82 (Fed. Cir. 2003) (“The language of the claim, not the patent owner’s commercial product, is the measure of infringement.”).

Literal infringement does not require intent. *See Warner-Jenkinson Co.*, 520 U.S. at 35 (“Application of the doctrine of equivalents, therefore, is akin to determining literal infringement, and neither requires proof of intent.”); *Intel Corp. v. United States Int’l Trade Comm’n*, 946 F.2d 821, 832 (Fed. Cir. 1991) (“there is no intent element to direct infringement.”).

B. Invalidity

A defendant challenging the validity of a patent bears the burden of proving invalidity by clear and convincing evidence. *Microsoft Corp. v. i4i Ltd.*, 564 U.S. 91, 95 (2011). “A patent shall be presumed valid.” 35 U.S.C. § 282. A defendant that challenges patent validity “must

overcome that presumption to prevail on an invalidity defense,” *Microsoft Corp.*, 564 U.S. at 100 (2011), and a court may conclude that a patent is valid “solely on the failure of the patent challenger’s evidence to convincingly establish the contrary.” *Orthokinetics, Inc. v. Safety Travel Chairs, Inc.*, 806 F.2d 1565, 1570 (Fed. Cir. 1986) (emphasis in original).

1. Priority

When a party seeks the benefit of an earlier-filed United States patent application, the earlier application must meet the requirements of 35 U.S.C. § 120 and 35 U.S.C. § 112 ¶ 1, which means the earlier application must contain a written description of the subject matter and must meet the enablement requirement. *See Hyatt v. Boone*, 146 F.3d 1348, 1352 (Fed. Cir. 1998). 35 U.S.C. § 120 allows a later-filed patent application to claim the benefit of an earlier filing date in the United States if “the claims of the later-filed application [are] supported by the written description in the parent ‘in sufficient detail that one skilled in the art can clearly conclude that the inventor invented the claimed invention as of the filing date sought.’” *EnOcean GmbH v. Face Intern. Corp.*, 742 F.3d 955, 960 (Fed. Cir. 2014).

If the party challenging validity comes forward with clear and convincing evidence of invalidating prior art that puts at issue the priority date of any claim of a patent, the burden shifts to the patentee “to come forward with evidence to prove entitlement to claim priority to a filing date that predates the filing date of the patent.” *Fairchild Semiconductor Corp. v. Power Integrations*, 100 F. Supp. 3d 357, 368 (D. Del. 2015) (citing *PowerOasis, Inc. v. T-Mobile USA, Inc.*, 522 F.3d 1299, 1305-06 (Fed. Cir. 2008)). To meet this burden, the patentee must demonstrate that “the disclosure of the earlier application provides support for the claims of the later application, as required by 35 U.S.C. § 112.” *PowerOasis*, 522 F.3d at 1306 (citing *In re Chu*, 66 F.3d 292, 297 (Fed. Cir. 1995)).

A “prior application need not contain precisely the same words as are found in the asserted claims,” but “the prior application must indicate to a person skilled in the art that the inventor was ‘in possession’ of the invention as later claimed.” *Id.* (citations omitted). “[I]t is unnecessary to spell out every detail of the invention in the specification; only enough must be included to convince a person of skill in the art that the inventor possessed the invention.” *LizardTech Inc. v. Earth Resource Mapping, Inc.*, 424 F.3d 1336, 1345 (Fed. Cir. 2005); *see also Eiselstein v. Frank*, 52 F.3d 1035, 1038 (Fed. Cir. 1995) (“[T]he prior application need not describe the claimed subject matter in exactly the same terms as used in the claims; it must simply indicate to persons skilled in the art that as of the earlier date the applicant had invented what is now claimed.”).

A prior inventor’s testimony concerning conception, reduction to practice, and diligence must be reasonably corroborated by evidence, and such corroborating evidence is considered “as a whole” under a “rule of reason.” *Price v. Symsek*, 988 F.2d 1195-96 (Fed. Cir. 1993); *see also Cooper v. Goldfarb*, 154 F.3d 1321, 1331 (Fed. Cir. 1998) (“[t]he law does not impose an impossible standard of ‘independence’ on corroborative evidence by requiring that every point of a reduction to practice be corroborated by evidence having a source totally independent of the inventor; indeed, such a standard is the antithesis of the rule of reason.”) (citation omitted).

2. Personal of Ordinary Skill in the Art

The person of ordinary skill in the art is an objective legal construct presumed to think along conventional lines without undertaking to innovate, whether by systematic research or by extraordinary insights. Inventors, as a class, according to concepts underlying the Constitution and the statutes that have created the patent system, possess something—call it what you will—which sets them apart from workers of ordinary skill, and one should not go about determining obviousness under 35 U.S.C. § 103 by inquiring into what patentees ... would have known or

would likely have done, faced with the revelations of references. *See Life Technologies, Inc. v. Clontech Laboratories, Inc.*, 224 F.3d 1320 (Fed. Cir. 2000).

Factors that may be considered in determining the ordinary level of skill in the art include: 1) the types of problems encountered in the art; 2) the prior art solutions to those problems; 3) the rapidity with which innovations are made; 4) the sophistication of the technology; and 5) the educational level of active workers in the field. “Not all such factors may be present in every case, and one or more of them may predominate.” *Ruiz v. A.B. Chance Co.*, 234 F.3d 654 (Fed. Cir. 2000).

The foundation for both the obviousness and claim construction determinations is “the level of ordinary skill in the pertinent art.” *Phillips v. AWH Corp.*, 415 F.3d 1303 (Fed. Cir. 2005). A person of ordinary skill is also a person of ordinary creativity, not an automaton. *KSR Intern. Co. v. Teleflex Inc.*, 550 U.S. 398 (2007). Applications of the standard have confirmed that this standard envisions persons of relative sophistication within the field of the invention. *Helifix Ltd. v. Block-Lok, Ltd.*, 26 F. Supp. 2d 294 (D. Mass. 1998), judgment vacated on other grounds, 208 F.3d 1339 (Fed. Cir. 2000).

C. Remedies

1. Patent Damages

35 U.S.C. § 284 provides “[u]pon finding for the claimant the court shall award the claimant damages adequate to compensate for the infringement, but in no event less than a reasonable royalty for the use made of the invention by the infringer, together with interest and costs as fixed by the court.” “[T]he amount of a prevailing party’s damages is a finding of fact on which the plaintiff bears the burden of proof by a preponderance of the evidence.” *Smithkline Diagnostics, Inc. v. Helena Labs. Corp.*, 926 F.2d 1161, 1164 (Fed. Cir. 1991). The patent statute

“imposes no limitation on the types of harm resulting from infringement that the statute will redress. The section’s broad language awards damages for any injury as long as it resulted from the infringement.” *King Instruments Corp. v. Perego*, 65 F.3d 941, 947 (Fed. Cir. 1995).

A patentee need not prove its damages with absolute certainty. *See W.R. Grace & Co.-Conn. v. Intercat, Inc.*, 60 F. Supp. 2d 316, 321 (D. Del. 1999) (citing *Lam, Inc. v. Johns-Manville Corp.*, 718 F.2d 1056, 1065 (Fed. Cir. 1983)). “[I]t will be enough if the evidence show [sic] the extent of the damages as a matter of just and reasonable inference, although the result be only approximate.” *Story Parchment Co. v. Patterson Paper Co.*, 282 U.S. 555, 563 (1931). “Any doubt about the correctness [of damages] is resolved against the infringer.” *State Indus., Inc. v. Mor-Flo Indus., Inc.*, 883 F.2d 1573, 1577 (Fed. Cir. 1989).

(i) Lost Profits

“A patentee may seek to recover actual damages, usually, the amount of profits actually lost” *SmithKline Diagnostics, Inc. v. Helena Labs. Corp.*, 926 F.2d 1161, 1164 (Fed. Cir. 1991) (citations omitted). “[T]he amount of a prevailing party’s damages is a finding of fact on which the plaintiff bears the burden of proof by a preponderance of the evidence.” *Id.* “The patent owner bears the burden to present evidence sufficient to show a reasonable probability that it would have made the asserted profits absent infringement.” *King Instruments*, 65 F.3d at 952.

“[T]he statutory measure of ‘damages’ is ‘the difference between [the patent owner’s] pecuniary condition after the infringement, and what his condition would have been if the infringement had not occurred.’” *Grain Processing Corp. v. American Maize-Products Co.*, 185 F.3d 1341, 1350 (Fed. Cir. 1999). To prove lost profits, a patentee must reconstruct the market to show “likely outcomes with infringement factored out of the economic picture.” *Id.*

To recover lost profits based on lost sales, the patent owner has an initial burden to show “but for” the infringement the patent owner would have made the infringer’s sales. *Crystal Semiconductor Corp. v. Tritech Microelectronics Int’l, Inc.*, 246 F.3d 1336, 1353 (Fed. Cir. 2001). “But the patent holder does not need to negate all possibilities that a purchaser might have bought a different product or might have foregone the purchase altogether.” *State Indus., Inc. v. Mor-Flo Indus., Inc.*, 883 F.2d 1573, 1577 (Fed. Cir. 1989) (quotation and citation omitted). Once the patent owner has met its initial burden, “[t]he burden then shifts to the infringer to show that the [‘but for’ claim] is unreasonable for some or all of the lost sales.” *Rite-Hite Corp. v. Kelley Co., Inc.*, 56 F.3d 1538, 1545 (Fed. Cir. 1995). In a two-supplier market, it may be inferred that the patentee would have made the infringer’s sales or charged higher prices but for the competition. *See State Indus.*, 883 F.2d at 1573.

One recognized method by which a plaintiff may prove the amount of its lost profits is based on the *Panduit* factors: (1) demand for the patented product; (2) absence of acceptable non-infringing substitute products; (3) manufacturing and marketing capability to meet the demand; and (4) the amount of the profit that would have been earned. *See Panduit Corp. v. Stahl Bros. Fibre Works, Inc.*, 575 F.2d 1152, 1156 (6th Cir. 1978); *Versata Software, Inc. v. SAP Am., Inc.*, 717 F.3d 1255, 1265 (Fed. Cir. 2013). “A showing under Panduit permits a court to reasonably infer that the lost profits claimed were in fact caused by the infringing sales, thus establishing a patentee’s prima facie case with respect to ‘but for’ causation.” *Rite-Hite*, 56 F.3d at 1545.

With regard to the first factor:

All that the first factor states, and thus requires, is “demand for the patented product.” *Panduit*, 575 F.2d at 1156. This factor does not require any allocation of consumer demand among the various limitations recited in a patent claim. Instead, the first Panduit factor simply asks whether demand existed for the “patented product,” i.e., a product that is “covered by the patent in suit” or that “directly

competes with the infringing device.”

DePuy Spine, Inc. v. Medtronic Sofamor Danek, Inc., 567 F.3d 1314, 1330 (Fed. Cir. 2009).

Commercial success is compelling evidence of demand. *See Gyromat Corp. v. Champion Spark Plug, Co.*, 735 F.2d 549, 552 (Fed. Cir. 1984).

With regard to the second factor:

When an alleged alternative is not on the market during the accounting period, a trial court may reasonably infer that it was not available as a noninfringing substitute at that time ... The accused infringer then has the burden to overcome this inference by showing that the substitute was available during the accounting period ... Mere speculation or conclusory assertions will not suffice to overcome the inference. After all, the infringer chose to produce the infringing, rather than noninfringing, product. Thus, the trial court must proceed with caution in assessing proof of the availability of substitutes not actually sold during the period of infringement. Acceptable substitutes that the infringer proves were available during the accounting period can preclude or limit lost profits; substitutes only theoretically possible will not.

Grain Processing, 185 F.3d at 1353. “While there may be competing devices available in the marketplace, the ‘mere existence of a competing device does not make that device an acceptable substitute.’” *Kalman v. Berlyn Corp.*, 914 F.2d 1473, 1484 (Fed. Cir. 1990) (citation omitted). “It is clear that ‘[a] product lacking the advantages of [the] patented [device] can hardly be termed a substitute ‘acceptable’ to the customer who wants those advantages.’” *Id.* (citation omitted).

The patent owner may prove the third *Panduit* factor—capacity—by showing that it had the ability to meet the demand for the quantity of sales that it claims to have lost. *See Fonar Corp. v. Gen. Elec. Co.*, 107 F.3d 1543, 1553 (Fed. Cir. 1997).

The patent owner may prove the fourth *Panduit* factor—the amount of profits it lost—by reasonably quantifying the incremental profits it would have made from the sales it lost. *See Paper Converting Machine Co. v. Magna-Graphics Corp.*, 745 F.2d 11, 22 (Fed. Cir. 1984). Classic computation of lost sales to infringing products applies the patent owner’s profit margin to the

revenue the patent owner would have generated based on the number of infringing units the infringer sold. *See King Instruments Corp.*, 65 F.3d at 953. “[F]ixed costs—those costs which do not vary with increases in production, such as management salaries, property taxes, and insurance—are excluded when determining profits.” *Paper Converting*, 745 F.2d at 22 (citations omitted).

(ii) Reasonable Royalty

A plaintiff is entitled to damages equivalent to a reasonable royalty, or the amount that the defendant would have paid for a license to the asserted patents if the parties had negotiated a license at the time of first alleged infringement. *See LaserDynamics, Inc. v. Quanta Computer, Inc.*, 694 F.3d 51, 60 (Fed. Cir. 2012). “The district court must award damages in an amount no less than a reasonable royalty.” *Dow Chem. Co. v. Mee Indust., Inc.*, 341 F.3d 1370, 1381-82 (Fed. Cir. 2003) (citing 35 U.S.C. § 284).

The reasonable royalty may be based on a determination of “the royalty upon which the parties would have agreed had they successfully negotiated an agreement just before infringement began,” i.e., the “hypothetical negotiation.” *Lucent Techs., Inc. v. Gateway, Inc.*, 580 F.3d 1301, 1324 (Fed. Cir. 2009); *see also Transocean Offshore Deepwater Drilling, Inc. v. Maersk Drilling USA, Inc.*, 699 F.3d 1340, 1357 (Fed. Cir. 2012). If the record does not fully support either party’s royalty estimate, then the fact finder must determine what constitutes a reasonable royalty from the record evidence. *See Apple, Inc. v. Motorola, Inc.*, 757 F.3d 1286, 1328 (Fed. Cir. 2014).

To determine a reasonable royalty, courts may apply the fifteen factors established in *Georgia-Pacific v. U.S. Plywood Corp.*:

1. Any royalties received by the licensor for the licensing of the Asserted Patents, proving or tending to prove an established royalty.

2. The rates paid by Defendant to license other patents comparable to the Asserted Patents.
3. The nature and scope of the license, as exclusive or non-exclusive, or as restricted or non-restricted in terms of its territory or with respect to whom the manufactured product may be sold.
4. The licensor's established policy and marketing program to maintain its right to exclude others from using the patented invention by not licensing others to use the invention, or by granting licenses under special conditions designed to preserve that exclusivity.
5. The commercial relationship between the licensor and the licensee, such as whether or not they are competitors in the same territory in the same line of business.
6. The effect of selling the patented product in promoting other sales of the licensee; the existing value of the invention to the licensor as a generator of sales of its nonpatented items; and the extent of such collateral sales.
7. The duration of the Asserted Patents and the term of the license.
8. The established profitability of the product made under the Asserted Patents; its commercial success; and its popularity.
9. The utility and advantages of the patented invention over the old modes or devices, if any, that had been used for achieving similar results.
10. The nature of the patented invention; the character of the commercial embodiment of it as owned and produced by or for the licensor; and the benefits to those who have used the invention.

11. The extent to which Defendant has made use of the invention; and any evidence that shows the value of that use.
12. The portion of the profit or of the selling price that may be customary in the particular business or in comparable businesses to allow for the use of the invention or analogous inventions.
13. The portion of the profit that arises from the patented invention itself as opposed to profit arising from unpatented features, such as the manufacturing process, business risks, or significant features or improvements added by the accused infringer.
14. The opinion testimony of qualified experts.
15. The amount that a licensor and a licensee if both sides had been reasonably and voluntarily trying to reach an agreement; that is, the amount which a prudent licensee—who desired, as a business proposition, to obtain a license to manufacture and sell a particular article embodying the patented invention—would have been willing to pay as a royalty and yet be able to make a reasonable profit and which amount would have been acceptable by a patentee who was willing to grant a license.
16. Any other economic factor that a normally prudent business person would, under similar circumstances, take into consideration in negotiating the hypothetical license.

See Georgia-Pacific Corp. v. United States Plywood Corp., 318 F. Supp. 1116 (S.D.N.Y. 1970), mod. and aff'd, 446 F.2d 295 (2d Cir. 1971).

“In determining a reasonable royalty, parties frequently rely on comparable license agreements.” *Bio-Rad Lab's, Inc. v. 10X Genomics Inc.*, 967 F.3d 1353, 1372 (Fed. Cir. 2020) (citing *Georgia-Pacific Corp.*, 318 F. Supp. at 1120). “Assessing the comparability of licenses requires a consideration of whether the license at issue involves comparable technology, is

economically comparable, and arises under comparable circumstances as the hypothetical negotiation.” *Id.* at 1372-73. “Such a model begins with rates from comparable licenses and then ‘account[s] for differences in the technologies and economic circumstances of the contracting parties.’” *Commonwealth Sci. & Indus. Research Organisation v. Cisco Sys., Inc.*, 809 F.3d 1295, 1303 (Fed. Cir. 2015), cert. denied, 136 S. Ct. 2530, 195 L. Ed. 2d 859 (2016). “Where the licenses employed are sufficiently comparable, this method is typically reliable because the parties are constrained by the market’s actual valuation of the patent.” *Id.* When the comparable license approach is used, apportionment to the smallest salable patent-practicing unit is not required. *See id.*

When a patentee seeks damages on unpatented components sold with a patented apparatus, courts have applied a formulation known as the ‘entire market value rule’ to determine whether such components should be included in the damage computation, whether for reasonable royalty purposes [] or for lost profits purposes[]. ... The entire market value rule has typically been applied to include in the compensation base unpatented components of a device when the unpatented and patented components are physically part of the same machine. *See, e.g., Western Elec. Co. v. Stewart–Warner Corp.*, 631 F.2d 333, 208 USPQ 183 (4th Cir. 1980), cert. denied, 450 U.S. 971, 101 S.Ct. 1492, 67 L.Ed.2d 622 (1981). The rule has been extended to allow inclusion of physically separate unpatented components normally sold with the patented components. *See, e.g., Paper Converting*, 745 F.2d at 23, 223 USPQ at 599. However, in such cases, the unpatented and patented components together were considered to be components of a single assembly or parts of a complete machine, or they together constituted a functional unit. *See, e.g., Velo–Bind, Inc. v. Minnesota Mining & Mfg. Co.*, 647 F.2d 965, 211 USPQ 926 (9th Cir.), cert. denied, 454 U.S. 1093, 102 S.Ct. 658, 70 L.Ed.2d 631 (1981).

Rite-Hite, 56 F.3d at 154-50. The combination of the royalty base and royalty rate must reflect the value attributable to the infringing features of the product. *See Ericsson, Inc. v. D-Link Sys. Inc.*, 773 F.3d 1201, 1226 (Fed. Cir. 2014).

When a patent claims a novel combination of conventional elements, “the question is how much new value is created by the novel combination, beyond the value conferred by the

conventional elements alone.” *AstraZeneca AB v. Apotex Corp.*, 782 F.3d 1324, 1339 (Fed. Cir. 2015).

(iii) Attorneys’ Fees

“The court in exceptional cases may award reasonable attorney fees to the prevailing party.” 35 U.S.C. § 285. “An “‘exceptional’ case is “one that stands out from others with respect to the substantive strength of a party’s litigating position (considering both the governing law and the facts of the case) or the unreasonable manner in which the case was litigated.” *Octane Fitness, LLC v. ICON Health & Fitness, Inc.*, 134 S. Ct. 1749, 1756 (2014). “District courts may determine whether a case is “exceptional” in the case-by-case exercise of their discretion, considering the totality of the circumstances.” *Id.* Relevant factors for consideration include “frivolousness, motivation, objective unreasonableness (both in the factual and legal components of the case) and the need in particular circumstances to advance considerations of compensation and deterrence.” *Id.* at 1756 n.6 (quotation and citation omitted).

(iv) Prejudgment and Post-Judgment Interest

The patent statute authorizes awards of prejudgment interest. 35 U.S.C. § 284. The Supreme Court has held that “prejudgment interest should ordinarily be awarded where necessary to afford the plaintiff full compensation for the infringement.” *Gen. Motors Corp. v. Devex Corp.*, 461 U.S. 648, 654 (1983). “An award of prejudgment interest serves to make the patentee whole because the patentee also lost the use of its money due to infringement.” *Crystal Semiconductor Corp. v. TriTech Microelectronics Int’l, Inc.*, 246 F.3d 1336, 1361 (Fed. Cir. 2001).

“The rate of prejudgment interest and whether it should be compounded or un compounded are matters left largely to the discretion of the district court.... In exercising that discretion, however, the district court must be guided by the purpose of prejudgment interest, which is ‘to

ensure that the patent owner is placed in as good a position as he would have been had the infringer entered into a reasonable royalty agreement.” *Bio-Rad Labs, Inc. v. Nicolet Instrument Corp.*, 807 F.2d 964, 969 (Fed. Cir. 1986) (citations omitted). “The prime rate is by far the most common practice in the District of Delaware.” *ArcherDX, LLC v. Qiagen Sciences, LLC*, No. 18-1019 (MN), 2022 WL 4597877, at *18 (D. Del. Sep. 30, 2022) (collecting cases).

Post-judgment interest is mandated in civil cases at “a rate equal to the weekly average 1-year constant maturity Treasury yield [] for the calendar week preceding the date of the judgment.” 28 U.S.C. § 1961. Post-judgment interest on the total money award is computed daily and compounded annually. *See id.*

(v) Costs

“Federal Rule of Civil Procedure 54(d) gives courts the discretion to award costs to prevailing parties.” *Taniguchi v. Kan Pac. Saipan, Ltd.*, 132 S. Ct. 1997, 2001 (2012). “Unless a federal statute, these rules, or a court order provides otherwise, costs—other than attorney’s fees—should be allowed to the prevailing party.” Fed. R. Civ. P. 54(d)(l).

2. Permanent Injunction

Upon the request of a patentee, the Court may permanently enjoin the infringer, during the life of the patent, from continuing with the activity found to have infringed the patent. *See eBay Inc. v. MercExchange, L.L.C.*, 547 U.S. 388 (2006).

To grant a permanent injunction, a patent holder must demonstrate (1) that it has suffered an irreparable injury; (2) that remedies available at law, such as monetary damages, are inadequate to compensate for that injury; (3) that, considering the balance of hardships between the patentee and infringer, a remedy in equity is warranted; and (4) the public interest would not be disserved by a permanent injunction. *See eBay Inc.*, 547 U.S. at 391.

II. RESPONSE TO DEFENDANT’S STATEMENT OF ISSUES OF LAW ON WHICH DEFENDANTS BEAR THE BURDEN OF PROOF

A. Validity Of The Patents-In-Suit

1. Person Of Ordinary Skill In The Art

Labcorp incorporates its statement in Part I.B.2. *See supra*.

2. Presumption of Validity

A defendant challenging the validity of a patent bears the burden of proving invalidity by clear and convincing evidence. *Microsoft Corp. v. i4i Ltd.*, 564 U.S. 91, 95 (2011). “A patent shall be presumed valid.” 35 U.S.C. § 282. A defendant that challenges patent validity “must overcome that presumption to prevail on an invalidity defense,” *Microsoft Corp.*, 564 U.S. at 100 (2011), and a court may conclude that a patent is valid “solely on the failure of the patent challenger’s evidence to convincingly establish the contrary.” *Orthokinetics, Inc. v. Safety Travel Chairs, Inc.*, 806 F.2d 1565, 1570 (Fed. Cir. 1986) (emphasis in original).

3. Priority Date and Prior Art Status

Labcorp incorporates its statement in Part I.B.1. *See supra*.

Whether an alleged reference is prior art, presents a question of law based on underlying factual inquiries. *TypeRight Keyboard Corp. v. Microsoft Corp.*, 374 F.3d 1151, 1157 (Fed. Cir. 2004). The challenger to a patent's validity, as part of proving its case of invalidity, bears the burden of proving, by clear and convincing evidence, that an asserted invalidating reference qualifies as prior art. *Mahurkar v. C.R. Bard, Inc.*, 79 F.3d 1572, 1576 (Fed. Cir. 1996)

As a consequence of the statutory presumption of validity, a party that asserts the invalidity of any claim of a patent has the initial burden of production and always has the burden of persuasion of proving invalidity. 35 U.S.C.A. § 282. The accused infringer, rather than the patentee, bears the burden of showing that alleged prior art was not considered by the Patent Office.

Richdel, Inc. v. Sunspool Corp., 714 F.2d 1573, 1579, 219 U.S.P.Q. 8 (Fed. Cir. 1983). “Genum, having the ultimate burden of proving its defense of invalidity based on anticipating prior art, then has the burden of going forward with evidence that there is such anticipating prior art.” *Tech. Licensing Corp. v. Videotek, Inc.*, 545 F.3d 1316, 1327 (Fed. Cir. 2008); *see also Dynamic Drinkware, LLC v. National Graphics, Inc.*, 800 F.3d 1375, 1379. (Fed. Cir. 2015)

4. Prior art Before a Patent Examiner

Under 35 U.S.C. § 282(a), a patent and each of the claims therein are presumed to be valid. *See Microsoft Corp. v. I4I Ltd. Partnership*, 564 U.S. 91 (2011). The presumption of validity applies to all persons seeking to challenge the validity of the patent even if those persons had no involvement or right to be heard during the prosecution of the patent before the Patent Office. *See Radio Corporation of America v. Radio Engineering Laboratories*, 293 U.S. 1 (1934). The presumption of validity applies to all aspects of patent validity and exists at all stages of litigation. *Canon Computer Systems, Inc. v. Nu-Kote Intern., Inc.*, 134 F.3d 1085, 1088 (Fed. Cir. 1998) (“a patent is presumed valid, and this presumption exists at every stage of the litigation”—applying presumption to affirm preliminary injunction); *see also Hybritech Inc. v. Monoclonal Antibodies, Inc.*, 802 F.2d 1367, 1375 (Fed. Cir. 1986); *Panduit Corp. v. Dennison Mfg. Co.*, 810 F.2d 1561, 1570 (Fed. Cir. 1987). An accused infringer may not offer testimony calling into question the competence of PTO examiners absent “evidence that there actually were defects in the particular application process at issue in this case.” *Bausch & Lomb, Inc. v. Alcon Laboratories, Inc.*, 79 F. Supp. 2d 252, 255–56 (W.D. N.Y. 2000).

5. Patent Eligibility¹

The question of “whether a claim is directed to statutory subject matter is a question of law.” *Arrhythmia Research Technology, Inc. v. Corazonix Corp.*, 958 F.2d 1053, 1055, 22 U.S.P.Q.2d 1033 (Fed. Cir. 1992). Claims are patent eligible unless they are both (1) directed towards ineligible subject matter such as an abstract idea; and (2) fail to add an “inventive concept” to the ineligible subject matter to which they are directed. *See Alice Corp. Pty. v. CLS Bank Int’l*, 573 U.S. 208, 217-18 (2014).

“The concern underlying the exceptions to § 101 is not tangibility, but preemption.” *McRO, Inc. v. Bandai Namco Games America Inc.*, 837 F.3d 1299, 1314 (Fed. Cir. 2016). The Federal Circuit has “routinely held software claims patent eligible under *Alice* step one when they are directed to improvements to the functionality of a computer or network platform itself.” *Uniloc USA, Inc. v. LG Electronics USA, Inc.*, 957 F.3d 1303, 1307 (Fed. Cir. 2020). In *Enfish*, the Federal Circuit was emphatic that software inventions can be patent eligible:

Nor do we think that claims directed to software, as opposed to hardware, are inherently abstract and therefore only properly analyzed at the second step of the *Alice* analysis. Software can make non-abstract improvements to computer technology just as hardware improvements can, and sometimes the improvements can be accomplished through either route.

Enfish, LLC v. Microsoft Corp., 822 F.3d 1327, 1336 (Fed. Cir. 2016).

In *McRo*, the claims found eligible were directed to an improved software approach to computer animation. *McRo*, 837 F.3d at 1314. The Federal Circuit explained that the improvement was in the computerized rules set forth in the claims, not the mere computerization

¹ Labcorp objects to Defendant’s statement of the patentable subject matter issue as an issue that remains to be litigated at the jury trial. This issue has already been resolved by the Court, finding the claims were not directed to an abstract idea under *Alice* step one. Dkt. No. 28.

of the animation process. *Id.* (“It is the incorporation of the claimed rules, not the use of the computer, that improved the existing technological process by allowing the automation of further tasks.”) (alterations omitted). In *Enfish*, the claims found eligible were directed to a self-referential table that stores computer data. *Enfish*, 822 F.3d at 1339. The claimed software table was innovative relative to prior art tables in very specific ways that were claimed. *Id.* at 1138 (“For example, step three of the algorithm described above explains that the table stores information related to each column in rows of that very same table, such that new columns can be added by creating new rows in the table.”). The Federal Circuit explained that, given the particulars of the table, “the claims are directed to a specific implementation of a solution to a problem in the software arts.” *Id.* at 1339. In *Data Engine*, the claims found eligible were directed to a specific method for navigating through three-dimensional electronic spreadsheets. *Data Engine Techs. LLC v. Google LLC*, 906 F.3d 999, 1008 (Fed. Cir. 2018). The Federal Circuit recognized that the claim “provides a specific solution to then-existing technological problems in computers and prior art electronic spreadsheets.” *Id.* The Federal Circuit explained that the claims specifically described the steps that would improve the spreadsheet performance. *Id.* (“The claim recites specific steps detailing the method of navigating through spreadsheet pages within a three-dimensional spreadsheet environment using notebook tabs.”).

6. Anticipation

A patent claim is invalid as anticipated if “the claimed invention was patented, described in a printed publication, or in public use, on sale, or otherwise available to the public before the effective filing date of the claimed invention.” 35 U.S.C. § 102(a). A defendant must demonstrate by clear and convincing evidence that “each and every” element and limitation of the claim was previously described in a single prior art reference, either expressly or inherently. *See Allergan*,

Inc. v. Apotex Inc., 754 F.3d 952, 958 (Fed. Cir. 2014). See also *Merck & Co., Inc. v. Teva Pharmaceuticals USA, Inc.*, 347 F.3d 1367, 1372 (Fed. Cir. 2003) (“An ‘anticipating’ reference must describe all of the elements and limitations of the claim in a single reference, and enable one of skill in the field of the invention to make and use the claimed invention.”); *Kyocera Wireless Corp. v. International Trade Com’n*, 545 F.3d 1340, 1351 (Fed. Cir. 2008); *Dewey & Almy Chem. Co v. Mimex Co*, 124 F.2d 986, 989 (2d Cir. 1942). Showing that a “prior art reference discloses part of the claimed invention, which an ordinary artisan might supplement to make the whole, or that it includes multiple, distinct teachings that the artisan might somehow combine to achieve the claimed invention” is not enough for anticipation. *Net MoneyIN, Inc. v. VeriSign, Inc.*, 545 F.3d 1359, 1371 (Fed. Cir. 2008).

In order to constitute an invalidating prior-art reference, a printed publication “must sufficiently describe the claimed invention to have placed the public in possession of it.” *In re Donohue*, 766 F.2d 531, 533 (Fed. Cir. 1985). In particular, the proper test for whether the public is in possession is “whether one skilled in the art to which the invention pertains could take the description of the invention in the printed publication and combine it with his own knowledge of the particular art and from this combination be put in possession of the invention on which a patent is sought. In particular, one must be able to make the claimed invention without undue experimentation.” *In re Elsner*, 381 F.3d 1125, 1128 (Fed. Cir. 2004). Showing that a “prior art reference discloses part of the claimed invention, which an ordinary artisan might supplement to make the whole, or that it includes multiple, distinct teachings that the artisan might somehow combine to achieve the claimed invention” is not enough for anticipation. *Net MoneyIN, Inc. v. VeriSign, Inc.*, 545 F.3d 1359, 1371 (Fed. Cir. 2008).

Further, the anticipating reference must be enabling. *Sanofi-Synthelabo*, 550 F.3d at 1082. “[I]nvalidity by anticipation requires that the four corners of a single, prior art document describe every element of the claimed invention, either expressly or inherently, such that a person of ordinary skill in the art could practice the invention without undue experimentation.” *Advanced Display Sys. Inc. v. Kent State Univ.*, 212 F.3d 1272, 1282 (Fed. Cir. 2000). In trying to show anticipation, “one skilled in the art cannot supply missing elements through his or her knowledge.” *Forest Labs., Inc. v. Ivax Pharms., Inc.*, 438 F. Supp. 2d 479, 485 (D. Del. 2006), *aff’d*, 501 F.3d 1263 (Fed. Cir. 2007). For anticipation, “[t]here must be no difference between the claimed invention and the reference disclosure, as viewed by a person of ordinary skill in the field of the invention.” *Scripps Clinic & Research Found. v. Genentech, Inc.*, 927 F.2d 1565, 1576 (Fed. Cir. 1991), *overruled in part for other reasons by Abbott Labs. v. Sandoz, Inc.*, 566 F.3d 1282 (Fed. Cir. 2009). A prior-art reference that does not disclose a limitation may inherently anticipate the limitation when the reference must “include the unstated limitation.” *Transclean Corp. v. Bridgewood Servs., Inc.*, 290 F.3d 1364, 1373 (Fed. Cir. 2002). For a reference to be inherently anticipatory, the missing element *must necessarily be present*, not merely “probably or possibly present.” *Trintec Indus. Inc. v. Top-U.S.A. Corp.*, 295 F.3d 1292 (Fed. Cir. 2002) (citing *In re Robertson*, 169 F.3d 743, 745 (Fed. Cir. 1999)). Inherent anticipation cannot “be established by probabilities or possibilities. The mere fact that a certain thing may result from a given set of circumstances is not sufficient.” *Cont’l Can Co. USA v. Monsanto Co.*, 948 F.2d 1264, 1268-69 (Fed. Cir. 1991) (internal quotation marks omitted).

Public policy prohibits the use of non-public works as prior art to defeat a patent claim. *W.L. Gore & Associates, Inc. v. Garlock, Inc.*, 721 F.2d 1540, 1550, (Fed. Cir. 1983) (holding that secret use is not prior art under 35 U.S.C.A. § 102(a),(b)—“There is no reason or statutory basis,

however, on which Budd's and Cropper's secret commercialization of a process, if established, could be held a bar to the grant of a patent to Gore on that process. ... The district court therefore erred as a matter of law in applying the statute and in its determination that Budd's secret use of the Cropper machine and sale of tape rendered all process claims of the '566 patent invalid under § 102(b).") *International Glass Co. v. U. S.*, 408 F.2d 395, 402 (1969) (prior invention of a process did not invalidate a patent on the same process under § 102(g) because the prior inventors did nothing to make the invention known to the public).

7. Non-Obviousness

Obviousness is a matter of law and depends on the following factual inquiries: (1) the scope and content of the prior art; (2) the differences between the claims and the prior art; (3) the level of ordinary skill in the relevant art; and (4) any objective indicia of nonobviousness. *KSR Int'l Co. v. Teleflex Inc.*, 550 U.S. 398, 406 (2007) (citing *Graham v. John Deere Co.*, 383 U.S. 1, 17 (1966)). 35 U.S.C. § 103 provides the following:

A patent for a claimed invention may not be obtained, notwithstanding that the claimed invention is not identically disclosed as set forth in section 102, if the differences between the claimed invention and the prior art are such that the claimed invention as a whole would have been obvious before the effective filing date of the claimed invention to a person having ordinary skill in the art to which the claimed invention pertains. Patentability shall not be negated by the manner in which the invention was made.

35 U.S.C. § 103. A party seeking to invalidate a patent based on obviousness must demonstrate "by clear and convincing evidence that a skilled artisan would have been motivated to combine the teachings of the prior art references to achieve the claimed invention, and that the skilled artisan would have had a reasonable expectation of success in doing so." *Pfizer, Inc. v. Apotex, Inc.*, 480 F.3d 1348, 1361 (Fed. Cir. 2007); see also *In re Cyclobenzaprine Hydrochloride Extended-Release*

Capsule Patent Litig., 676 F.3d 1063, 1068-69 (Fed. Cir. 2012). In analyzing obviousness, “a patent composed of several elements is not proved obvious merely by demonstrating that each of its elements was, independently, known in the prior art.” *KSR Inter. Co.*, 550 U.S. at 418.

Both the suggestion and the reasonable expectation of success “must be founded in the prior art, not in the applicant’s disclosure.” *Noelle v. Lederman*, 355 F.3d 1343, 1352 (Fed. Cir. 2004). “Obviousness requires more than a mere showing that the prior art includes separate references covering each separate limitation in a claim under examination,” *Unigene Labs., Inc. v. Apotex, Inc.*, 655 F.3d 1352, 1360 (Fed. Cir. 2011), and “[a] solution is not obvious simply because it was obvious to conduct experiments to try to solve the problem.” *Vanda Pharms. Inc. v. Roxane Labs., Inc.*, 203 F. Supp. 3d 412, 427 (D. Del. 2016), *aff’d*, 887 F.3d 1117 (Fed. Cir. 2018); *see also Abbott Labs.*, 334 F.3d at 1357.

To avoid “distortion caused by hindsight bias,” there must be “a reason that would have prompted a person of ordinary skill in the relevant field to combine the elements in the way the claimed new invention does.” *KSR Inter. Co.*, 550 U.S. at 418, 421; *see also id.* at 421 (“A factfinder should be aware, of course, of the distortion caused by hindsight bias and must be cautious of arguments reliant upon ex post reasoning.”); *Novartis Pharms. Corp. v. Par Pharm., Inc.*, 48 F. Supp. 3d 733, 752 (D. Del. 2014) (a party seeking to invalidate a patent claim “must show that a PHOSITA would be motivated to combine the claimed combinations with a reasonable expectation of success.”).

8. Secondary Considerations of Non-Obviousness

An obviousness determination requires consideration of the objective indicia of nonobviousness (or “secondary considerations”) such as licensing, praise, unexpected results, commercial success, copying, skepticism, failure of others, and long-felt but unresolved need.

KSR, 550 U.S. at 406; *Apple Inc. v. Samsung Elecs. Co., Ltd.*, 839 F.3d 1034, 1048 (Fed. Cir. 2016) (*en banc*) (“Objective indicia of nonobviousness must be considered in every case where present.”). There must also be a nexus between the objective indicia and the claimed invention. *Demaco Corp. v. F. Von Langsdorff Licensing Ltd.*, 851 F.2d 1387, 1392 (Fed. Cir. 1988).

9. Written Description

Pursuant to 35 U.S.C. § 112(a), “[t]he specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art . . . to make and use the same.” To overcome the presumed validity of a patent, a defendant challenging whether a patent meets the written description requirement of 35 U.S.C. § 112(a) “must show that the claims lack a written description by clear and convincing evidence.” *Hynix Semiconductor Inc. v. Rambus Inc.*, 645 F.3d 1336, 1351 (Fed. Cir. 2011).

Pursuant to Section 112(a) of the Patent Act, “[t]he specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art . . . to make and use the same.” 35 U.S.C. § 112(a). To overcome the presumed validity of a patent, a defendant challenging whether a patent meets the written description requirement of 35 U.S.C. § 112(a) “must show that the claims lack a written description by clear and convincing evidence.” *Hynix Semiconductor Inc. v. Rambus Inc.*, 645 F.3d 1336, 1351 (Fed. Cir. 2011). The inventor is not required to satisfy this requirement by “any particular form of disclosure.” *Ariad Pharms., Inc. v. Eli Lilly & Co.*, 598 F.3d 1336, 1352 (Fed. Cir. 2010) (*en banc*). The level of disclosure that is required is subject to a variety of considerations “such as the existing knowledge in a particular field, the extent and content of the prior art, the maturity of the science or technology, the

predictability of the aspect at issue, and other considerations appropriate to the subject matter.”
Capon v. Eshhar, 418 F.3d 1349, 1359 (Fed. Cir. 2005).

10. Definiteness²

Section 112(b) of the Patent Act requires claims to “particularly point[] out and distinctly claim[] the subject matter which the inventor or a joint inventor regards as the invention.” 35 U.S.C. § 112(b). A determination of claim definiteness is a question of law. *Personalized Media Commc’ns, LLC v. Int’l Trade Comm’n*, 161 F.3d 696, 705 (Fed. Cir. 1998). A defendant challenging a patent’s validity has the burden to prove the indefiniteness requirement by clear and convincing evidence. *BSAF Corp. v. Johnson Matthey Inc.*, 875 F.3d 1360, 1365 (Fed. Cir. 2017).

Indefiniteness of a claim is evaluated from the perspective of a person skilled in the relevant art. *See Nautilus, Inc. v. BioSig Instruments, Inc.*, 572 U.S. 898, 908 (2014). Moreover, the claim is evaluated in light of the patent’s specification and prosecution history, and measured as of the time of the patent application. *Id.* Thus, reference to publications or patents in the specification are part of that disclosure, and are included in the inquiry of whether a claim, read in light of the specification and prosecution history, informs “with reasonable certainty” those skilled in the art about the scope of the invention, even if such references are not incorporated by reference. *Atmel Corp. v. Information Storage Devices, Inc.*, 198 F.3d 1374 1383 (Fed. Cir. 1999) (stating that “the district court erred by failing to consider the knowledge of one skilled in the art that indicated, based on unrefuted testimony, that the specification disclosed sufficient structure corresponding

² Labcorp objects to Defendant’s statement of the definiteness issue as a contested fact that remains to be litigated at the jury trial. “A determination of claim definiteness is a question of law.” *Personalized Media Commc’ns, LLC v. Int’l Trade Comm’n*, 161 F.3d 696, 705 (Fed. Cir. 1998). *See also Atmel Corp. v. Info. Storage Devices, Inc.*, 198 F.3d 1374, 1378 (Fed. Cir. 1999) (“Indefiniteness, therefore, like claim construction, is a question of law that we review de novo.”); *Nature Simulation Sys. Inc. v. Autodesk, Inc.*, 50 F.4th 1358, 1360 (Fed. Cir. 2022).

to the high-voltage means limitation” by citing, but not describing, a technical article); *see also Eli Lilly & Co. v. Teva Parenteral Medicines Inc.*, 845 F.3d 1357, 1370-72 (Fed. Cir. 2017) (holding the claim term “vitamin B12” as not indefinite when a person of ordinary skill in the art would understand the claim term in the context of the claim language, specification, and prosecution history).

“The claims as granted are accompanied by a presumption of validity based on compliance with, *inter alia*, § 112 ¶ 2.” *S3 Inc. v. Nvidia Corp.*, 259 F.3d 1364, 1367 (Fed. Cir. 2001). A patent claim is not indefinite if “viewed in light of the specification and prosecution history,” the claim “inform[s] those skilled in the art about the scope of the invention with reasonable certainty.” *Nautilus*, 572 U.S. at 910. The definiteness requirement is analyzed “not in a vacuum, but always in light of the teachings of the prior art and of the particular application disclosure as it would be interpreted by one possessing the ordinary level of skill in the pertinent art.” *Energizer Holdings v. ITC*, 435 F.3d 1366, 1370 (Fed. Cir. 2006). The definiteness requirement “ensure[s] that patent claims are written in such a way that they give notice to the public of what is claimed, thus enabling [others] to determine whether they infringe.” *Bayer Pharma AG v. Watson Labs., Inc.*, No. 12-1726-LPS, 2014 WL 4954617, at *3 (D. Del. Sept. 30, 2014).

A patent is “invalid for indefiniteness if its claims, read in light of the specification delineating the patent, and the prosecution history, fail to inform, with reasonable certainty, those skilled in the art about the scope of the invention.” *Nautilus, Inc. v. BioSig Instruments, Inc.*, 572 U.S. 898, 901, 909-10 (2014) (also noting that “the definiteness requirement must take into account the inherent limitations of language” as “absolute precision is unattainable.”).

11. Enablement

Enablement requires that the specification of a patent teach a person skilled in the art how to make and use the claimed invention without undue experimentation. 35 U.S.C. § 112; *In re Wands*, 858 F.2d 731, 736-37 (Fed. Cir. 1988). The Federal Circuit has set forth eight factors that can be considered in the analysis of whether a patent is properly enabled: (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims. *In re Wands*, at 737. These factors are “illustrative, not mandatory.” *Amgen, Inc. v. Chugai Pharmaceutical Co., Ltd.*, 927 F.2d 1200, 1213 (Fed. Cir. 1991). Further, “[t]he fact that some experimentation is necessary does not preclude enablement; what is required is that the amount of experimentation must not be unduly extensive.” *PPG Industries, Inc. v. Guardian Industries Corp.*, 75 F.3d 1558, 1564 (Fed. Cir. 1996) (internal quotations and citations omitted). The consideration of whether experimentation is undue “is not merely quantitative, since a considerable amount of experimentation is permissible, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed.” *Id.*; *see also Cephalon, Inc. v. Watson Pharms., Inc.*, 707 F.3d 1330, 1338-39 (Fed. Cir. 2013) (“extensive experimentation does not necessarily render the experiments unduly extensive where the experiments involve repetition of known or commonly used techniques.”). The patentee is also not required to “describe how to make and use every possible variant of the claimed invention.” *AK Steel Corp. v. Sollac & Ugine*, 344 F.3d 1234 (Fed. Cir. 2003).

B. Attorney's Fees And Costs³

Labcorp incorporates its statement in Parts I.C.1.iii & v. *See supra*.

³ Defendant bears the burden of proving it is entitled to any alleged remedies, including whether it is entitled to costs and attorneys' fees under 35 U.S.C. § 285. Labcorp, to the extent necessary, will introduce evidence to rebut Defendant's assertion that it are entitled to any remedies, including whether it is entitled to costs and attorneys' fees under 35 U.S.C. § 285.

EXHIBIT 5

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

**EXHIBIT 5: DEFENDANT'S STATEMENT OF ISSUES OF LAW
THAT REMAIN TO BE LITIGATED**

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Natera respectfully submits the following issues of law that remain to be litigated. This statement is based on Natera's claims, counterclaims, and defenses, Natera's current understanding of Plaintiff's claims and defenses, and the proceedings in this action to date. Should the Court determine that any issue identified in this list is more properly considered an issue of fact, it shall be so considered and Natera incorporates such issue into Natera's Statement of Issues of Fact That Remain to Be Litigated (Ex. 3 to Proposed Final Pretrial Order). To the extent that Natera's Statement of Issues of Fact That Remain to be Litigated contains issues that the Court deems to be issues of law, those issues are incorporated herein by reference. Natera reserves the right to revise, modify, supplement, or change the issues of law to be litigated in response to subsequent Court rulings and/or Labcorp's revised identification of issues of law and fact to be litigated or any new issues Labcorp may raise, or for other good cause. The following statement of issues of law is not exhaustive, and Natera reserves the right to prove any matters identified in the pleadings, and discovery responses, including in its contentions, interrogatory responses, expert reports, by experts at depositions, and by fact witnesses at depositions. Natera further intends to offer evidence to rebut evidence offered by Labcorp. By identifying the following issues, Natera does not necessarily concede that each of these issues, in whole or in part, is a pure issue of law. Further, insofar as the following issues, as a matter of law and precedent, themselves turn on additional or subsidiary legal issues or elements, those legal issues or elements are incorporated.

I. INVALIDITY OF THE ASSERTED PATENTS

Natera provides the below issues to be litigated and legal authorities.

A. Issues of Law to Be Litigated

1. Whether Natera has proven by clear and convincing evidence that claims 1–13 and 15–16 of the '799 Patent, claims 1–13 and 15–18 of the '863 Patent, and claims 1, 4–9, 12, and 15–27 of the '308 Patent are invalid under 35 U.S.C. §§ 101, 102, 103, and/or 112.

2. Whether Natera has proven by clear and convincing evidence that the asserted prior art qualifies as prior art under 35 U.S.C. § 102.

B. Person of Ordinary Skill in the Art

3. “The ‘person of ordinary skill in the art’ is a theoretical construct.” *eSpeed, Inc. v. Brokertec USA, L.L.C.*, 404 F. Supp. 2d 575, 579 (D. Del. 2005) (quoting *Endress + Hauser, Inc. v. Hawk Measurement Sys. Pty. Ltd.*, 122 F.3d 1040, 1042 (Fed. Cir. 1997)). “Factors that may be considered in determining the ordinary level of skill in the art include: 1) the types of problems encountered in the art; 2) the prior art solutions to those problems; 3) the rapidity with which innovations are made; 4) the sophistication of the technology; and 5) the educational level of active workers in the field. ‘Not all such factors may be present in every case, and one or more of them may predominate.’” *Ruiz v. A.B. Chance Co.*, 234 F.3d 654, 666–67 (Fed. Cir. 2000) (quoting *Custom Accessories, Inc. v. Jeffrey–Allan Indus., Inc.*, 807 F.2d 955, 962 (Fed. Cir. 1986)). The hypothetical person of ordinary skill in the art is presumed to know all of the teachings of the prior art references in the field of the invention at the time the invention was made. *See Union Carbide Corp. v. Am. Can Co.*, 724 F.2d 1567, 1576 (Fed. Cir. 1984).

C. Presumption of Validity

4. Patents are presumed to be valid. 35 U.S.C. § 282. “The presumption is, like all presumptions in law, a starting place and a procedural device assigning the burden of proof. To treat the presumption as irrebuttable would be to oust the courts of their jurisdiction to consider a challenge to the validity of patents before them.” *Chore-Time Equip., Inc. v. Cumberland Corp.*, 713 F.2d 774, 780 (Fed. Cir. 1983). A challenger must prove by clear and convincing evidence that a patent is invalid. *Microsoft Corp. v. I4I Ltd. P’ship*, 564 U.S. 91, 111 (2011).

D. Priority Date

5. Labcorp “bears the burden of establishing that its claimed invention is entitled to an earlier priority date than an asserted prior art reference.” *In re Magnum Oil Tools Int’l, Ltd.*, 829 F.3d 1364, 1376 (Fed. Cir. 2016). “To obtain the benefit of the filing date of a parent application, the claims of the later-filed application must be supported by the written description in the parent ‘in sufficient detail that one skilled in the art can clearly conclude that the inventor invented the claimed invention as of the filing date sought.’” *Anascope, Ltd. v. Nintendo of Am., Inc.*, 601 F.3d 1333, 1335 (Fed. Cir. 2010) (quoting *Lockwood v. Am. Airlines, Inc.*, 107 F.3d 1565, 1572 (Fed. Cir. 1997)).

6. To claim a priority date earlier than the effective filing date of a patent application, the patentee must establish conception and “reduction to practice prior to the effective date of the reference, or conception of the invention prior to the effective date of the reference coupled with due diligence from prior to said date to a subsequent reduction to practice or to the filing of the application.” *In re Steed*, 802 F.3d 1311, 1316 (Fed. Cir. 2015) (internal quotations and citations omitted). Labcorp bears the burden of proving that any patent claim is entitled to a priority date earlier than its effective filing date. *See PowerOasis, Inc. v. T-Mobile USA, Inc.*, 522 F.3d 1299, 1305–06 (Fed. Cir. 2008).

7. Conception requires “formation in the mind of the inventor of a definite and permanent idea of the complete and operative invention, as it is hereafter to be applied in practice.” *Burroughs Wellcome Co. v. Barr Lab’ys., Inc.*, 40 F.3d 1223, 1228 (Fed. Cir. 1994). To establish conception, a party must show possession of every feature recited in the claim, and that every limitation of the claim was known to the inventor at the time of the alleged conception. *See Coleman v. Dines*, 754 F.2d 353, 359 (Fed. Cir. 1985). Conception may not be complete if those skilled in the art express uncertainty that “undermines the specificity of the inventor’s idea that it

is not yet a definite and permanent reflection of the complete invention as it will be used in practice.” *Burroughs Wellcome Co.*, 40 F.3d at 1229.

8. A party seeking to prove its entitlement to an earlier priority date, where it claims it is “first to conceive but second to reduce to practice,” must also “demonstrate reasonable diligence toward reduction to practice.” *Mahurkar v. C.R. Bard, Inc.*, 79 F.3d 1572, 1578 (Fed. Cir. 1996). To establish actual reduction to practice, the party asserting an earlier priority date “must satisfy a two-prong test: (1) the party constructed an embodiment or performed a process that met every element of the [claim], and (2) the embodiment or process operated for its intended purpose.” *Eaton v. Evans*, 204 F.3d 1094, 1097 (Fed. Cir. 2000). Actual reduction to practice requires that “the constructed embodiment or performed process include the precise elements recited” in the claims. *See id.* Thus, “there can be no actual reduction to practice if the constructed embodiment or performed process lacks an element recited in the [claims] or uses an equivalent of that element.” *Id.* Moreover, there must be “some recognition of successful testing prior to the critical date for an invention to be reduced to practice.” *Estee Lauder Inc. v. L’Oreal, S.A.*, 129 F.3d 588, 593 (Fed. Cir. 1997).

E. Prior Art Before a Patent Examiner

9. “A court is not bound by the PTO’s actions and must make its own independent determination of patent validity.” *Medrad, Inc. v. MRI Devices Corp.*, 401 F.3d 1313, 1322 (Fed. Cir. 2005); *see Gardner v. TEC Sys., Inc.*, 725 F.2d 1338, 1345 (Fed. Cir. 1984); *see also Athletic Alternatives, Inc. v. Benetton Trading USA, Inc.*, 174 F. App’x 571, 574 (Fed. Cir. 2006) (holding that a court has a right to consider prior art that was before an examiner).

F. Patent Eligibility

10. Patent eligibility under 35 U.S.C. § 101 is “ultimately an issue of law” that “may contain underlying issues of fact.” *Berkheimer v. HP Inc.*, 881 F.3d 1360, 1365 (Fed. Cir. 2018),

cert. denied, 140 S. Ct. 911 (2020). Patent eligibility is governed by the two-step analysis in *Alice Corp. Pty. v. CLS Bank Int'l*, 573 U.S. 208, 217–18 (2014). Step one of the *Alice* inquiry asks whether the patent claims are directed to ineligible subject matter, *e.g.*, an abstract idea. *See Berkheimer*, 881 F.3d at 1366. If the claims are directed to an abstract idea, then at step two the Court determines whether the claims include an “inventive concept sufficient to transform the abstract idea into a patent-eligible application.” *Id.* at 1369. The Court “consider[s] the elements of each claim both individually and ‘as an ordered combination’ to determine whether the additional elements ‘transform the nature of the claim’ into a patent-eligible application.” *Alice*, 573 U.S. at 217 (quoting *Mayo Collaborative Servs. v. Prometheus Labs., Inc.*, 566 U.S. 66, 78–79 (2012)). Where the “additional features” recite nothing more than “well-understood, routine, conventional activity,” the claim is ineligible for patenting. *Intellectual Ventures I LLC v. Erie Indemnity Co.*, 850 F.3d 1315, 1328 (Fed. Cir. 2017); *see, e.g., Digitech Image Techs., LLC v. Elecs. For Imaging, Inc.*, 758 F.3d 1344, 1351 (Fed. Cir. 2014) (claim reciting “taking two data sets and combining them into a single data set” was directed to an abstract idea because the data sets were drawn from “existing information” and simply organized “into a new form”); *see also RecogniCorp, LLC v. Nintendo Co.*, 855 F.3d 1322, 1327 (Fed. Cir. 2017) (claims that recited “a process that started with data, added an algorithm, and ended with a new form of data” were directed to an abstract idea); *Berkheimer*, 881 F.3d at 1366 (claims “directed to the abstract idea of parsing, comparing, storing, and editing data”); *Elec. Power Group, LLC v. Alstom S.A.*, 830 F.3d 1350, 1353 (Fed. Cir. 2016) (claims focused on “collecting information, analyzing it, and displaying certain results of the collection and analysis” directed to an abstract idea). It is not enough “to merely improve a fundamental practice or abstract process by invoking a computer merely as a tool.” *Customedia Techs., LLC v. Dish Network Corp.*, 951 F.3d 1359, 1364 (Fed.

Cir. 2020) (citing *Affinity Labs. of Texas, LLC v. DIRECTV, LLC*, 838 F.3d 1253, 1258 (Fed. Cir. 2016)). Claims are ineligible where they are “merely implemented ‘using some unspecified, generic computer’ and [do] not ‘purport to improve the functioning of the computer itself.’” *Customedia*, 951 F.3d at 1362 (quoting *Alice*, 573 U.S. at 225–26); see, e.g., *Univ. of Fla. Rsch. Found., Inc. v. Gen. Elec. Co.*, 916 F.3d 1363, 1367 (Fed. Cir. 2019) (rejecting “do it on a computer” patents that merely sought “to automate ‘pen and paper methodologies’ to conserve human resources and minimize errors”); accord, e.g., *In re Stanford*, 991 F.3d 1245, 1250–51 (Fed. Cir. 2021) (claims were abstract because focused on “the use of mathematical calculations and statistical modeling” to manipulate genetic data and were not drawn to any “practical, technological improvements extending beyond improving the accuracy of a mathematically calculated statistical prediction”); *Accenture Glob. Servs., GmbH v. Guidewire Software, Inc.*, 728 F.3d 1336, 1339, 1342 (Fed. Cir. 2013); *Intell. Ventures I LLC v. Symantec Corp.*, 838 F.3d 1307, 1318–19 (Fed. Cir. 2016) (holding the mere application of a generic computer is not a technological improvement); *In-Depth Test, LLC v. Maxim Integrated Prods., Inc.*, C.A. Nos. 14-887-CFC, 114-888-CFC, 2018 WL 6617142, at *4 (D. Del. Dec. 18, 2018) (citing *Enfish, LLC v. Microsoft Corp.*, 822 F.3d 1327, 1334 (Fed. Cir. 2016)).

G. Anticipation

11. “Anticipation is an issue of fact.” *In re Schreiber*, 128 F.3d 1473, 1477 (Fed. Cir. 1997). Under pre-AIA 35 U.S.C. § 102(a), a patent claim is invalid if it is not novel, including if “the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for patent.” Under 35 U.S.C. § 102(b), a patent claim is invalid if “the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of the application for patent in the United States.” Under 35 U.S.C.

§ 102(e)(2), a patent claim is invalid as anticipated if the invention was described in “a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent.” A patent claim is anticipated under 35 U.S.C. § 102(g)(2) where, before the applicant’s invention thereof, “the invention was made in this country by another inventor who had not abandoned, suppressed, or concealed it.”

12. A patent claim is anticipated if “a single prior art reference discloses, either expressly or inherently, each limitation of the claim.” *In re Cruciferous Sprout Litig.*, 301 F.3d 1343, 1349 (Fed. Cir. 2002); *see, e.g., Billups-Rothenberg, Inc. v. Assoc. Reg’l & Univ. Pathologists, Inc.*, 642 F.3d 1031, 1038 (Fed. Cir. 2011) (“A patent claim is anticipated if each and every limitation is found either expressly or inherently in a single prior art reference.”); *Schering Corp. v. Geneva Pharms.*, 339 F.3d 1373, 1379 (Fed. Cir. 2003) (“[A] prior art reference which expressly or inherently contains each and every limitation of the claimed subject matter anticipates and invalidates.”). A patent claim may therefore be anticipated even if a prior-art reference does not expressly point out each limitation of the claim. *Id.* Such inherent disclosure does not need to be recognized by a person of ordinary skill in the art if practice of the prior art inevitably produces the claimed feature. *In re Omeprazole Patent Litig.*, 483 F.3d 1364, 1373 (Fed. Cir. 2007); *Abbott Labs. v. Baxter Pharm. Prods. Inc.*, 471 F.3d 1363, 1368 (Fed. Cir. 2006) (“Inherent anticipation does not require that a person of ordinary skill in the art at the time would have recognized the inherent disclosure.”) (citation omitted).

13. “Anticipation is a question of fact that considers whether a single reference describes the claimed invention ‘with sufficient precision and detail to establish that the subject matter existed in the prior art.’” *In re ThermoLife Int’l LLC*, 796 F. App’x 726, 730 (Fed. Cir. 2020) (quoting *Verve, LLC v. Crane Cams, Inc.*, 311 F.3d 1116, 1120 (Fed. Cir. 2002)). “[A]

reference can anticipate a claim even if it ‘d[oes] not expressly spell out’ all the limitations arranged or combined as in the claim, if a person of skill in the art, reading the reference, would ‘at once envisage’ the claimed arrangement or combination.” *Blue Calypso, LLC v. Groupon, Inc.*, 815 F.3d 1331, 1341 (Fed. Cir. 2016) (quoting *In re Petering*, 301 F.2d. 676, 681 (C.C.P.A. 1962)).

14. “As long as the reference discloses all of the claim limitations and enables the ‘subject matter that falls within the scope of the claims at issue,’ the reference anticipates—no ‘actual creation or reduction to practice’ is required.” *In re Gleave*, 560 F.3d 1331, 1334 (Fed. Cir. 2009) (quoting *Schering*, 339 F.3d at 1380–81). “This is so despite the fact that the description provided in the anticipating reference might not otherwise entitle its author to a patent.” *Id.*; see also *Duke Univ. v. BioMarin Pharm. Inc.*, 685 F. App’x 967, 973 (Fed. Cir. 2017) (“An anticipatory reference must be enabled, but no actual creation or reduction to practice is required.”) (quotations omitted). A “prior art reference need not demonstrate utility in order to serve as an anticipating reference under section 102.” *Rasmusson v. SmithKline Beecham Corp.*, 413 F.3d 1318, 1326 (Fed. Cir. 2005).

15. Patent claims may be anticipated by prior art products or systems that are capable of performing the functions or methods covered by a patent claim, or publications describing the same. See, e.g., *In re Hallman*, 655 F.2d 212, 215 (C.C.P.A. 1981); see, e.g., *Lockwood*, 107 F.3d at 1570 (holding software was prior art under pre-AIA Sections 102(a) and (b)); *Alexsam, Inc. v. Gap, Inc.*, 621 F. App’x 983, 988–89 (Fed. Cir. 2015) (reversing JMOL of no anticipation under pre-AIA Section 102(g) based on “electronic gift card system” prior art). Patent claims may also be anticipated by prior art products or systems that would infringe if they did not pre-date the priority date of the patent, because “[t]hat which infringes if later anticipates if earlier.” *Brown v. 3M*, 265 F.3d 1349, 1352 (Fed. Cir. 2001). It is well settled that multiple pieces of evidence may

be relied upon to prove that a single prior-art product or system anticipates under 35 U.S.C. §§ 102(a) and (g). *See IOENGINE, LLC v. PayPal Holdings, Inc.*, 607 F. Supp. 3d 464, 518–19 (D. Del. 2022) (“[I]t is permissible for a defendant to establish anticipation by using several documents that reveal how a single prior art system works.”); *see also Finjan, Inc. v. Symantec Corp.*, C.A. No. 10-593-GMS, 2013 WL 5302560, at *17 (D. Del. Sept. 19, 2013), *aff’d*, 577 F. App’x 999 (Fed. Cir. 2014) (rejecting challenge that defendant relied on “distinct pieces of prior art that cannot be characterized as a single product” because they were used “simply to demonstrate and support how [the prior-art product] functioned at the time, not as distinct references”).

16. A patent claim may also be invalid under § 102 in view of prior public knowledge or use of the relevant patented features. *See UCB, Inc. v. Watson Labs., Inc.*, 927 F.3d 1272, 1289–91 (Fed. Cir. 2019); *see also, e.g., Novo Nordisk Pharm., Inc. v. Bio-Tech. Gen. Corp.*, 424 F.3d 1347, 1355–56 (Fed. Cir. 2005) (affirming finding of anticipation under § 102(a) based on enabling disclosure in prior printed publication); *BroadSoft, Inc. v. CallWave Commc’ns, LLC*, 282 F. Supp. 3d 771, 790–91 (D. Del. 2017) (holding prior art software system anticipated patents because relevant features were publicly known and on sale before critical date); *UCB, Inc. v. Actavis Labs., UT, Inc.*, C.A. No. 19-474-KAJ, 2021 U.S. Dist. LEXIS 90952, at *62–63 (D. Del. Mar. 26, 2021); *Gillette Co. LLC v. Dollar Shave Club, Inc.*, C.A. No. 15-1158-LPS-CJB, 2019 U.S. Dist. LEXIS 46865, at *6–7 (D. Del. Mar. 21, 2019). “Prior knowledge and use by a single person is sufficient” to defeat patentability under Section 102(a). *UCB*, 927 F.3d at 1289 (quoting *Coffin v. Ogden*, 85 U.S. 120, 124 (1873)). “[T]he ‘known or used’ prong of [pre-AIA] Section 102(a) [] mean[s] ‘knowledge or use which is accessible to the public.’” *BASF Corp. v. SNF Holding Co.*, 955 F.3d 958, 964 (Fed. Cir. 2020) (quoting *Carella v. Starlight Archery & Pro Line Co.*, 804 F.2d 135, 139 (Fed. Cir. 1986)); *see also* MPEP § 2132 at I.A. Actual public use or knowledge is not required,

and the invention need only be “publicly accessible,” *i.e.*, accessible to the public “upon reasonable inquiry.” *BASF Corp.*, 804 F.3d at 965.

17. Public use includes “any use of [the claimed] invention by a person other than the inventor who is under no limitation, restriction, or obligation of secrecy to the inventor.” *Netscape Commc’ns Corp. v. Konrad*, 295 F.3d 1315, 1320 (Fed. Cir. 2002) (quoting *Petrolite Corp. v. Baker Hughes Inc.*, 96 F.3d 1423, 1425 (Fed. Cir. 1996)). A product is “on sale” if it satisfies the two-part test set forth in *Pfaff v. Wells Elecs., Inc.*, 525 U.S. 55 (1998), namely, whether the claimed invention was (1) the subject of a commercial offer for sale; and (2) ready for patenting at the time of that offer for sale. *See Meds. Co. v. Hospira, Inc.*, 827 F.3d 1363, 1368 (Fed. Cir. 2016) (en banc) (citing *Pfaff*, 525 U.S. at 67–68). Whether a patent is invalid for a public use or on sale is a question of law based on the underlying facts. *Id.* at 1371; *see also Pronova BioPharma Norge AS v. Teva Pharm. USA, Inc.*, 549 F. App’x 934, 938–39 (Fed. Cir. 2013).

18. To the extent the Asserted Claims are entitled to an effective filing date before March 16, 2013, under pre-AIA 35 U.S.C. § 102(g), “[a] person shall be entitled to a patent unless . . . before such person’s invention thereof, the invention was made in this country by another inventor who had not abandoned, suppressed, or concealed it.” A patent claim may therefore be invalidated by the prior invention of another. *Apotex USA, Inc. v. Merck & Co.*, 254 F.3d 1031, 1035 (Fed. Cir. 2001); *see also, e.g., TC Tech., LLC v. Sprint Corp.*, 379 F. Supp.3d 305, 318 (D. Del. 2019) (citing *Solvay S.A. v. Honeywell Int’l, Inc.*, 742 F.3d 998, 1000 (Fed. Cir. 2014)). The party asserting invalidity “need only prove either that they first reduced the invention to practice, or that [the prior inventor] conceived of the invention first and were diligent in reducing it to practice.” *bioMerieux, S.A. v. Hologic, Inc.*, C.A. No. 18-21-LPS, 2020 U.S. Dist. LEXIS 25318, at *29–30 (D. Del. Feb. 7, 2020) (citing *Fox Grp., Inc. v. Cree, Inc.*, 700 F.3d 1300, 1304 (Fed.

Cir. 2012)); *see also, e.g., Tyco Healthcare Grp. LP v. Ethicon Endo-Surgery, Inc.*, 774 F.3d 968, 974–75 (Fed. Cir. 2014). Moreover, where the prior inventors are “non-parties and their testimony concern[s] an unpatented prior invention” the corroboration rule—requiring corroboration of inventor testimony directed to establishing their invention as anticipating the claims at issue—is not triggered because “this [situation] does not rise to the level of self-interest required to justify triggering application of the corroboration rule.” *Thomson, S.A. v. Quixote Corp.*, 166 F.3d 1172, 1175–76 (Fed. Cir. 1999).

H. Obviousness

19. “Obviousness is a question of law based on underlying findings of fact.” *Wyers v. Master Lock Co.*, 616 F.3d 1231, 1237 (Fed. Cir. 2010). “These underlying factual determinations include: (1) the scope and content of the prior art; (2) the level of ordinary skill in the art; (3) the differences between the claimed invention and the prior art; and (4) the extent of any proffered objective indicia of nonobviousness,” termed “secondary considerations.” *Weatherchem Corp. v. J.L. Clark, Inc.*, 163 F.3d 1326, 1334 (Fed. Cir. 1998) (citing *Graham v. John Deere Co.*, 383 U.S. 1, 17–18, 86 S. Ct. 684, 694 (1966)).

20. Under 35 U.S.C. § 103, a patent claim is invalid if the “differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains.” As the Supreme Court held in *KSR Int’l Co. v. Teleflex Inc.*:

Under § 103, the scope and content of the prior art are to be determined; differences between the prior art and the claims at issue are to be ascertained; and the level of ordinary skill in the pertinent art resolved. Against this background, the obviousness or nonobviousness of the subject matter is determined.

550 U.S. 398, 406 (2007) (quoting *Graham v. John Deere Co.*, 383 U.S. 1, 17–18 (1966)); *see also Allergan, Inc. v. Sandoz Inc.*, 796 F.3d 1293, 1303 (Fed. Cir. 2015). That is, “[w]hen a work is available in one field of endeavor, design incentives and other market forces can prompt variations of it, either in the same field or a different one. If a person of ordinary skill can implement a predictable variation, § 103 likely bars its patentability.” *Id.* at 417. Moreover, “if a technique has been used to improve one device, and a person of ordinary skill in the art would recognize that it would improve similar devices in the same way, using the technique is obvious unless its actual application is beyond his or her skill.” *Id.* A “combination of familiar elements according to known methods is likely to be obvious when it does no more than yield predictable results.” *Id.* at 416. The Supreme Court reasoned: “[g]ranting patent protection to advances that would occur in the ordinary course without real innovation retards progress and may, in the case of patents combining previously known elements, deprive prior inventions of their value or utility.” *Id.* at 419.

21. Obviousness may be based on one or more references, although either the prior art as a whole, or knowledge generally available to one of ordinary skill in the art, may suggest the obviousness of combining and modifying the prior art to arrive at the claimed invention. *See SIBIA Neurosciences, Inc. v. Cadus Pharm. Corp.*, 225 F.3d 1349, 1356 (Fed. Cir. 2000); *see also KSR*, 550 U.S. at 420. “As long as some motivation or suggestion to combine the references is provided by the prior art taken as a whole, the law does not require that the references be combined for the reasons contemplated by the inventor.” *In re Beattie*, 974 F.2d 1309, 1312 (Fed. Cir. 1992). It is sufficient that a combination of elements was “obvious to try” because “[w]hen there is a design need or market pressure to solve a problem and there are a finite number of identified, predictable solutions, a person of ordinary skill has good reason to pursue the known options within his or her

technical grasp. If this leads to the anticipated success, it is likely the product not of innovation but of ordinary skill and common sense.” *KSR*, 550 U.S. at 421. Indeed, “in many cases a person of ordinary skill will be able to fit the teachings of multiple patents together like pieces of a puzzle.” *Id.* at 420. “In that instance the fact that a combination was obvious to try might show that it was obvious under § 103.” *Id.* It is established that “a rejection for obviousness under § 103 can be based on a reference which happens to anticipate the claimed subject matter.” *In re application of Meyer*, 599 F.2d 1026, 1031 (C.C.P.A. 1979).

22. “[T]he ultimate determination of obviousness ‘does not require absolute predictability of success. . . . [A]ll that is required is a reasonable expectation of success.’” *Brown & Williamson Tobacco Corp. v. Philip Morris Inc.*, 229 F.3d 1120, 1125 (Fed. Cir. 2000). The factfinder inquires whether a person of ordinary skill in the art would have been motivated to combine the prior art in the manner claimed and would have had a reasonable expectation of success in doing so. *See Intelligent Bio-Sys., Inc. v. Illumina Cambridge Ltd.*, 821 F.3d 1359, 1366–67 (Fed. Cir. 2016). The Federal Circuit’s “case law does not require that a particular combination must be the preferred, or the most desirable, combination described in the prior art in order to provide motivation for the current invention.” *In re Fulton*, 391 F.3d 1195, 1200 (Fed. Cir. 2004). Moreover, “[c]onclusive proof of efficacy is not necessary to show obviousness. All that is required is a reasonable expectation of success.” *Hoffmann-La Roche Inc. v. Apotex Inc.*, 748 F.3d 1326, 1331 (Fed. Cir. 2014); *see also Valeant Pharm. Int’l, Inc. v. Mylan Pharm. Inc.*, 955 F.3d 25, 34 (Fed. Cir. 2020).

23. The factfinder may also consider whether there is a “showing of a suggestion, teaching, or motivation to combine the prior art references.” *See Brown & Williamson Tobacco Corp.*, 229 F.3d at 1124; *see also KSR*, 550 U.S. at 419. A “suggestion, teaching, or motivation

to combine the relevant prior art teachings to achieve the claimed invention does not have to be found explicitly in the prior art references sought to be combined, but rather ‘may be found in any number of sources, including common knowledge, the prior art as a whole, or the nature of the problem itself.’” *Pfizer, Inc. v. Apotex, Inc.*, 480 F.3d 1348, 1362 (Fed. Cir. 2007) (citations omitted). Multiple references can be combined to show a patent is invalid, provided a prima facie case is shown and there is motivation to combine the references such that a person skilled in the art would be able to make the claimed invention. *See In re Kahn*, 441 F.3d 977, 988–91 (Fed. Cir. 2006).

24. In view of *KSR*, the United States Patent and Trademark Office issued a set of new Examination Guidelines. *See Examination Guidelines for Determining Obviousness Under 35 U.S.C. § 103*, 72 Fed. Reg. 57526 (Oct. 10, 2007). These Guidelines identify various rationales under *KSR* for finding a claim obvious at the time of the filing of the application for the patent, including those based on other precedents, including but not limited to (1) combining prior art elements according to known methods to yield predictable results; (2) simple substitution of one known element for another to obtain predictable results; (3) use of known technique to improve similar devices (methods, or products) in the same way; (4) applying a known technique to a known device (method, or product) ready for improvement to yield predictable results; (5) “[o]bvious to try”—choosing from a finite number of identified, predictable solutions, with a reasonable expectation of success; (6) known work in one field of endeavor may prompt variations of it for use in either the same field or a different one based on design incentives or other market forces if the variations would have been predictable to one of ordinary skill in the art; and (7) some teaching, suggestion, or motivation in the prior art that would have led one of ordinary skill to

modify the prior art reference or to combine prior art reference teachings to arrive at the claimed invention.

25. Patent claims may be deemed obvious in light of prior art products or systems, or publications describing same, that are capable of performing the functions or methods covered by a patent claim. *See, e.g., In re Hallman*, 655 F.2d 212, 215, 210 U.S.P.Q. 609 (C.C.P.A. 1981).

I. Secondary Considerations of Nonobviousness

26. “Once a prima facie case of obviousness has been established, the burden shifts to the applicant to come forward with evidence of secondary considerations of non-obviousness to overcome the prima facie case.” *Aventis Pharma S.A. v. Hospira, Inc.*, 743 F. Supp. 2d 305, 344 (D. Del. 2010), *aff’d*, 675 F.3d 1324 (Fed. Cir. 2012). ““Under § 103, the scope and content of the prior art are to be determined; differences between the prior art and the claims at issue are to be ascertained; and the level of ordinary skill in the pertinent art resolved. Against this background, the obviousness or nonobviousness of the subject matter is determined. Such secondary considerations as commercial success, long felt but unsolved needs, failure of others, etc., might be utilized to give light to the circumstances surrounding the origin of the subject matter sought to be patented.”” *KSR Int’l Co.*, 550 U.S. at 406 (quoting *Graham*, 383 U.S. at 17–18).

27. “[S]econdary considerations of nonobviousness . . . simply cannot overcome a strong prima facie case of obviousness.” *Wyers*, 616 F.3d at 1246. Once a challenger has put forth a prima facie case of invalidity, a patentee can proffer evidence of secondary considerations by a preponderance of evidence. *See Apple Inc. v. Samsung Elecs. Co.*, 839 F.3d 1034, 1053 (Fed. Cir. 2016) (en banc); *see also Hospira, Inc. v. Amneal Pharm., LLC*, 285 F. Supp. 3d 776, 784 (D. Del. 2018), *appeal dismissed*, C.A. No. 2018-1522, 2018 WL 4382057 (Fed. Cir. June 25, 2018), *and aff’d*, 748 F. App’x 1024 (Fed. Cir. 2019) (“There must be enough evidence, however, for a finding that a given secondary consideration, if presented, exists by a preponderance of the evidence. If

there is, then the probative value of each secondary consideration will be considered in light of the evidence produced.”); *Amazon.com, Inc. v. Barnesandnoble.com, Inc.*, 239 F.3d 1343, 1366 (Fed. Cir. 2001) (allegedly copied feature must be an embodiment of the patented claims).

28. “The patentee bears the burden of showing that a nexus exists” between the alleged secondary considerations of nonobviousness and the patented invention. *Fox Factory, Inc. v. SRAM, LLC*, 944 F.3d 1366, 1373 (Fed. Cir. 2019). “[C]ase law clearly establishes that the patentee must establish a nexus between the evidence of commercial success and the patented invention.” *Wyers*, 616 F.3d at 1246. “So too if the feature that creates the commercial success was known in the prior art, the success is not pertinent.” *Ormco Corp. v. Align Tech., Inc.*, 463 F.3d 1299, 1312 (Fed. Cir. 2006). “When the thing that is commercially successful is not coextensive with the patented invention—for example, if the patented invention is only a component of a commercially successful machine or process, the patentee is not entitled to a presumption of nexus.” *Fox Factory*, 944 F.3d at 1373 (internal citations omitted). “A patent claim is not coextensive with a product that includes a ‘critical’ unclaimed feature that is claimed by a different patent and that materially impacts the product’s functionality.” *Id.* at 1375. Similarly, nexus must be shown between the “merits of the claimed invention” and the evidence of long-felt need. *Merck Sharp & Dohme Corp. v. Hospira Inc.*, C.A. No. 14-915-RGA, 2016 WL 5872620, at *11 (D. Del. July 10, 2016), *aff’d*, 874 F.3d 724 (Fed. Cir. 2017). Nexus must also be shown “between industry praise and the patented *technology*.” *Alarm.com, Inc. v. SecureNet Techs. LLC*, C.A. No. 15-807-RGA, 2019 WL 133228, at *4 (D. Del. Jan. 8, 2019) (emphasis in original).

29. The patentee bears the burden of demonstrating that the relevant commercial success is attributable to the claimed invention “as opposed to other economic and commercial

factors unrelated to the technical quality of the patented subject matter.” *Cable Elec. Prods, Inc. v. Genmark, Inc.*, 770 F. 2d 1015, 1027 (Fed. Cir. 1987); *see Windsurfing Int’l Inc. v. AMF*, 782 F. 2d 995, 999–1000 (Fed. Cir. 1986) (considerations such as intervening, non-covered technological innovations, popularity of accessories, and advertising expense are all relevant to the nexus determination). “If commercial success is due to an element in the prior art, no nexus exists.” *Tokai Corp. v. Easton Enters., Inc.*, 632 F.3d 1358, 1369–70 (Fed. Cir. 2011); *see, e.g., In re Huai-Hung Kao*, 639 F.3d 1057, 1068 (Fed. Cir. 2011) (“Where the offered secondary consideration actually results from something other than what is both claimed and novel in the claim, there is no nexus to the merits of the claimed invention.”) (emphasis in original); *Ormco*, 463 F.3d at 1312 (“[I]f the feature that creates the commercial success was known in the prior art, the success is not pertinent.”). Similarly, the patentee must show alleged industry praise is due to the allegedly novel features of the Asserted Claims, rather than to features present in the prior art. *See Muniauction, Inc. v. Thomson Corp.*, 532 F.3d 1318, 1328 (Fed. Cir. 2008). Evidence of unexpected results must tend to “establish that there is a difference between the results obtained and those of the closest prior art, and that the difference would not have been expected by one of ordinary skill in the art at the time of the invention.” *Bristol-Myers Squibb Co. v. Teva Pharm. USA, Inc.*, 752 F.3d 967, 977 (Fed. Cir. 2014).

J. Written Description

30. The written description requirement mandates that “[t]he specification shall contain a written description of the invention and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same, and shall set forth the best mode contemplated by the inventor of carrying out his invention.” 35 U.S.C. § 112, ¶ 1. “A determination that a patent is invalid for failure to meet the written description requirement of

35 U.S.C. § 112, ¶ 1 is a question of fact.” *Ariad Pharm., Inc. v. Eli Lilly & Co.*, 598 F.3d 1336, 1355 (Fed. Cir. 2010) (en banc).

31. The written description, drawings, and claims in a patent must clearly allow a person of ordinary skill in the art to understand and recognize that the patentee invented what is claimed. *Gentry Gallery, Inc. v. Berkline Corp.*, 134 F.3d 1473, 1479 (Fed. Cir. 1998). In this regard, the patent must demonstrate by disclosure in the specification to those skilled in the art that the patentee had “possession” of what is now asserted to be the claimed invention. *Vas-Cath Inc. v. Mahurkar*, 935 F.2d 1555, 1561 (Fed. Cir. 1991). The written description must actually or inherently disclose every claim element. *PowerOasis, Inc. v. T-Mobile USA, Inc.*, 522 F.3d 1299, 1306–07 (Fed. Cir. 2008). It is not enough to say that undisclosed subject matter would have been obvious or within the normal skill set of a person of ordinary skill. *ICU Med., Inc. v. Alaris Med. Sys., Inc.*, 558 F.3d 1368, 1377 (Fed. Cir. 2009). A written description that discloses only a certain method does not “necessarily support a broad claim as to every possible type of [method], no matter how different in structure or operation from the inventor’s [discussion].” *LizardTech, Inc. v. Earth Res. Mapping, Inc.*, 424 F.3d 1336, 1346 (Fed. Cir. 2005). That is, an inventor’s description of one type of method does not entitle the inventor to claim “any and all means for achieving that objective.” *Id.*; see also *ICU Med.*, 558 F.3d at 1377–79.

32. For the written description requirement, “the test for sufficiency is whether the disclosure of the application relied upon reasonably conveys to those skilled in the art that the inventor had possession of the claimed subject matter as of the filing date.” *Ariad Pharms. v. Eli Lilly & Co.*, 598 F.3d 1336, 1351 (Fed. Cir. 2010) (en banc). Possession requires a “show[ing] that the inventor actually invented the invention claimed.” *Id.* The “level of detail required to satisfy the written description requirement varies depending on the nature and scope of the claims

and on the complexity and predictability of the relevant technology.” *Id.* “[T]he purpose of the written description requirement is to ‘ensure that the scope of the right to exclude, as set forth in the claims, does not overreach the scope of the inventor’s contribution to the field of art as described in the patent specification.’” *ICU Med.*, 558 F. 3d at 1376–79 (citations omitted).

33. The use of patentee’s contention that the claims cover the accused product may be used to illustrate the breadth of the claims and lack of support. *See Rivera v. ITC*, 857 F.3d 1315, 1319–21 (Fed. Cir. 2017) (“Thus, even applying the ‘broad’ definition of ‘pod’ . . . written description support for broad claims covering a receptacle with integrated filter such as Solofill’s accused products and [the patent holder’s products] is lacking.”). The written description requirement is not satisfied where one example is described but it is “not representative of the full variety or scope of the genus.” *AbbVie Deutschland GmbH & Co., KG v. Janssen Biotech, Inc.*, 759 F.3d 1285, 1300–01 (Fed. Cir. 2014); *see e.g., Amgen Inc. v. Sanofi*, 872 F.3d 1367, 1374 (Fed. Cir. 2017) (permissible to use the accused product to show that the specification examples are “not representative of the entire genus.”). “Post-priority-date evidence can be considered where . . . it is used to evaluate whether the disclosed species sufficiently represent the claimed genera.” *MorphSys, Inc. v. Janssen Biotech, Inc.*, 358 F. Supp. 3d 354, 365 (D. Del. 2019). Even if a patent contains working examples, there must be “meaningful guidance” to provide adequate written description. *See Idenix Pharm. LLC v. Gilead Scis. Inc.*, 941 F.3d 1149, 1164–65 (Fed. Cir. 2019).

K. Indefiniteness

34. Where the claims of a patent, read in light of its specification and prosecution history, fail to inform those skilled in the art about the scope of the invention with reasonable certainty, such claims are invalid under 35 U.S.C. § 112 for indefiniteness. *Nautilus, Inc. v. Biosig Instruments, Inc.*, 134 S. Ct. 2120, 2124 (2014). Indefiniteness is a question of law which may be

based on underlying facts. *See Berkheimer*, 881 F.3d at 1368 (Fed. Cir. 2018). To determine whether a claim is indefinite, the court looks to “the claims, specification, and prosecution history—to ascertain if they convey to one of skill in the art with reasonable certainty the scope of the invention claimed.” *Teva Pharm. USA, Inc. v. Sandoz, Inc.*, 789 F.3d 1335, 1341 (Fed. Cir. 2015).

35. A claim may be indefinite where elements specified by the claim may be measured or assessed by a variety of means, none of which are written into the claim. *Media Rights Techs., Inc. v. Capital One Fin. Corp.*, 800 F.3d 1366, 1371 (Fed. Cir. 2015) (quoting *Nautilus, Inc.*, 572 U.S. at 911). In such instances, where something falls within the scope of the claim when assessed or measured by one means, but is excluded from the scope of the claim when assessed or measured by another means, the claim is invalid for indefiniteness. *Dow Chem. Co. v. NOVA Chems. Corp. (Canada)*, 803 F.3d 620, 634–35 (Fed. Cir. 2015); *Teva Pharm. USA, Inc. v. Sandoz, Inc.*, 789 F.3d 1335, 1344–45 (Fed. Cir. 2015). “[P]atent claims with descriptive words or terms of degree must provide objective boundaries for those of skill in the art in the context of the invention to be definite.” *Niazi Licensing Corp. v. St. Jude Med. S.C., Inc.*, 30 F.4th 1339, 1349 (Fed. Cir. 2022).

L. Enablement

36. “Enablement is a question of law based on underlying factual findings.” *MagSil Corp. v. Hitachi Global Storage Techs., Inc.*, 687 F.3d 1377, 1380 (Fed. Cir. 2012). To satisfy the enablement requirement, the specification of a patent must enable a person of skill in the art, as of the filing date, to practice the full scope of the claimed invention without undue experimentation. *ALZA Corp. v. Andrx Pharms., LLC*, 603 F.3d 935, 941–42 (Fed. Cir. 2010); *Sitrick v. Dreamworks, LLC*, 516 F.3d 993, 999 (Fed. Cir. 2008).

37. “Enabling the full scope of each claim is part of the quid pro quo of the patent bargain.” *Id.* at 999 (quoting *AK Steel Corp. v. Sollac*, 344 F.3d 1234, 1244 (Fed. Cir. 2003))

(quotations omitted)). If a patent enables some embodiments within the scope of a claim, but not others, then the claim is invalid. *ALZA*, 603 F.3d at 939–43 (affirming judgment that claims encompassing medicinal tablets in both osmotic and non-osmotic dosage forms were invalid where specification taught only osmotic dosage forms); *Sitrick*, 516 F.3d at 999–1001 (affirming summary judgment that claims encompassing both video games and movies held invalid where specification only taught use of invention in video games); *Auto. Tech. Int’l, Inc. v. BMW of N. Am., Inc.*, 501 F.3d 1274, 1281–85 (Fed. Cir. 2007) (affirming summary judgment that claims encompassing both mechanical and electronic side-impact sensors were invalid where specification taught only mechanical sensors).

38. The focus of an enablement inquiry is on the teachings in the specification. *See* 35 U.S.C. § 112 (“The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains . . . to make and use the same. . . .”). To satisfy the plain language of 35 U.S.C. § 112, the patentee is “required to provide an adequate enabling disclosure in the specification; it cannot simply rely on the knowledge of a person of ordinary skill to serve as a substitute for the missing information in the specification.” *ALZA*, 603 F.3d at 941; *see also Auto. Tech.*, 501 F.3d at 1283–84 (claims encompassing electronic sensors held invalid despite the fact that known technologies could be used to create the electronic sensors, where specification did not teach electronic sensors).

39. The Federal Circuit has identified several factors, referred to as the *Wands* factors, that a court may consider when deciding whether the specification requires undue experimentation: “(1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of

the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims.” *Amgen Inc. v. Sanofi, Aventisub LLC*, 987 F.3d 1080, 1084 (Fed. Cir. 2021), *aff’d sub nom. Amgen Inc. v. Sanofi*, 598 U.S. 594 (2023) (citing *In re Wands*, 858 F.2d 731, 737 (Fed. Cir. 1988)). “A court need not consider each of the *Wands* factors, for they ‘are illustrative, not mandatory.’” *Baxalta Inc. v. Genentech, Inc.*, 579 F. Supp. 3d 595, 608 (D. Del. 2022), *aff’d*, 81 F.4th 1362 (Fed. Cir. 2023) (quoting *Amgen, Inc. v. Chugai Pharm. Co.*, 927 F.2d 1200, 1213 (Fed. Cir. 1991)). Moreover, “when there is no disclosure of any specific starting material or of any of the condition under which a process can be carried out, undue experimentation is required.” *ALZA*, 603 F.3d at 941 (quoting *Auto. Tech.*, 501 F.3d at 1283–84).

II. REMEDIES AVAILABLE TO NATERA

A. Issues of Law to Be Litigated

40. Whether Natera has proven by a preponderance of the evidence that this is an exceptional case pursuant 35 U.S.C. § 285.

41. Whether Natera has proven by a preponderance of the evidence that it is entitled to attorneys’ fees, expenses, or costs, and the amount.

B. Attorney’s Fees and Costs

42. Under 35 U.S.C. § 285, “[t]he court in exceptional cases may award reasonable attorney fees to the prevailing party.” “An ‘exceptional’ case is simply one that stands out from others with respect to the substantive strength of a party’s litigating position (considering both the governing law and the facts of the case) or the unreasonable manner in which the case was litigated. District courts may determine whether a case is ‘exceptional’ in the case-by-case exercise of their discretion, considering the totality of the circumstances.” *Octane Fitness, LLC v. ICON Health & Fitness, Inc.*, 572 U.S. 545, 554 (2014).

43. “Unless a federal statute, these rules, or a court order provides otherwise, costs—other than attorney’s fees—should be allowed to the prevailing party.” Fed. R. Civ. P. 54(d)(1); *see also* D. Del. L.R. 54.1(a). Costs include: “(1) Fees of the clerk and marshal; (2) Fees for printed or electronically recorded transcripts necessarily obtained for use in the case; (3) Fees and disbursements for printing and witnesses; (4) Fees for exemplification and the costs of making copies of any materials where the copies are necessarily obtained for use in the case; (5) Docket fees under section 1923 of this title; (6) Compensation of court appointed experts, compensation of interpreters, and salaries, fees, expenses, and costs of special interpretation services under section 1828 of this title.” 28 U.S.C. § 1920; *see also* D. Del. L.R. 54.1 (b).

III. ALLEGED INFRINGEMENT OF THE ASSERTED PATENTS

A. Alleged Direct Infringement Under 35 U.S.C. § 271

44. Direct infringement occurs when “whoever without authority makes, uses, offers to sell, or sells any patented invention, within the United States or imports into the United States any patented invention during the term of the patent therefor” 35 U.S.C. § 271(a).

45. “Infringement, whether literal or under the doctrine of equivalents, is a question of fact.” *Cook Biotech Inc. v. Acell, Inc.*, 460 F.3d 1365, 1373 (Fed. Cir. 2006). As noted *supra*, Natera discusses infringement in its discussion of legal issues herein to provide citations to relevant legal authority, without waiver of any argument regarding whether a particular issue is one of fact or law.

46. Direct infringement of a method claim requires the patentee to demonstrate that every step of the claimed method is practiced by the accused infringer. *Niazi Licensing Corp. v. St. Jude Med. S.C., Inc.*, 30 F.4th 1339, 1351 (Fed. Cir. 2022); *see also Exergen Corp. v. Wal-Mart Stores, Inc.*, 575 F.3d 1312, 1320 (Fed. Cir. 2009) (“Direct infringement requires a party to perform each and every step or element of a claimed method or product” (quotations and citations

omitted).). “[A]n accused product or process is not infringing unless it contains each limitation of the claim, either literally or by an equivalent.” *Freedman Seating Co. v. Am. Seating Co.*, 420 F.3d 1350, 1358 (Fed. Cir. 2005).

47. “[I]nfringement requires ‘specific instances of direct infringement or that the accused device necessarily infringes the patent in suit.’” *Ball Aerosol & Specialty Container, Inc. v. Ltd. Brands, Inc.*, 555 F.3d 984, 995 (Fed. Cir. 2009) (quoting *ACCO Brands, Inc. v. ABA Locks Mfr. Co.*, 501 F.3d 1307, 1313 (Fed. Cir. 2007)). Labcorp’s burden of proof is preponderance of the evidence. *See Cross Med. Prods., Inc. v. Medtronic Sofamor Danek, Inc.*, 424 F.3d 1293, 1310 (Fed. Cir. 2005). “[W]hen no reasonable jury could find that every limitation recited in a properly construed claim is found in the accused device either literally or under the doctrine of equivalents,” infringement may be decided as a matter of law. *Advanced Steel Recovery, LLC v. X-Body Equip., Inc.*, 808 F.3d 1313, 1317 (Fed. Cir. 2015) (internal citations omitted).

48. “[L]imitations cannot be read into the claims from the specification or the prosecution history.” *Burke, Inc. v. Bruno Indep. Living Aids, Inc.*, 183 F.3d 1334, 1340 (Fed. Cir. 1999). “If an accused product does not infringe an independent claim, it also does not infringe any claim depending thereon.” *Motivation Innovations LLC v. Ulta Salon Cosmetics & Fragrance Inc.*, 59 F. Supp. 3d 663, 669 (D. Del. 2014).

B. Doctrine of Equivalents

49. “[A] product or process that does not literally infringe upon the express terms of a patent claim may nonetheless be found to infringe if there is ‘equivalence’ between the elements of the accused product or process and the claimed elements of the patented invention.” *Warner-Jenkinson Co. v. Hilton Davis Chem. Co.*, 520 U.S. 17, 21 (1997) (quoting *Graver Tank & Mfg. Co. v. Linde Air Prods. Co.*, 339 U.S. 605, 609 (1950)). Infringement under the doctrine of equivalents is a question of fact. *Stryker Corp. v. Davol Inc.*, 234 F.3d 1252, 1258 (Fed. Cir.

2000). The doctrine of equivalents is “a limited remedy available in special circumstances.” *Schoell v. Regal Marine Indus., Inc.*, 247 F.3d 1202, 1210 (Fed. Cir. 2001).

50. The doctrine of equivalents (DOE) requires a claim limitation-by-limitation analysis. *See Akzo Nobel Coatings, Inc. v. Dow Chem. Co.*, 811 F.3d 1334, 1342 (Fed. Cir. 2016). The patentee must prove by a preponderance of the evidence that each and every difference between the accused process and the literal scope of the claimed features is insubstantial. *See Graver Tank & Mfg. Co.*, 339 U.S. at 608. The “all limitations” or “all-elements” rule “holds that an accused product or process is not infringing unless it contains each limitation of the claim, either literally or by an equivalent.” *Freedman Seating Co.*, 420 F.3d at 1358. A claim limitation’s equivalent is found in an accused product only “where an equivalent differs from the claimed limitation only insubstantially.” *Enzo Biochem Inc. v. Applera Corp.*, 702 F. App’x 971, 976 (Fed. Cir. 2017) (internal citation and quotation omitted). “Whether a component in the accused subject matter performs substantially the same function as the claimed limitation in substantially the same way to achieve substantially the same result may be relevant to this determination.” *Id.* (internal citation and quotation omitted).

51. A DOE argument must be established by claim-limitation-specific evidence, with analysis as to the substantial similarity between each specific claim limitation for which equivalency is alleged and the specific feature or operation of the allegedly infringing product or process that is accused for that claim limitation:

Such evidence must be presented on a limitation-by-limitation basis. Generalized testimony as to the overall similarity between the claims and the accused infringer’s product or process will not suffice.

Tex. Instruments Inc. v. Cypress Semiconductor Corp., 90 F.3d 1558, 1567 (Fed. Cir. 1996).

52. A patentee cannot generically allege equivalence to a product as a whole, but must do so for each claim limitation, with particularized testimony and linking arguments as to how the accused product's features or operations are equivalent to each claim limitation for which equivalency is alleged. See *Network Com., Inc. v. Microsoft Corp.*, 422 F.3d 1353, 1363 (Fed. Cir. 2005); *Horizon Medicines LLC v. Alkem Lab 'ys Ltd.*, 503 F. Supp. 3d 118, 148 (D. Del. 2020), *aff'd*, No. 2021-1480, 2021 WL 5315424 (Fed. Cir. Nov. 16, 2021) (finding no DOE infringement where plaintiff applied DOE theory to two claim limitations simultaneously); *Galderma Lab 'ys, L.P. v. Amneal Pharms. LLC*, 806 F. App'x 1007, 1014 (Fed. Cir. 2020) (reversing judgment of DOE infringement because plaintiff relied on same testimony to support equivalency for two distinct limitations, thus failing to "present particularized testimony and linking argument" on a limitation-by-limitation basis); *Inline Connection Corp. v. AOL Time Warner Inc.*, 364 F. Supp. 2d 417, 447–48 (D. Del. 2005) (granting summary judgment of no DOE infringement where plaintiff "impermissibly subsumed [its DOE arguments] in its arguments for literal infringement and provides insufficient particularized linking testimony to raise a genuine question of material fact"). Similarly, "[a] patentee, bearing the burden of showing equivalence, cannot merely point to other claim limitations to satisfy the doctrine of equivalents. Doing so runs afoul of the 'all-elements rule' articulated in *Warner-Jenkinson*." *Advanced Steel Recovery, LLC v. X-Body Equip., Inc.*, 808 F.3d 1313, 1320 (Fed. Cir. 2015); see also *Cooper Notification, Inc. v. Twitter, Inc.*, 867 F. Supp. 2d 485, 496–97 (D. Del. 2012).

C. Claim Vitiating

53. As a matter of law, an element of an accused process cannot be deemed an equivalent if such a finding would entirely vitiate the claim limitation. See *Warner-Jenkinson*, 520 U.S. at 39 n.8 ("[I]f a theory of equivalence would entirely vitiate a particular claim element, partial or complete judgment should be rendered by the court, as there would be no further *material*

issue for the jury to resolve.”) (emphasis original); *see also, e.g., Virnetx, Inc. v. Cisco Sys., Inc.*, 767 F.3d 1308, 1322–23 (Fed. Cir. 2014). A theory of infringement under the doctrine of equivalents “thus fails if it renders a claim limitation inconsequential or ineffective.” *Akzo*, 811 F.3d at 1342; *see also United Access Techs., LLC v. AT & T Corp.*, 265 F. Supp. 3d 446, 453 (D. Del. 2017) (Stark, J.), *rev’d in part on other grounds by United Access Techs., LLC v. AT & T Corp.*, 757 Fed. App’x 960 (Fed. Cir. 2019). The doctrine applies equally to the Court’s construction of a claim term as to the words written in the patent claims themselves. *See Augme Techs., Inc. v. Yahoo! Inc.*, 755 F.3d 1326, 1332, 1335–37 (Fed. Cir. 2014); *United Access Techs.*, 265 F. Supp. 3d at 453. Claim vitiation is “important to ensure that the application of [] [DOE], even as to an individual element, is not allowed such broad play as to effectively eliminate that element in its entirety.” *See Warner-Jenkinson*, 520 U.S. at 29.

54. “The vitiation concept has its clearest application where the accused device contain[s] the antithesis of the claimed structure.” *See Brilliant Instruments, Inc. v. GuideTech, LLC*, 707 F.3d 1342, 1347 (Fed. Cir. 2013) (citation omitted); *see also Abbott Lab’ys v. Andrx Pharms., Inc.*, 473 F.3d 1196, 1211 (Fed. Cir. 2007) (“[T]he concept of equivalency cannot embrace a structure that is specifically excluded from the scope of the claims.” (citation omitted)); *Deere & Co. v. Bush Hog, LLC*, 703 F.3d 1349, 1356 (Fed. Cir. 2012) (“[C]ourts properly refuse to apply the doctrine of equivalents where the accused device contain[s] the antithesis of the claimed structure.” (citation omitted)).

55. “[V]itiation comes into play when the alleged equivalent is ‘diametrically opposed’ to the missing claim element.” *Bio-Rad Lab’ys, Inc. v. 10X Genomics Inc.*, 967 F.3d 1353, 1367 (Fed. Cir. 2020) (citation omitted); *see also, e.g., United Access Techs., LLC v. AT&T Corp.*, Nos. 2021-2002 & 2021-2007, 2022 WL 1124961, at *5 (Fed. Cir. Apr. 15, 2022) (affirming summary

judgment of no DOE infringement because theory “would ‘embrace a structure that is specifically excluded from the scope of the claims’” (citation omitted)); *EMED Techs. Corp. v. Repro-Med Sys., Inc.*, 809 F. App’x 885, 892 (Fed. Cir. 2020) (affirming summary judgment of no DOE infringement where alleged equivalent was excluded from the properly construed claim limitation); *XMTT, Inc. v. Intel Corp.*, C.A. No. 18-1810-MFK, 2023 WL 2163242, at *8 (D. Del. Feb. 22, 2023) (granting summary judgment of no DOE infringement because accused product performed the “antithesis” of the claimed element).

56. A patentee’s theory of equivalence, in light of the claim language and alleged evidence of infringement, can itself mandate the legal conclusion that the alleged equivalent would vitiate the claim limitations. *See Warner-Jenkinson*, 520 U.S. at 39 n.8 (“[I]f a theory of equivalence would entirely vitiate a particular claim element, partial or complete judgment should be rendered by the court, as there would be no further material issue for the jury to resolve.”); *Duncan Parking Techs., Inc. v. IPS Grp., Inc.*, 914 F.3d 1347, 1361–62 (Fed. Cir. 2019) (summary judgment of no infringement under DOE due to vitiation); *Rembrandt Pat. Innovations, LLC v. Apple, Inc.*, 716 F. App’x 965, 977–78 (Fed. Cir. 2017) (same).

D. Ensnarement

57. “The doctrine of equivalents cannot be applied to encompass the prior art as ‘this court has consistently limited the doctrine of equivalents to prevent its application to ensnare prior art.’” *Gemalto S.A. v. HTC Corp.*, 754 F.3d 1364, 1374–75 (Fed. Cir. 2014) (citations omitted). “This limitation is imposed even if a jury has found equivalence as to each claim element.” *DePuy Spine, Inc. v. Medtronic Sofamor Danek, Inc.*, 567 F.3d 1314, 1322–23 (Fed. Cir. 2009) (citations omitted).

58. To test whether an alleged equivalent would ensnare the prior art, “[a] hypothetical claim may be constructed to literally cover the accused device. If such a claim would be

unpatentable under 35 U.S.C. §§ 102 or 103, then the patentee has overreached, and the accused device is noninfringing as a matter of law.” *Interactive Pictures Corp. v. Infinite Pictures, Inc.*, 274 F.3d 1371, 1380 (Fed. Cir. 2001) (internal citations omitted).

IV. ALLEGED REMEDIES SOUGHT BY LABCORP

A. Issues of Law to Be Litigated

59. If the Asserted Claims are found valid and infringed, whether Labcorp has proven by a preponderance of the evidence that it is entitled to damages, in the form of lost profits, a reasonable royalty, pre-judgment and/or post-judgment interest, and attorneys’ fees and costs.

60. If the Asserted Claims are found valid and infringed, whether Labcorp has proven by a preponderance of the evidence that it is entitled to a permanent injunction.

B. Damages in General

61. Under 35 U.S.C. § 284, upon a finding of infringement, “the court shall award the claimant damages adequate to compensate for the infringement, but in no event less than a reasonable royalty for the use made of the invention by the infringer, together with interest and costs as fixed by the court.” “[T]he amount of a prevailing party’s damages is a finding of fact on which the plaintiff bears the burden of proof by a preponderance of the evidence.” *Smithkline Diagnostics, Inc. v. Helena Labs. Corp.*, 926 F.2d 1161, 1164 (Fed. Cir. 1991). It is plaintiff’s initial burden to prove damages, including to apportion any proposed royalty so that it reflects “the value attributable to the infringing features of the product, and no more.” *See Ericsson, Inc. v. D-Link Sys., Inc.*, 773 F.3d 1201, 1226 (Fed. Cir. 2014); *ResQNet.com, Inc. v. Lansa, Inc.*, 594 F.3d 860, 872 (Fed. Cir. 2010) (“But it was ResQNet’s burden, not Lansa’s, to persuade the court with legally sufficient evidence regarding an appropriate reasonable royalty.”); *W.L. Gore & Assocs. v. C.R. Bard, Inc.*, 2015 WL 12731924, at *4, *6–7 (D. Del. Nov. 4, 2015).

C. Lost Profits

62. “To recover lost profits, the patent owner must show ‘causation in fact,’ establishing that ‘but for’ the infringement, he would have made additional profits.” *Grain Processing Corp. v. Am. Maize-Prod. Co.*, 185 F.3d 1341, 1349 (Fed. Cir. 1999). “When basing the alleged lost profits on lost sales, the patent owner has an initial burden to show a reasonable probability that he would have made the asserted sales ‘but for’ the infringement. Once the patent owner establishes a reasonable probability of ‘but for’ causation, ‘the burden then shifts to the accused infringer to show that [the patent owner’s “but for” causation claim] is unreasonable for some or all of the lost sales.’” *Id.*

63. “To obtain as damages the profits on sales he would have made absent the infringement, *i.e.*, the sales made by the infringer, a patent owner must prove: (1) demand for the patented product, (2) absence of acceptable noninfringing substitutes, (3) his manufacturing and marketing capability to exploit the demand and (4) the amount of profit he would have made.” *Panduit Corp. v. Stahl Bros. Fibre Works, Inc.*, 575 F.2d 1152, 1156 (6th Cir. 1978).

64. “With such multi-component products, it may often be the case that no one patentee can obtain lost profits on the overall product—the *Panduit* test is a demanding one. A patentee cannot obtain lost profits unless it and only it could have made the sale—there are no non-infringing alternatives or, put differently, the customer would not have purchased the product without the infringing feature.” *Mentor Graphics Corp. v. EVE-USA, Inc.*, 851 F.3d 1275, 1289 (Fed. Cir. 2017). “An award of lost profits may not be speculative. Rather the patent owner must show a reasonable probability that, absent the infringement, it would have made the infringer’s sales.” *BIC Leisure Prod., Inc. v. Windsurfing Int’l, Inc.*, 1 F.3d 1214, 1218 (Fed. Cir. 1993).

65. “[A] fair and accurate reconstruction of the ‘but for’ market also must take into account, where relevant, alternative actions the infringer foreseeably would have undertaken had

he not infringed,” such as offering a non-infringing version of the accused product. *Grain Processing*, 185 F.3d at 1350–51. This analysis is necessary because “[t]he competitor in the ‘but for’ marketplace is hardly likely to surrender its complete market share when faced with a patent, if it can compete in some other lawful manner.” *Id.* at 1351; *see also id.* (“[U]nless the law wishes to systematically overreward patented inventions, it is necessary to inquire about the nature and value of the product that the infringer could have made had he not infringed.”) (quoting Schlicher, Patent Law: Legal and Economic Principles § 9.05[2][1] (1997)). An accused infringer need not have an actual working example in order for it to be considered available in the but-for world. *See Grain Processing*, 185 F.3d at 1351 (explaining that “next-best available alternative(s)” need to be considered “regardless of whether the alternative(s) were actually produced and sold during the infringement [period]”).

66. The patentee bears the burden to establish all four *Panduit* factors, including proving the “absence of non-infringing alternatives.” *Mentor Graphics*, 851 F.3d at 1285. Although the accused infringer has the burden to show that a “substitute was available during the accounting period” if the alleged substitute was not on the market, *Grain Processing*, 185 F.3d at 1353, it remains the patentee’s burden to prove the “absence of non-infringing alternatives.” *Mentor Graphics*, 851 F.3d at 1285.

D. Reasonable Royalty

67. “A patentee receives a reasonable royalty for any of the infringer’s sales not included in the lost profit calculation.” *Crystal Semiconductor Corp. v. TriTech Microelecs. Int’l, Inc.*, 246 F.3d 1336, 1354 (Fed. Cir. 2001).

68. While the patent statute provides a floor of “a reasonable royalty for the use made of the invention by the infringer,” 35 U.S.C. § 284, it provides no method for defining a “reasonable” royalty, an exercise that “is not an exact science.” *Summit 6, LLC v. Samsung Elecs.*

Co., 802 F.3d 1283, 1296, 1299 (Fed. Cir. 2015). One approach to determining a reasonable royalty is the “hypothetical negotiation approach,” which the Federal Circuit has held is a reasonable method. *See Summit 6*, 802 F.3d at 1299. The hypothetical negotiation approach “‘attempts to ascertain the royalty upon which the parties would have agreed had they successfully negotiated an agreement just before infringement began.’” *Id.* (quoting *Lucent Techs., Inc. v. Gateway, Inc.*, 580 F.3d 1301, 1324 (Fed. Cir. 2009)). The fifteen factors identified in *Georgia-Pacific Corp. v. United States Plywood Corp.*, 318 F. Supp. 1116, 1120 (S.D.N.Y. 1970), are most commonly used for this analysis. The *Georgia-Pacific* factors are:

1. The royalties received by the patentee for the licensing of the patent in suit, proving or tending to prove an established royalty.
2. The rates paid by the licensee for the use of other patents comparable to the patent in suit.
3. The nature and scope of the license, as exclusive or non-exclusive; or as restricted or non-restricted in terms of territory or with respect to whom the manufactured product may be sold.
4. The licensor’s established policy and marketing program to maintain his patent monopoly by not licensing others to use the invention or by granting licenses under special conditions designed to preserve that monopoly.
5. The commercial relationship between the licensor and licensee, such as, whether they are competitors in the same territory in the same line of business; or whether they are inventor and promoter.
6. The effect of selling the patented specialty in promoting sales of other products of the licensee; that existing value of the invention to the licensor as a generator of sales of his non-patented items; and the extent of such derivative or convoyed sales.
7. The duration of the patent and the term of the license.
8. The established profitability of the product made under the patent; its commercial success; and its current popularity.
9. The utility and advantages of the patent property over the old modes or devices, if any, that had been used for working out similar results.
10. The nature of the patented invention; the character of the commercial embodiment of it as owned and produced by the licensor; and the benefits to those who have used the invention.

11. The extent to which the infringer has made use of the invention; and any evidence probative of the value of that use.
12. The portion of the profit or of the selling price that may be customary in the particular business or in comparable businesses to allow for the use of the invention or analogous inventions.
13. The portion of the realizable profit that should be credited to the invention as distinguished from non-patented elements, the manufacturing process, business risks, or significant features or improvements added by the infringer.
14. The opinion testimony of qualified experts.
15. The amount that a licensor (such as the patentee) and a licensee (such as the infringer) would have agreed upon (at the time the infringement began) if both had been reasonably and voluntarily trying to reach an agreement.

318 F. Supp. at 1120.

69. Where the accused product includes both an allegedly patented feature and unpatented or conventional features, “damages awarded for patent infringement ‘must reflect the value attributable to the infringing features of the product, and no more.’” *CSIRO v. Cisco Sys., Inc.*, 809 F.3d 1295, 1301 (Fed. Cir. 2015) (quoting *Ericsson, Inc. v. D-Link Sys.*, 773 F. 3d 1201, 1226 (Fed. Cir. 2014)); *see also Exmark Mfg. Co., Inc. v. Briggs & Stratton Power Prod. Grp., LLC*, 879 F.3d 1332, 1347–48, 350 (Fed. Cir. 2018). “The essential requirement is that the ultimate reasonable royalty award must be based on the incremental value that the patented invention adds to the end product.” *Exmark Mfg.*, 879 F.3d at 1348 (quoting *Ericsson*, 773 F. 3d at 1226). Thus, a patentee must “apportion or separate the damages between the patented improvement and the conventional components of the multicomponent product.” *Id.* Such an apportionment can be applied to the royalty rate or the royalty base, or a combination of both. *Id.* The apportionment analysis must be based on evidence that is “reliable and tangible, and not conjectural or speculative.” *LaserDynamics, Inc. v. Quanta Comp., Inc.*, 694 F.3d 51, 67 (Fed. Cir. 2012) (quoting *Garretson v. Clark*, 111 U.S. 120, 121 (1884)).

70. “The entire market value rule is a narrow exception to [the] general rule” that “royalties be not based on the entire product, but instead on the ‘smallest salable patent-practicing unit.’” *LaserDynamics*, 694 F.3d at 67. “The entire market value rule allows for the recovery of damages based on the value of an entire apparatus containing several features, when the feature patented constitutes the basis for customer demand.” *Id.* Under the entire market value rule, “[i]t is not enough to merely show that the [claimed method] is viewed as valuable, important, or even essential to the use of the [device at issue]. Nor is it enough to show that a [device] without an ODD practicing the [claimed] method would be commercially unviable. Were this sufficient, a plethora of features of a [device at issue] could be deemed to drive demand for the entire product.” *Id.* at 68. Further apportionment beyond the smallest salable patent-practicing unit is required “if that unit still contains significant unpatented features.” *Virnetx, Inc. v. Cisco Sys., Inc.*, 767 F.3d 1308, 1329 (Fed. Cir. 2014).

71. “[Q]ualitative testimony that an invention is valuable – without being anchored to a quantitative market valuation – [is] insufficiently reliable.” *CSIRO*, 809 F.3d at 1302. “[T]he district court may reject the extreme figures proffered by the litigants as incredible and substitute an intermediate figure as a matter of its judgment from all of the evidence.” *SmithKline Diagnostics, Inc. v. Helena Labs. Corp.*, 926 F.2d 1161, 1168 (Fed. Cir. 1991). Methods to calculate reasonable royalty using licenses must be based on sufficiently comparable licenses. *See CSIRO*, 809 F.3d at 1303–04. “Grounds for exclusion in [the Federal Circuit’s] past cases have included, but are not limited to: the license being a litigation settlement agreement, and the patented technology’s lack of a relationship to the licensed technology.” *Id.* at 1304 n.2 (internal citations omitted). Further, the license comparability analysis must be based on evidence of technological comparability between the licensed technology and the claimed invention. *See*

ResQNet.com, Inc. v. Lansa, Inc., 594 F.3d 860, 871 (Fed. Cir. 2010) (“This trial court, like the one in *Lucent*, made no effort to link certain licenses to the infringed patent.”); *Lucent*, 580 F.3d at 1329.

E. Prejudgment Interest

72. Under 35 U.S.C. § 284, upon a finding of infringement, “the court shall award the claimant damages adequate to compensate for the infringement, but in no event less than a reasonable royalty for the use made of the invention by the infringer, together with interest and costs as fixed by the court.” 35 U.S.C. § 284 (emphasis added). The prejudgment interest on a damages award “merely serves to make the patent owner whole, since his damages consist not only of the value of the royalty payments but also the foregone use of the money between the time of infringement and the date of the judgment.” *Gen. Motors Corp. v. Devex Corp.*, 461 U.S. 648, 656 (1983). The District Court has discretion to determine the applicable rate. *Edwards Lifesciences AG v. CoreValve, Inc.*, No. C.A. 08-91-GMS, 2011 WL 446203, at *13 (D. Del. Feb. 7, 2011), *aff’d in part, remanded in part*, 699 F.3d 1305 (Fed. Cir. 2012).

F. Post-Judgment Interest

73. Post-judgment interest is governed by 28 U.S.C. § 1961. According to 28 U.S.C. § 1961(a):

Interest shall be allowed on any money judgment in a civil case recovered in a district court. Execution therefor may be levied by the marshal, in any case where, by the law of the State in which such court is held, execution may be levied for interest on judgments recovered in the courts of the State. Such interest shall be calculated from the date of the entry of the judgment, at a rate equal to the weekly average 1-year constant maturity Treasury yield, as published by the Board of Governors of the Federal Reserve System, for the calendar week preceding[] the date of the judgment. The Director of the Administrative Office of the United States Courts shall distribute notice of that rate and any changes in it to all Federal judges.

74. The District Court has discretion to determine the applicable rate. *See Edwards Lifesciences AG*, 2011 WL 446203, at *13; *TruePosition Inc. v. Andrew Corp.*, 611 F. Supp. 2d 400, 413 n.15 (D. Del. 2009), *aff'd*, 389 F. App'x 1000 (Fed. Cir. 2010).

G. Permanent Injunctive Relief

75. Under 35 U.S.C. § 283, courts “may grant injunctions in accordance with the principles of equity to prevent the violation of any right secured by patent, on such terms as the court deems reasonable.” “According to well-established principles of equity, a plaintiff seeking a permanent injunction must satisfy a four-factor test before a court may grant such relief. A plaintiff must demonstrate: (1) that it has suffered an irreparable injury; (2) that remedies available at law, such as monetary damages, are inadequate to compensate for that injury; (3) that, considering the balance of hardships between the plaintiff and defendant, a remedy in equity is warranted; and (4) that the public interest would not be disserved by a permanent injunction.” *eBay Inc. v. MercExchange, L.L.C.*, 547 U.S. 388, 391 (2006).

H. Attorney’s Fees and Costs

Natera incorporates by reference as though fully set forth herein its statements of legal authorities set forth *supra* Section II.B.

EXHIBIT 6

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-669 (GBW)
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-1635 (GBW)
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	

EXHIBIT 6: PLAINTIFF'S WITNESS LIST

Plaintiff Invitae Corporation (“Invitae”) identifies the following fact witnesses that it may call live or by deposition at trial. Invitae reserves the right to modify this list in accordance with Fed. R. Civ. P. 26(a)(3), D. Del. LR 16.3, or in view of other events or changed circumstances that may occur before or during trial. Invitae expressly reserves the right to call live or by deposition any witness on its witness list or any witness on the witness list of Defendant. This list is not a commitment that Invitae will call any particular witness at trial, or a representation that any witness listed is available or will appear for trial. If any Invitae, Defendant, or third-party witness is unavailable or refuses to testify live, Invitae reserves the right to use their deposition testimony. With respect to Defendant’s witnesses, Invitae reserves the right to introduce testimony through deposition or live examination, as appropriate. In addition, Invitae reserves the right to call any witness, whether listed below or not, to establish authenticity and/or admissibility of any trial exhibit whose authenticity or admissibility is challenged by Defendant. Notwithstanding providing this list, Invitae makes no representation regarding its ability to force any witness to appear at trial unwillingly.

Invitae also reserves the right to call in its case in chief any witness identified by Defendant and to call by deposition any witness identified by Defendant who does not testify at trial or who is unavailable. Invitae also reserves the right to call any witness in its list either in its case in chief, or as a rebuttal witness, or both.

I. INVITAE INTENDS TO CALL THE FOLLOWING WITNESSES AT TRIAL:

1. Gregory Porreca (Live)
2. Nirav Malani (Live)
3. Joshua Earl (Live)
4. Dan Krane (Live)

5. Alexander Clemons (Live)

II. INVITAE MAY CALL THE FOLLOWING WITNESSES AT TRIAL:

1. Mary Freivogel
2. Richard Lusk
3. Nirav Malani
4. Eric Olivares
5. Joshua Paul
6. Jim Stuart
7. Sajani Swamy
6. Andrea Velenich
7. Gregory Porreca
8. David Bessette
9. John Fesko
10. Kevin Masukawa
11. Solomon Moshkevich
12. Raheleh Salari
13. Hsin-Ta Wu
14. Eric Banks
15. Ryan Poplin
16. All witnesses named on Natera's trial witness list

EXHIBIT 7

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

EXHIBIT 7: DEFENDANT'S WITNESS LIST

OF COUNSEL:

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Daniel J. Klein
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Natera identifies the following fact witnesses that it may call live or by deposition at trial. Natera reserves the right to modify this list in accordance with Fed. R. Civ. P. 26(a)(3), D. Del. L.R. 16.3, or in view of other events or changed circumstances that may occur before or during trial. Natera expressly reserves the right to call live or by deposition any witness on its witness list or any witness on the witness list of Labcorp. This list is not a commitment that Natera will call any particular witness at trial, or a representation that any witness listed is available or will appear for trial. If any Natera, Labcorp, or third-party witness is unavailable or refuses to testify live, Natera reserves the right to use their deposition testimony. With respect to Labcorp's witnesses, Natera reserves the right to introduce testimony through deposition or live examination, as appropriate. In addition, Natera reserves the right to call any witness, whether listed below or not, to establish authenticity and/or admissibility of any trial exhibit whose authenticity or admissibility is challenged by Labcorp. Notwithstanding providing this list, Natera makes no representation regarding its ability to force any witness to appear at trial unwillingly.

Natera also reserves the right to call in its case in chief live or by deposition any witness identified by Labcorp and to call by deposition any witness identified by Labcorp who does not testify at trial or who is unavailable. Natera also reserves the right to call live or by deposition any witness in its list either in its case in chief, or as a rebuttal witness, or both. Natera further reserves the right to amend or supplement this disclosure of witnesses it may call at trial in view of the Court's rulings on any of the parties' objections to the other's witness list.

I. FACT WITNESSES

1. Eric Banks (Live)
2. John Fesko (Live)
3. George Gemelos (Live)
4. Solomon Moshkevich (Live)

5. Ryan Poplin (Live)
6. David Bessette (Deposition)
7. Hsin-Ta Wu (Deposition)
8. Raheleh Salari (Deposition)
9. Mary Freivogel (Deposition)
10. Richard Lusk (Deposition)
11. Nirav Malani (Deposition)
12. Kevin Masukawa (Deposition)
13. Hila Moyal (Deposition)
14. Eric Olivares (Deposition)
15. Joshua Paul (Deposition)
16. Gregory Porreca (Deposition)
17. Jim Stuart (Deposition)
18. Sajani Swamy (Deposition)
19. Andrea Velenich (Deposition)
20. Plaintiff Labcorp's Corporate Representative(s) (Live or Deposition)
21. All witnesses named on Plaintiff Labcorp's Trial Witness List (Pretrial Order, Ex. 6) (Live or Deposition)

II. EXPERT WITNESSES

Natera lists below the names of the expert witnesses it may call at trial. Natera intends to call its expert witnesses live at trial and does not currently intend to seek to introduce their testimony by deposition designation unless one or more of its expert witnesses becomes unavailable and/or is unable or unwilling to travel or testify live at trial.

1. Istvan Albert, Ph.D.
2. Michael Metzker, Ph.D.

3. Nisha Mody, Ph.D.

EXHIBIT 8

Pursuant to D. Del. LR 16.3, Plaintiff Labcorp Corporation of America Holdings ("Plaintiff") hereby submits its list of deposition designations that it may offer at trial.

Plaintiff makes these disclosures without prejudice to amending or supplementing the disclosures in the future if necessary, including but not limited to further reducing the designations set forth below. Plaintiff reserves the right to use any deposition testimony, whether designated or not, for purposes of cross-examination, impeachment, and/or rebuttal. Plaintiff reserves the right to designate additional deposition testimony or call any witness for live testimony in response to any of Natera, Inc.'s ("Defendant") deposition designations or for any other reason. Plaintiff's designations include all exhibits that are referenced in the specified pages and lines, whether or not such exhibits are separately identified. Plaintiff reserves the right to use any deposition testimony designated by Defendant. Inclusion on this list is neither an admission nor a representation as to the admissibility of or relevance to any issue of any deposition designation. By designating deposition testimony, Plaintiff is neither representing nor admitting that Plaintiff has the burden of proof on any topic.

Plaintiff generally objects to any deposition testimony counter-designated by Defendant that is the subject of the parties' stipulations, agreed motions in limine (if any), Plaintiff's motions in limine, motions to exclude certain evidence, Daubert motions and challenges to experts, and any dispositive motions. Plaintiff reserves the right to make additional objections leading up to and at trial.

Plaintiff reserves the right to add to, remove from, and/or supplement these lists of objections to Defendant's counter-designations and Plaintiff's counter-counter designations.

Regarding Plaintiff's objections to Defendant's counter-designations, Plaintiff reserves the right to assert any one, part, or all of its objections. Plaintiff also reserves the right to assert additional objections or counter-counter designations. Plaintiff also reserves the right to assert its original affirmative designation as a counter-counter designation to any counter-designation listed by Defendant.

Pursuant to D. Del. LR 16.3, Defendant Natera, Inc. ("Natera") hereby submits its objections and counter-designations to Invitae's deposition designations.

Defendant makes these objections and disclosures without prejudice to amending or supplementing the objections and disclosures in the future if necessary, including but not limited to reducing the counter-designations set forth in this document, reducing the objections set forth in this document, and/or amending counter-designations in light of Plaintiff's objections and counter-counter-designations. Defendant reserves the right to use any deposition testimony designated by Plaintiff, even if Plaintiff chooses not to use such testimony at trial. Defendant reserves the right to use any deposition testimony, whether designated or not, for purposes of impeachment and/or in rebuttal to any evidence or testimony introduced by Plaintiff. Inclusion on this list is neither an admission nor a representation as to the admissibility of any testimony or exhibits referenced in such testimony.

Defendant generally objects to any deposition testimony designated by Plaintiff that is the subject of the parties' stipulations, agreed motions in limine, Defendant's motions in limine, motions to exclude certain evidence, Daubert motions and challenges to experts, and any dispositive motions. Defendant reserves the right to make additional objections leading up to and at trial.

Defendant's Objection Key

Code	Meaning
402	Not relevant
403	Prejudicial, confusing, and/or waste of time
602	Lack of foundation
701	Opinion testimony by a lay witness
C	Attorney colloquy or objection/not testimony
702/703	Improper foundation/basis for expert testimony
802	Hearsay
NR	Not related
NS	Nonsensical
NQP	No question posed
NA	No answer
I	Incomplete
MIL	Subject of a MIL
V	Vague and ambiguous
HYP	Improper hypothetical
AF	Assumes facts not in evidence
MIS	Mischaracterizes evidence/testimony or is misleading
S	Calls for speculation
Cmpd.	Compound
Scope	Outside the scope of 30(b)(6) designations
NBE	Not best evidence
LC	Calls for legal conclusion
A&A	Asked and answered

	Plaintiff's Objection Key
AA	Asked and answered; Fed. R. Evid. 611(a).
ARG	Argumentative, or attorney argument; Fed. R. Evid. 611(a).
BTS	Beyond the scope of examination or of 30(b)(6) topic; Fed R. Evid. 611, Fed. R. Civ. P. 30(b)(6).
BSD	Counter-Designation Beyond the Scope of the Designation(s).
CP	Compound question.
F	No foundation or assumes facts not in evidence; Fed. R. Evid. 602, 703, 901.
FOW	An objection to form is waived if it was not timely made during the deposition, Fed. R. Civ. P. 32(d)(3)(B).
H	Hearsay if offered for the truth of the matter asserted; Fed. R. Evid. 801, 803, 805.
I	Incomplete designation; Fed. R. Evid. 106, 403.
IH	Incomplete Hypothetical.
L	Leading; Fed. R. Evid. 611(c).
LC	Calls for Legal Conclusion; Fed. R. Evid. 701.
LW	Witness will be testifying live at trial.
MIL	Subjec to motion in limine
MIS	Mischaracterization of testimony or evidence.
NARR	Narrative.
NR	Not responsive; Fed. R. Evid. 611(a).
O	Unqualified Opinion; Calls for improper expert opinion from lay witness; Fed. R. Evid. 701, 702.
OB	Attorney Objection improperly designated/Improper designation.
P	Privileged; Fed. R. Evid. 501, Fed. R. Civ. P. 26(b)(3),(4).
PK	Lack of personal knowledge; Fed. R. Evid. 602.
R	Not relevant; Fed. R. Evid. 401, 402.
SPEC	Calls for Speculation; Fed. R. Evid. 602, 701, 702.
403	Unfairly prejudicial; cumulative, waste of time, Fed. R. Evid. 403.
V	Vague or ambiguous; Fed. R. Evid. 611(a).

Labcorp Corporation of America Holdings v. Natera, Inc. (Case No. 1:21-cv-00669-GBW)			
Witness: Banks, Eric			
Date of Desposition: 2023-04-20			
Labcorp's Opening Designations	Natera's Objections	Natera's Counter-Designations	Labcorp's Objections
7:11-15			
9:5-12			
9:16-10:3			
10:7-16			
12:23-13:14		13:24-14:19	
16:10-22		16:8-9; 22:22-23:4	BSD
17:2-18:12		19:14-16; 19:18-20; 20:4-6; 20:9-10; 20:12-20	R, 403
18:14			
18:16-22	MIS, V	19:14-16; 19:18-20; 20:4-6; 20:9-10; 20:12-20; 21:13-15; 21:23-22:1	R, 403, BSD
18:24-19:2		19:14-16; 19:18-20; 20:4-6; 20:9-10; 20:12-20; 21:13-15; 21:23-22:1	R, 403, BSD
19:4-6	MIS, V	19:14-16; 19:18-20; 20:4-6; 20:9-10; 20:12-20; 21:13-15; 21:23-22:1	R, 403, BSD
19:12	MIS, V	19:14-16; 19:18-20; 20:4-6; 20:9-10; 20:12-20; 21:13-15; 21:23-22:1	R, 403, BSD
27:13-15	MIS, AF, 602	25:21-26:8; 26:10-14; 26:24-25; 27:2-4; 189:22-193:2	R, 403, BSD, L, V
27:17	MIS, AF	25:21-26:8; 26:10-14; 26:24-25; 27:2-4; 189:22-193:2	R, 403, BSD, L, V
27:19-28:3	MIS	25:21-26:8; 26:10-14; 26:24-25; 27:2-4; 189:22-193:2	R, 403, BSD, L, V
28:5	MIS	25:21-26:8; 26:10-14; 26:24-25; 27:2-4; ; 189:22-193:2	R, 403, BSD, L, V
28:8-29:2	MIS	112:20-113:11; 186:2-12; 187:10-188:6	R, 403
29:4-5	MIS	112:20-113:11; 186:2-12; 187:10-188:6	R, 403
29:8-11	MIS	112:20-113:11; 186:2-12; 187:10-188:6	R, 403

Labcorp Corporation of America Holdings v. Natera, Inc. (Case No. 1:21-cv-00669-GBW)			
Witness: Banks, Eric			
Date of Desposition: 2023-04-20			
Labcorp's Opening Designations	Natera's Objections	Natera's Counter-Designations	Labcorp's Objections
29:13-16	MIS	112:20-113:11; 186:2-12; 187:10-188:6	R, 403
29:25-30:2	MIS, V, S		
30:4-5	MIS, V, S		
30:7-9			
30:11			
31:11-32:11	V		
32:13	V		
32:15-33:15		33:23-34:4	R, 403
34:5-9		34:19-21; 34:23-35:6; 35:19-36:1	R, 403
36:2-19	MIS, V		
36:21-23			
36:25-37:3		34:19-21; 34:23-35:6; 35:19-36:1	R, 403
37:16-24			
38:1			
38:3-8			
39:24-25	V, AF	22:2-8; 38:15-16; 38:18-19; 38:21-39:10; 39:12; 39:14-15; 39:17	R, 403
40:2	V, AF		
41:20-42:16	602, I, V, S	12:7-9; 12:13-22; 43:4-5; 43:7-11; 46:13-17; 46:21; 50:14-23	R, 403, BSD, PK, SPEC
42:18-19	602, I, V, S	12:7-9; 12:13-22; 43:4-5; 43:7-11; 46:13-17; 46:21; 50:14-23	R, 403, BSD, PK, SPEC
42:21-23	602, I, V, S	12:7-9; 12:13-22; 43:4-5; 43:7-11; 46:13-17; 46:21; 50:14-23	R, 403, BSD, PK, SPEC
42:25-43:2	602, I, V, S	12:7-9; 12:13-22; 43:4-5; 43:7-11; 46:13-17; 46:21; 50:14-23	R, 403, BSD, PK, SPEC
43:13-14	602, I, V, S	12:7-9; 12:13-22; 43:4-5; 43:7-11; 45:21-22; 45:24-46:4; 46:13-17; 46:21; 50:14-23	R, 403, BSD, PK, SPEC, V

Labcorp Corporation of America Holdings v. Natera, Inc. (Case No. 1:21-cv-00669-GBW)			
Witness: Banks, Eric			
Date of Desposition: 2023-04-20			
Labcorp's Opening Designations	Natera's Objections	Natera's Counter-Designations	Labcorp's Objections
43:16-44:1	602, I, V, S	12:7-9; 12:13-22; 43:4-5; 43:7-11; 45:21-22; 45:24-46:4; 46:13-17; 46:21; 50:14-23	R, 403, BSD, PK, SPEC, V
47:8-48:5		50:6-8	
52:11-13		52:14-16	
53:21-54:6			
54:10-15			
55:15-17	MIS		
55:19-20	MIS		
55:23-56:4			
56:10-12			
56:14-57:9			
57:12-15		57:16-18	BSD
57:19-22		57:16-18	
57:24-58:10			
58:19-25			
62:6-8			
62:16-63:17			
65:21-22	V, MIS	66:20-25	
65:24-66:1		66:20-25	
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70:2-19			
71:1-3			
71:5-7			
71:9-11			
71:13-14			
72:15-23			
72:25-73:3			
73:5	V		
73:7-8	V		
73:10-74:2	V		
74:4	V		
74:6-10	V, MIS		
74:12			
74:22-23	V, MIS		
75:25	V, MIS		
75:2-5	V, MIS		
75:7	V, MIS		
75:9-12	V, MIS		

Labcorp Corporation of America Holdings v. Natera, Inc. (Case No. 1:21-cv-00669-GBW)			
Witness: Banks, Eric			
Date of Desposition: 2023-04-20			
Labcorp's Opening Designations	Natera's Objections	Natera's Counter-Designations	Labcorp's Objections
75:14	V, MIS		
75:16-22	V, MIS		
75:24-25	V, MIS		
76:2-3	V, MIS		
76:5	V, MIS		
76:7-11	V, MIS		
76:17-18	V, MIS		
77:11-17	V, MIS		
77:19-23	V, MIS		
78:17-23		189:22-193:2	R, 403, BSD, L, V
79:1	I, NQP, V	78:24-25; 80:23-81:1	R, 403
79:3			
86:10-11		91:25-92:12; 92:15-17; 92:19; 96:21-25; 97:2	R, 403, BSD
86:23		91:25-92:12; 92:15-17; 92:19; 96:21-25; 97:2	R, 403, BSD
86:25-87:1		91:25-92:12; 92:15-17; 92:19; 96:21-25; 97:2	R, 403, BSD
87:4-5		91:25-92:12; 92:15-17; 92:19; 96:21-25; 97:2	R, 403, BSD
87:8-11	V	91:25-92:12; 92:15-17; 92:19; 96:21-25; 97:2	R, 403, BSD
87:13	V	91:25-92:12; 92:15-17; 92:19; 96:21-25; 97:2	R, 403, BSD
87:15-88:1	V	91:25-92:12; 92:15-17; 92:19; 96:21-25; 97:2	R, 403, BSD
88:3-4	V	91:25-92:12; 92:15-17; 92:19; 96:21-25; 97:2	R, 403, BSD
88:6-9		91:25-92:12; 92:15-17; 92:19; 96:21-25; 97:2	R, 403, BSD
88:11-12		91:25-92:12; 92:15-17; 92:19; 96:21-25; 97:2	R, 403, BSD
97:4-6			
97:10			
97:16-18	402, 403, 802		
97:24-98:3	402, 403, 802		
98:8-9	402, 403, 802		
98:11-15	402, 403, 802		
98:23-99:24		100:1-10; 189:22-193:2	BSD

Labcorp Corporation of America Holdings v. Natera, Inc. (Case No. 1:21-cv-00669-GBW)			
Witness: Banks, Eric			
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103:23-104:14	V, MIS	189:22-193:2	R, 403, BSD, L, V
104:17-21	V, MIS	189:22-193:2	R, 403, BSD, L, V
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105:9-22		106:12-16; 106:18; 189:22-193:2	R, 403, BSD, L, V,
106:20-107:3	V	189:22-193:2	R, 403, BSD, L, V
107:5		189:22-193:2	R, 403, BSD, L, V
107:7-11		189:22-193:2	R, 403, BSD, L, V
107:18-108:4	V	189:22-193:2	R, 403, BSD, L, V
108:6-8		189:22-193:2	R, 403, BSD, L, V
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109:25-110:7		109:13-18; 109:20-23; 189:22-193:2	R, 403, BSD, L, V
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119:11-12	S		
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120:3-5			
120:7-17	MIS; I	120:20-21	
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121:1-10			
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121:16	V		
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122:5-123:24	V		
125:15-126:5	MIS, AF		
126:7-11	MIS, AF		
126:13-127:13	Cmpd.		
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128:4-6			
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151:10-152:5		189:22-193:2	R, 403, BSD, L, V
152:7-153:18	MIS	189:22-193:2	R, 403, BSD, L, V
153:20	MIS	189:22-193:2	R, 403, BSD, L, V
153:22-154:16		189:22-193:2	R, 403, BSD, L, V
154:19-155:7		189:22-193:2	R, 403, BSD, L, V
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177:11	V, S		
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178:13-15		177:20-178:9; 185:15-17; 185:19-22	R, 403, PK
178:17-179:15		177:20-178:9; 185:15-17; 185:19-22	R, 403, PK
179:18-180:2	I	177:20-178:9; 180:6-11; 185:15-17; 185:19-22	R, 403, PK
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182:20-183:4		177:20-178:9; 185:15-17; 185:19-22	R, 403, PK
183:7-184:6		177:20-178:9; 185:15-17; 185:19-22	R, 403, PK
184:9-185:5	V	177:20-178:9; 185:15-17; 185:19-22	R, 403, PK
185:7	V	177:20-178:9; 185:15-17; 185:19-22	R, 403, PK
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31:17-33:4	I, 602, AF, V, HYP	26:22-27:21; 27:24-27:24; 28:2-28:2; 28:5-28:10; 28:21-28:23; 29:1-29:4; 34:14-34:19	R, 403, O, BSD, PK, V
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34:1-3	I, 602, V, HYP, S, Scope, PK, 402, 403	29:22-29:24; 30:3-30:7; 30:9-30:11; 30:14-30:16	R, 403, O, BSD, PK, V
34:6-9	NQP, 602, V, HYP, AF, S, Scope, PK, 402, 403	29:22-29:24; 30:3-30:7; 30:9-30:11; 30:14-30:16	R, 403, O, BSD, PK, V
34:11-19	NQP, 602, V, HYP, AF, I, Scope, PK, 402, 403	29:22-29:24; 30:3-30:7; 30:9-30:11; 30:14-30:16	R, 403, O, BSD, PK, V
35:5-12	602, I, AF, V, S, Scope, PK, 402, 403	29:22-29:24; 30:3-30:7; 30:9-30:11; 30:14-30:16	R, 403, O, BSD, PK, V
35:14-19	NQP, 602, I, AF, V, S, Scope, PK, 402, 403	29:22-29:24; 30:3-30:7; 30:9-30:11; 30:14-30:16	R, 403, O, BSD, PK, V
35:23-36:2	NQP, 602, I, AF, V, S, Scope, PK, 402, 403	29:22-29:24; 30:3-30:7; 30:9-30:11; 30:14-30:16	R, 403, O, BSD, PK, V
36:4-8	NQP, 602, I, AF, V, S, Scope, PK, 402, 403	29:22-29:24; 30:3-30:7; 30:9-30:11; 30:14-30:16;	R, 403, O, BSD, PK, V
36:10-20	NQP, 602, I, AF, V, S, Scope, PK, 402, 403	28:21-28:23; 29:1-4; 29:22-29:24; 30:3-30:7; 30:9-30:11; 30:14-30:16	R, 403, O, BSD, PK, V
36:23	NQP, 602, I, AF, V, S, Scope, PK, 402, 403	28:21-28:23; 29:1-4; 29:22-29:24; 30:3-30:7; 30:9-30:11; 30:14-30:16	R, 403, O, BSD, PK, V
36:25-37:2	602, I, AF, V, S, Scope, PK, 402, 403	28:21-28:23; 29:1-4; 29:22-29:24; 30:3-30:7; 30:9-30:11; 30:14-30:16	R, 403, O, BSD, PK, V
37:4-6	602, I, AF, V, S, Scope, PK, 402, 403	28:21-28:23; 29:1-4; 29:22-29:24; 30:3-30:7; 30:9-30:11; 30:14-30:16	R, 403, O, BSD, PK, V
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42:5-12	I	42:13-45:2	R, 403, BSD, PK, O
45:3	602, I, AF, V, Scope	45:23-45:24; 46:2-46:3; 46:5-46:6; 46:10-46:21; 47:14-47:19; 48:14-49:1	R, 403, NARR
45:5-9	602, I, AF, V, Scope	45:23-45:24; 46:2-46:3; 46:5-46:6; 46:10-46:21; 47:14-47:19; 48:14-49:1	R, 403, NARR
45:11-22	602, I, AF, V, Scope	45:23-45:24; 46:2-46:3; 46:5-46:6; 46:10-46:21; 47:14-47:19; 48:14-49:1	R, 403, NARR
49:2-3	602, I, AF, V, Scope	49:24-50:3; 50:11-50:13; 50:17-50:23; 52:2-52:3; 52:7-52:25; 53:8-53:10	R, 403, H
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49:10-17	602, I, AF, V, Scope	49:24-50:3; 50:11-50:13; 50:17-50:23; 52:2-52:3; 52:7-52:25; 53:8-53:10	R, 403, H
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73:2-5	602, I, AF, V	72:11-72:18; 73:6-73:9; 73:12-73:17; 75:5-75:7	R, 403, H
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91:1-3	602, I		
91:23-25	602, I		
92:3-6	602, I		
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95:19-23	602, I, V		
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186:1-3	602, V, 402, 403, I, Scope, PK	182:11-182:14; 182:24-182:25; 184:16-184:17; 184:20-185:8	R, 403, BSD
186:7-17	602, V, 402, 403, I, Scope, PK	182:11-182:14; 182:24-182:25; 184:16-184:17; 184:20-185:8	R, 403, BSD
186:19-20	602, V, 402, 403, I, Scope, PK	182:11-182:14; 182:24-182:25; 184:16-184:17; 184:20-185:8	R, 403, BSD
186:22-24	602, V, 402, 403, I, Scope, PK	182:11-182:14; 182:24-182:25; 184:16-184:17; 184:20-185:8	R, 403, BSD
187:2-4	602, V, 402, 403, I, Scope, PK	182:11-182:14; 182:24-182:25; 184:16-184:17; 184:20-185:8	R, 403, BSD
187:7-8	602, V, 402, 403, I, Scope, PK	182:11-182:14; 182:24-182:25; 184:16-184:17; 184:20-185:8	R, 403, BSD
188:7-189:8	602, V, 402, 403, I, Scope, PK, S		
191:16-192:8	602, V, I, 402, 403, AF, Scope, PK	192:11-192:20; 193:25-194:2; 194:11-194:17	R, 403, PK, BSD
192:21-193:11	602, V, I, 402, 403, AF, Scope, PK	192:11-192:20; 193:25-194:2; 194:11-194:17	R, 403, PK, BSD

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8:3-5	I, 602	7:21-8:2	R
65:16-22	I, 602, V, AF	64:12-64:14; 64:17-65:1; 65:4-65:5; 65:8-65:14	R, 403, BSD, PK, SPEC
68:23-69:3	I, 602, V, AF, 402, 403	54:2-54:5; 54:8-54:17; 54:20-54:22; 55:24-56:2; 56:5-56:18; 56:21-57:11; 57:14-57:20; 57:23-58:1; 64:12-64:14; 64:17-65:1; 65:8-65:14; 66:21-66:25; 67:3-67:17; 69:4-69:7; 69:10-69:14; 69:17; 70:4-70:7; 70:10-70:15; 70:24-71:2; 71:5-71:7	R, 403, BSD, PK, SPEC, V, O
69:19-70:3	I, 602, V, AF, 402, 403	54:2-54:5; 54:8-54:17; 54:20-54:22; 55:24-56:2; 56:5-56:18; 56:21-57:11; 57:14-57:20; 57:23-58:1; 64:12-64:14; 64:17-65:1; 65:8-65:14; 66:21-66:25; 67:3-67:17; 69:4-69:7; 69:10-69:14; 69:17; 70:4-70:7; 70:10-70:15; 70:24-71:2; 71:5-71:7	R, 403, BSD, PK, SPEC, V, O
70:17-18	I, 602, V, AF, 402, 403	54:2-54:5; 54:8-54:17; 54:20-54:22; 55:24-56:2; 56:5-56:18; 56:21-57:11; 57:14-57:20; 57:23-58:1; 64:12-64:14; 64:17-65:1; 65:8-65:14; 66:21-66:25; 67:3-67:17; 69:4-69:7; 69:10-69:14; 69:17; 70:4-70:7; 70:10-70:15; 70:24-71:2; 71:5-71:7	R, 403, BSD, PK, SPEC, V, O

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72:4-7	I, 602, V, AF, 402, 403	54:2-54:5; 54:8-54:17; 54:20-54:22; 55:24-56:2; 56:5-56:18; 56:21-57:11; 57:14-57:20; 57:23-58:1; 64:12-64:14; 64:17-65:1; 65:8-65:14; 66:21-66:25; 67:3-67:17; 69:4-69:7; 69:10-69:14; 69:17; 70:4-70:7; 70:10-70:15; 70:24-71:2; 71:5-71:7	R, 403, BSD, PK, SPEC, V, O
72:10	I, 602, V, AF, 402, 403	54:2-54:5; 54:8-54:17; 54:20-54:22; 55:24-56:2; 56:5-56:18; 56:21-57:11; 57:14-57:20; 57:23-58:1; 64:12-64:14; 64:17-65:1; 65:8-65:14; 66:21-66:25; 67:3-67:17; 69:4-69:7; 69:10-69:14; 69:17; 70:4-70:7; 70:10-70:15; 70:24-71:2; 71:5-71:7	R, 403, BSD, PK, SPEC, V, O
76:19-21	I, 602, AF, 403	77:11-77:14; 77:17-77:24	R, 403, PK, SPEC, V
76:24-77:2	I, 602, AF, 403	77:11-77:14; 77:17-77:24	R, 403, PK, SPEC, V
77:4-6	I, 602, AF, 403	77:11-77:14; 77:17-77:24	R, 403, PK, SPEC, V
77:9-10	I, 602, AF, 403	77:11-77:14; 77:17-77:24	R, 403, PK, SPEC, V
126:3-5	602, 402, 403, AF, MIS		

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126:16-19	602, 402, 403, AF, MIS		
130:17-131:1	602, 402, 403, I, AF	128:22-128:24; 129:2-129:7; 131:2-131:4; 131:7-131:25; 132:3-132:8; 132:11	R, 403, PK, SPEC, V, O
168:8-10	602, 402, 403, I, AF, V	169:9-169:11; 169:14-169:18; 171:19-171:24; 172:2-172:9; 172:12-172:17; 172:20-172:21	R, 403, PK, SPEC, V
168:13-169:1	NQP, 602, 402, 403, I, AF, V	169:9-169:11; 169:14-169:18; 171:19-171:24; 172:2-172:9; 172:12-172:17; 172:20-172:21	R, 403, PK, SPEC, V
169:19-170:22	602, 402, 403, I, AF, V, C, S	169:9-169:11; 169:14-169:18; 171:19-171:24; 172:2-172:9; 172:12-172:17; 172:20-172:21	R, 403, PK, SPEC, V
170:25-171:12	NQP, 602, 402, 403, I, AF, V, S	169:9-169:11; 169:14-169:18; 171:19-171:24; 172:2-172:9; 172:12-172:17; 172:20-172:21	R, 403, PK, SPEC, V
171:15-18	NQP, 602, 402, 403, I, AF, V	169:9-169:11; 169:14-169:18; 171:19-171:24; 172:2-172:9; 172:12-172:17; 172:20-172:21	R, 403, PK, SPEC, V
172:23-173:1	602, 402, 403, I, AF, V	173:2-173:3; 173:6-174:6; 174:17-174:19; 174:22-175:3; 175:5-173:13; 176:10-17; 177:6-177:7; 178:2-178:4; 179:5-8	R, 403, BSD, PK, SPEC, V, O, CP
174:7-8	602, 402, 403, I, AF, V	173:2-173:3; 173:6-174:6; 174:17-174:19; 174:22-175:3; 175:5-173:13; 176:10-17; 177:6-177:7; 178:2-178:4; 179:5-8	R, 403, BSD, PK, SPEC, V, O, CP

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177:11-12	602, 402, 403, I, AF, V	173:2-173:3; 173:6-174:6; 174:17-174:19; 174:22-175:3; 175:5-173:13; 176:10-17; 177:6-177:7; 178:2-178:4; 179:5-8	R, 403, BSD, PK, SPEC, V, O, CP
177:15-19	NQP, 602, 402, 403, I, AF, V	173:2-173:3; 173:6-174:6; 174:17-174:19; 174:22-175:3; 175:5-173:13; 176:10-17; 177:6-177:7; 178:2-178:4; 179:5-8	R, 403, BSD, PK, SPEC, V, O, CP
177:22-25	602, 402, 403, I, AF, V	173:2-173:3; 173:6-174:6; 174:17-174:19; 174:22-175:3; 175:5-173:13; 176:10-17; 177:6-177:7; 178:2-178:4; 179:5-8	R, 403, BSD, PK, SPEC, V, O, CP
178:5-6	602, 402, 403, I, AF, V	173:2-173:3; 173:6-174:6; 174:17-174:19; 174:22-175:3; 175:5-173:13; 176:10-17; 177:6-177:7; 178:2-178:4; 179:5-8	R, 403, BSD, PK, SPEC, V, O, CP
178:8-14	NQP, 602, 402, 403, I, AF, V	173:2-173:3; 173:6-174:6; 174:17-174:19; 174:22-175:3; 175:5-173:13; 176:10-17; 177:6-177:7; 178:2-178:4; 179:5-8	R, 403, BSD, PK, SPEC, V, O, CP
178:17-21	NQP, 602, 402, 403, I, AF, V	173:2-173:3; 173:6-174:6; 174:17-174:19; 174:22-175:3; 175:5-173:13; 176:10-17; 177:6-177:7; 178:2-178:4; 179:5-8	R, 403, BSD, PK, SPEC, V, O, CP
179:19-22	602, 402, 403, I, AF, V	173:2-173:3; 173:6-174:6; 174:17-174:19; 174:22-175:3; 175:5-173:13; 176:10-17; 177:6-177:7; 178:2-178:4; 179:5-8	R, 403, BSD, PK, SPEC, V, O, CP

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195:16-18	602, I, 402, 403, I, AF, V	196:18-196:24; 197:2-197:21	R, 403, BSD, PK, SPEC, V, O, CP
195:21-25	602, I, 402, 403, I, AF, V	196:18-196:24; 197:2-197:21	R, 403, BSD, PK, SPEC, V, O, CP
196:2-4	602, I, 402, 403, I, AF, V	196:18-196:24; 197:2-197:21	R, 403, BSD, PK, SPEC, V, O, CP
196:7-17	NQP, 602, I, 402, 403, I, AF, V	196:18-196:24; 197:2-197:21	R, 403, BSD, PK, SPEC, V, O, CP

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4:4-21	I	9:12-10:9; 10:23-11:9; 14:3-14:19	R, 403, BSD, PK, SPEC, V
11:23-12:5	I, 602, 402	10:23-11:9; 14:3-17:4; 17:7-17:12; 17:15-18:10	R, 403, BSD, PK, SPEC
12:8-13:19	I, 602, 402	10:23-11:9; 14:3-17:4; 17:7-17:12; 17:15-18:10	R, 403, BSD, PK, SPEC
18:14-19	NQP		
18:22-19:12	I, 602	9:12-10:9; 10:23-11:9; 14:3-14:15; 29:7-29:16	R, 403
19:16-20:14	I, 602, 402	10:23-11:9; 14:3-17:4; 17:7-17:12; 17:15-18:10; 18:7-10	R, 403, BSD, PK, SPEC
20:16-21:5	I, 602, 402	10:23-11:9; 14:3-17:4; 17:7-17:12; 17:15-18:10; 18:7-10	R, 403, BSD, PK, SPEC
21:17-24:1	I, 602, 402, Scope	10:23-11:9; 14:3-17:4; 17:7-17:12; 17:15-18:6	R, 403, BSD, PK, SPEC
24:6-9	I, 602, 402, Scope	10:23-11:9; 14:3-17:4; 17:7-17:12; 17:15-18:6	R, 403, BSD, PK, SPEC
27:20-24	I, 602	18:7-10; 26:6-26:16; 26:19-27:19	R
28:9-29:6	I, 602	18:7-10; 26:6-26:16; 26:19-27:19	R
31:21-24	NQP		
32:12-15	NQP		
32:22-24	I, 602	18:7-10; 29:12-29:16	
33:2-7	I, 602, AF	18:7-10; 29:12-29:16	
33:11-16	I, 602, AF	18:7-10; 29:12-29:16	
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36:1-15	I, 602, 402, 403, C	18:7-10; 29:12-29:16	
36:17-20	I, 602, AF, 402, 403, C, NBE, V	18:7-10; 29:12-29:16	
37:5	I, 602, AF, 402, 403, C, NBE, V	18:7-10; 29:12-29:16	

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38:20-22	I, 602, AF, V, Scope, 402, 403, PK	4:14-21; 9:12-10:9; 38:25-39:9	R, 403
39:13-16	602, I, V, NQP		
39:19-41:16	602, I, V, 402, 403, PK	4:14-21; 9:12-10:9; 38:25-39:9; 59:19-60:9	R, 403
41:18	602, I, V, 402, 403, PK	4:14-21; 9:12-10:9; 38:25-39:9; 59:19-60:9	R, 403
41:22-42:1	NQP, 602		
42:7-23	602, I, V, AF, LC, NBE, 402, 403, PK	18:7-10; 30:8-14	
43:4	602, I, V, AF, LC, NBE, 402, 403, PK	18:7-10; 30:8-14	
43:8-46:7	602, I, V, AF, LC, Scope, 402, 403, NBE, PK	18:7-10; 30:8-14	
46:20-47:18	602, I, V, AF, LC, Scope, 402, 403, NBE, PK	18:7-10; 30:8-14	
47:23-24	602, I, V, AF, LC, Scope, 402, 403, NBE, PK	18:7-10; 30:8-14	
48:23-49:1	NQP, 602		
49:7-51:6	602, I, V, AF, 402, 403, Scope, NBE		
51:12-19	602, I, V, AF, 402, 403, Scope		
52:3-14	602, I, V, AF, 402, 403, Scope		
52:16-18	602, I, V, AF, 402, 403, Scope		
53:9-54:5	602, I, V, 402, 403, Scope, AF		

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59:19-60:13	602, V, AF		
60:16	602, V, AF		
60:21-61:13	602, V, AF, MIS, 402, 403		
61:16-62:17	602, V, AF, MIS, 402, I, 403	62:18-62:23	R, 403, PK, SPEC, V
62:24-63:9	602, V, AF, MIS, 402, I, 403	62:18-62:23	R, 403, PK, SPEC, V
63:17-64:6	602, V, AF, MIS, 402, I, 403	62:18-62:23	R, 403, PK, SPEC, V
64:12-15	602, V, AF, MIS, 402, I, 403	62:18-62:23	R, 403, PK, SPEC, V
64:18-66:15	602, V, AF, MIS, 402, I, 403	62:18-62:23	R, 403, PK, SPEC, V
66:17-68:15	602, V, AF, MIS, 402, I, 403, Scope	62:18-62:23	R, 403, PK, SPEC, V
68:25-69:9	602, V, AF, MIS, 402, I, 403, Scope	62:18-62:23	R, 403, BSD, PK, SPEC, V
71:1-9	602, V, AF, MIS, 402, I, NQP, 403, Scope	62:18-62:23; 69:10-23	R, 403, BSD, PK, SPEC, V
72:12-:73:3	602, V, AF, MIS, 402, I, 403, Scope	62:18-62:23; 69:10-23	R, 403, BSD, PK, SPEC, V
73:7-13	602, V, AF, MIS, 402, I, Scope, 403	62:18-62:23; 69:10-23	R, 403, BSD, PK, SPEC, V
73:16-19	602, V, AF, MIS, 402, I, 403, Scope	62:18-62:23; 69:10-23	R, 403, BSD, PK, SPEC, V
73:22-74:2	602, V, AF, MIS, 402, I, 403, Scope	62:18-62:23; 69:10-23	R, 403, BSD, PK, SPEC, V
75:21-24	NQP, 602		
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78:15-19	I, 602, NQP, C, 402, 403	79:8-25; 82:24-83:6; 115:2-116:6	R, 403, BSD, PK, SPEC, V, O
79:20-80:4	I, 602, PK, 402, 403	79:8-25; 82:24-83:6; 115:2-116:6	R, 403, BSD, PK, SPEC, V, O
83:4-8	I, 602, AF	79:8-25; 82:24-83:6; 115:2-116:6	R, 403, BSD, PK, SPEC, V, O
83:11-12	I, 602, AF	79:8-25; 82:24-83:6; 115:2-116:6	R, 403, BSD, PK, SPEC, V, O
83:14-20	I, 602, AF, NQP	79:8-25; 82:24-83:6; 115:2-116:6	R, 403, BSD, PK, SPEC, V, O
84:8-17	I, 602	79:8-25; 82:24-83:6; 115:2-116:6	R, 403, BSD, PK, SPEC, V, O
85:10-13	NQP, 602		
85:19-87:9	I, 602, AF, Scope, V, 402, 403	91:22-92:21	R, 403, PK, SPEC
87:12-16	I, 602, AF, Scope, V, 402, 403	91:22-92:21	R, 403, PK, SPEC
87:19-22	I, 602, AF, Scope, V, 402, 403	91:22-92:21	R, 403, PK, SPEC
87:25-88:5	I, 602, AF, Scope, V, 402, 403	91:22-92:21	R, 403, PK, SPEC
88:12-90:1	I, 602, AF, Scope, V, 402, 403	91:22-92:21	R, 403, PK, SPEC
90:4-5	I, 602, AF, Scope, V, 402, 403	91:22-92:21	R, 403, PK, SPEC

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91:17-21	I, 602, AF, Scope, V, 402, 403, NBE	91:22-92:21	R, 403, PK, SPEC
96:2-23	I, 602, AF, Scope, V	96:24-97:1	
97:2-4	I, 602, AF, Scope, V	96:24-97:1	
97:7-15	I, 602, AF, Scope, V	96:24-97:1	
98:23-99:2	NQP, 602		
99:8-15	I, 602, AF, 403, NS	100:22-100:25; 103:16-104:1; 104:5-104:6; 106:12-106:20; 106:24-107:3; 107:5-107:13	R, 403, BSD, PK, SPEC
99:22-25	I, 602, AF, C, 403, NS	100:22-100:25; 103:16-104:1; 104:5-104:6; 106:12-106:20; 106:24-107:3; 107:5-107:13	R, 403, BSD, PK, SPEC
100:2-21	I, 602, AF, Scope	100:22-100:25; 103:16-104:1; 104:5-104:6; 106:12-106:20; 106:24-107:3; 107:5-107:13	R, 403, BSD, PK, SPEC
101:1-102:8	I, 602, AF, Scope	100:22-100:25; 103:16-104:1; 104:5-104:6; 106:12-106:20; 106:24-107:3; 107:5-107:13; 109:2-110:15; 116:8-116:20	R, 403, PK, SPEC, V
102:11-103:11	I, 602, AF, Scope	100:22-100:25; 103:16-104:1; 104:5-104:6; 106:12-106:20; 106:24-107:3; 107:5-107:13; 109:2-110:15; 116:8-116:20	R, 403, PK, SPEC, V

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181:12-182:2	602, I, V, AF, 402, 402, 403, AF	179:18-181:11; 175:18-176:10; 176:13-176:20; 176:22-177:10; 177:14-177:15; 177:17-177:24; 178:2-178:21; 178:24-179:7; 179:18-181:11; 182:6-182:12; 182:15-184:1; 185:1-186:10; 186:13-186:14	BSD, R, I, PK, 403
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202:17-20	NQP, I, V, AF, 602, 402, 403	194:24-195:15; 195:17-195:20; 195:24-196:13; 195:17-195:20; 196:15; 196:18-196:24; 197:2-197:11; 197:14-197:14	BSD, R, 403, PK, SPEC
202:23-203:17	I, V, AF, 602, 402, 403	194:24-195:15; 195:17-195:20; 195:24-196:13; 195:17-195:20; 196:15; 196:18-196:24; 197:2-197:11; 197:14-197:14	BSD, R, 403, PK, SPEC
203:20-23	I, V, AF, 602,402, 403	194:24-195:15; 195:17-195:20; 195:24-196:13; 195:17-195:20; 196:15; 196:18-196:24; 197:2-197:11; 197:14-197:14	BSD, R, 403, PK, SPEC
204:22-205:2	I, V, AF, 602, 402, 403	194:24-195:15; 195:17-195:20; 195:24-196:13; 195:17-195:20; 196:15; 196:18-196:24; 197:2-197:11; 197:14-197:14	BSD, R, 403, PK, SPEC
205:4	I, V, AF, 602, NQP, 402, 403	194:24-195:15; 195:17-195:20; 195:24-196:13; 195:17-195:20; 196:15; 196:18-196:24; 197:2-197:11; 197:14-197:14	BSD, R, 403, PK, SPEC
205:7-16	I, V, AF, 602, NQP, 402, 403	194:24-195:15; 195:17-195:20; 195:24-196:13; 195:17-195:20; 196:15; 196:18-196:24; 197:2-197:11; 197:14-197:14	BSD, R, 403, PK, SPEC

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208:23-209:14	602, I, V, AF, 402, 403	205:17-207:20; 208:2-4; 214:6-217:8; 219:3-219:5; 219:8-219:10; 219:13-219:16; 219:18-219:23; 219:25-219:25; 220:3-220:19; 220:25-222:12; 222:15-223:6; 223:9-225:24	BSD, R, 403, PK, SPEC, H
209:17	602, I, V, AF, 402, 403	205:17-207:20; 208:2-4; 214:6-217:8; 219:3-219:5; 219:8-219:10; 219:13-219:16; 219:18-219:23; 219:25-219:25; 220:3-220:19; 220:25-222:12; 222:15-223:6; 223:9-225:24	BSD, R, 403, PK, SPEC, H
213:12-214:5	602, I, V, AF, 402, 403	205:17-207:20; 208:2-4; 214:6-217:8; 219:3-219:5; 219:8-219:10; 219:13-219:16; 219:18-219:23; 219:25-219:25; 220:3-220:19; 220:25-222:12; 222:15-223:6; 223:9-225:24	BSD, R, 403, PK, SPEC, H

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217:14-219:2	602, I, V, AF, 402, 403	205:17-207:20; 208:2-4; 214:6-217:8; 219:3-219:5; 219:8-219:10; 219:13-219:16; 219:18-219:23; 219:25-219:25; 220:3-220:19; 220:25-222:12; 222:15-223:6; 223:9-225:24	BSD, R, 403, PK, SPEC, H
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247:10-11	NQP, I, 602	247:6-247:8; 247:12-247:15; 247:19-247:25; 249:10-249:19	
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25:24	Scope, I	26:4-27:10	
26:1-3	Scope		
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28:18-31:11	Scope, I, AF	26:4-27:10; 27:18-27:21; 27:25-28:17; 31:12-31:21	BSD, PK
31:24-32:2	Scope, I, AF, S, PK	32:4-32:7; 32:9-32:15	BSD, PK
32:16-21	Scope, I, AF, S, PK	32:4-32:7; 32:9-32:15;	BSD, PK
32:23-25	Scope, I, AF, S, PK	32:4-32:7; 32:9-32:15;	BSD, PK
33:1-21	Scope, I, AF, S, PK	32:4-32:7; 32:9-32:15;	BSD, PK
33:24	NQP		
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34:25-36:11	Scope, LC		
37:2-7	Scope, LC, I, AF, S, PK	32:4-32:7; 32:9-32:15; 38:12-38:24; 39:5-39:8; 39:10-39:14	BSD, PK, AA
37:9-10	Scope, LC, I, AF	32:4-32:7; 32:9-32:15; 38:12-38:24; 39:5-39:8; 39:10-39:14	BSD, PK, AA

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37:14-15	Scope, LC, I, AF	32:4-32:7; 32:9-32:15; 38:12-38:24; 39:5-39:8; 39:10-39:14	BSD, PK, AA
37:17-20	Scope, LC, I, AF, S, HYP, PK	32:4-32:7; 32:9-32:15; 38:12-38:24; 39:5-39:8; 39:10-39:14	BSD, PK, AA
37:22	Scope, LC, I, AF, S, HYP, PK	32:4-32:7; 32:9-32:15; 38:12-38:24; 39:5-39:8; 39:10-39:14	BSD, PK, AA
37:24	Scope, LC, I, AF, S, HYP	32:4-32:7; 32:9-32:15; 38:12-38:24; 39:5-39:8; 39:10-39:14	BSD, PK, AA
38:1-11	Scope, LC, I, AF, S, HYP	32:4-32:7; 32:9-32:15; 39:5-39:8; 39:10-39:14	BSD, PK, AA
39:15-20	Scope, LC, I, AF, S, HYP	32:4-32:7; 32:9-32:15; 39:5-39:8; 39:10-39:14	BSD, PK, AA
40:7-13	Scope, LC, I, AF, S, HYP	32:4-32:7; 32:9-32:15; 39:5-39:8; 39:10-39:14	BSD, PK, AA
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42:11-43:2	I, V, AF, Scope	41:6-41:17	BSD
43:12-13	I, V, AF, Scope, 402	41:6-41:17	BSD
43:15-17	I, V, AF, Scope, 402	41:6-41:17	BSD
43:19-20	I, V, AF, Scope, 402	41:6-41:17	BSD
43:22	I, V, AF, Scope, 402	41:6-41:17	BSD
43:24-44:8	I, V, AF, Scope, 402	41:6-41:17	BSD
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50:20-51:4	I		
51:7-10	I		
51:12-15	I		
52:5-7	I	51:17-52:2	OB
53:2-11	I		
53:14-17	I		
53:20-21	I		
53:23-54:7	I, 402, 403, MIS		
54:9-11	I, 402, 403, MIS		
55:3-10	I		
55:12-17	I		
57:9-14	I, V, 402, 403, MIS, Scope	60:10-60:18	BSD
57:21-25	I, V, 402, 403, MIS, Scope	60:10-60:18	BSD
58:1-2	I, V, 402, 403, MIS, Scope	60:10-60:18	BSD
58:12-16	I, V, A&A, 402, 403, Scope	60:10-60:18	BSD
58:18	I, V, 402, 403, MIS, Scope	60:10-60:18	BSD
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58:24	I, V, A&A, 402, 403, Scope	60:10-60:18	BSD
59:1-3	I, V, A&A, 402, 403, Scope	60:10-60:18	BSD
59:5-6	I, V, A&A, 402, 403, Scope	60:10-60:18	BSD
59:8-12	I, V, A&A, 402, 403, Scope	60:10-60:18	BSD
59:14-15	I, V, A&A, 402, 403, Scope	60:10-60:18	BSD
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63:19-23	I, V, A&A, 402, 403, Scope	60:10-60:18; 61:25-62:2; 65:13-66:14	
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65:5-11	I, V, A&A, 402, 403, Scope	60:10-60:18; 61:25-62:2; 65:13-66:14	
66:16-25	I, V, A&A, 402, 403, Scope	60:10-60:18; 61:25-62:2; 65:13-66:14	
67:2-6	I, V, A&A, 402, 403, Scope	60:10-60:18; 61:25-62:2; 65:13-66:14	
67:8-9	I	14:6-14:19	BSD
67:11-14	NQP, Scope, PK		
67:19-69:3	602, AF, LC, MIS, I, S, HYP, Scope, PK	69:6-69:8; 69:10-69:10; 69:12-71:10; 71:18-72:11; 72:13-72:17	BSD, PK
69:5	602, AF, LC, MIS, I, S, HY, Scope, PK	69:6-69:8; 69:10-69:10; 69:12-71:10; 71:18-72:11; 72:13-72:17	BSD, PK
71:11-17	602, AF, LC, MIS, I, S, HYP, Scope, PK	69:6-69:8; 69:10-69:10; 69:12-71:10; 71:18-72:11; 72:13-72:17	BSD, PK
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73:15-17	I, 602, LC, Scope, PK	73:1-73:2; 75:3-75:22; 76:7-76:12; 76:14-78:17; 78:19-78:20	BSD, PK
73:19-74:1	I, 602, LC, Scope, PK	73:1-73:2; 75:3-75:22; 76:7-76:12; 76:14-78:17; 78:19-78:20	BSD, PK

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74:23-75:2	I, 602, LC, Scope	73:1-73:2; 74:9-11; 74:21-22; 76:7-76:12; 76:14-78:17; 78:19-78:20	BSD, PK
75:23-76:6	I, 602, LC, Scope, PK	73:1-73:2; 75:3-75:22; 76:7-76:12; 76:14-78:17; 78:19-78:20	BSD, PK
78:21	NQP		
78:23-80:1	602, V, PK		
80:8-19	602, I, A&A, 402, 403	80:21-81:3; 81:24-82:5; 82:7-82:7	BSD, I, PK
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86:10-14	602, I, LC, Scope, 402, 403	81:24-82:5; 82:7-82:7	BSD, I, PK
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94:10-23	602, I	107:5-108:22; 108:24-109:5	BSD
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133:5-8	I, 602, AF, MIS	132:20-133:4; 136:5-136:9; 136:11-136:21; 137:14-138:12; 138:14-139:10	BSD
133:10-12	I, 602, AF, MIS	132:20-133:4; 136:5-136:9; 136:11-136:21; 137:14-138:12; 138:14-139:10	BSD
133:18-134:13	I, 602, AF, MIS	132:20-133:4; 136:5-136:9; 136:11-136:21; 137:14-138:12; 138:14-139:10	BSD
134:22-135:2	I, 602, AF, MIS	132:20-133:4; 136:5-136:9; 136:11-136:21; 137:14-138:12; 138:14-139:10	BSD
135:10-16	I, 602, AF, MIS	132:20-133:4; 136:5-136:9; 136:11-136:21; 137:14-138:12; 138:14-139:10	BSD
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135:23-136:4	I, 602, AF, MIS	132:20-133:4; 136:5-136:9; 136:11-136:21; 137:14-138:12; 138:14-139:10	BSD
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155:22-156:11	602, I	155:3-155:4; 155:6-155:7	BSD
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13:11-12			
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13:24	Cmpd., MIS	13:13-14; 13:16-19	
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23:19-24:1		23:17-18; 24:11-17; 26:24-28:7; 28:19-29:8	R, 403, BSD
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31:3	V	30:16-18; 30:20-24; 31:4-12; 31:14-15; 32:3-24; 33:3-6; 33:16-34:1	R, 403, BSD, PK
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44:2-23	602, V, S		
44:24-45:16	602, V, S		
45:22-23			
45:25-47:15			
48:2-18	MIS		
48:20-25	MIS		
49:2-22	MIS, S		
49:24-50:9	MIS, S		
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82:22	MIS	112:19-113:23; 113:25-116:6; 116:8-116:24; 117:2-4; 117:8-21; 117:23-25; 118:2-13; 118:17-119:17; 119:19-120:5; 120:7-17; 120:20-121:1; 121:3-16	R, 403, BTS, BSD, PK, SPEC

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122:4-13	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 120:21-23; 122:14-15; 122:17-18; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
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124:16-125:8	403, 602, 701, MIS, I	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 123:4-5; 123:7; 124:6-7; 124:9-11; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
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126:22-24	403, 602, 701, MIS, NBE, Cmpd.	36:3-5; 40:13-41:4; 41:6; 49:11-15; 46:9-11; 48:25-49:1; 49:3; 49:5-9; 106:3-4; 106:6; 123:4-5; 123:7; 124:6-7; 124:9-11; 128:12-15; 128:17-18; 128:21-22; 156:11-24; 157:1; 157:2-17; 157:19-21; 157:23-159:6; 159:8-13; 159:15-24; 160:5-7; 160:9-12; 160:14-17; 160:19-21; 160:23-25; 161:2-4; 161:6-8; 161:10-19; 161:21-162:17; 162:19-163:1; 166:20-25; 167:2-6	R, 403, MIS, O V, H, BSD, PK
127:1-128:3	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 128:12-15; 128:17-18; 128:21-22; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
128:5-8	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 128:12-15; 128:17-18; 128:21-22; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
128:10-11	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 128:12-15; 128:17-18; 128:21-22; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
128:23-129:2	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 128:12-15; 128:17-18; 128:21-22; 129:9-10; 129:12; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK

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129:4-6	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 128:12-15; 128:17-18; 128:21-22; 129:9-10; 129:12; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
129:8	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 128:12-15; 128:17-18; 128:21-22; 129:9-10; 129:12; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
129:18-20	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 129:9-10; 129:12; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
129:22-130:1	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 129:9-10; 129:12; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
130:3-5	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 128:12-15; 128:17-18; 128:21-22; 129:9-10; 129:12; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
130:7-9		36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 128:12-15; 128:17-18; 128:21-22; 129:9-10; 129:12; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
130:11-131:3	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 128:12-15; 128:17-18; 128:21-22; 129:9-10; 129:12; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK

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131:13-18	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 128:12-15; 128:17-18; 128:21-22; 129:9-10; 129:12; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
131:20-132:9	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 128:12-15; 128:17-18; 128:21-22; 129:9-10; 129:12; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
132:15	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 132:16-17; 132:19-20; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
132:21-133:1	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 132:16-17; 132:19-20; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
133:3	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 132:16-17; 132:19-20; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
133:8-10	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 132:16-17; 132:19-20; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK

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133:17-22	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 132:16-17; 132:19-20; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
133:24-134:4	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 132:16-17; 132:19-20; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
134:6-8	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 132:16-17; 132:19-20; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
134:10-14	403, 602, 701, MIS	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 132:16-17; 132:19-20; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
134:16-22	802	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
134:24	802	36:3-5; 40:13-41:4; 41:6; 106:3-4; 106:6; 161:11-19; 161:21-162:17; 162:19-163:1	R, 403, MIS, O V, H, BSD, PK
135:2-8	403, 602, 701, MIS		
135:10-20	403, 602, 701, I, MIS	135:22-24	R, 403
136:7-8	403, 602, 701, I, MIS	135:22-24	R, 403

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137:9-11	403, 602, 701, MIS, V	136:9-12; 136:14-16	R, 403
137:13-16	403, 602, 701, MIS, V, Cmpd.	136:9-12; 136:14-16	R, 403
137:18	403, 602, 701, MIS, V, Cmpd.	136:9-12; 136:14-16	R, 403
137:20-23		136:9-12; 136:14-16	R, 403
137:25-138:3	802	136:9-12; 136:14-16	R, 403
138:5-7	802	136:9-12; 136:14-16	R, 403
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144:5-7		144:8-9; 144:11-14; 144:16-17	R, 403
145:4-6	Cmpd.		
145:8-10			
145:12-15			
145:17-18			
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146:6-7			
154:23-25			
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163:8-23		105:3-4; 105:6; 164:14; 164:16-19; 164:21; 164:23-25	R, 403, MIS, O V, H, BSD, PK
164:9-13		105:3-4; 105:6; 164:14; 164:16-19; 164:21; 164:23-25	R, 403, MIS, O V, H, BSD, PK

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165:20-25		46:9-11; 48:25-49:1; 49:3; 49:5-9; 49:11-15; 156:11-24; 157:1; 157:2-17; 157:19-21; 157:23-159:6; 159:8-13; 159:15-24; 160:5-7; 160:9-12; 160:14-17; 160:19-21; 160:23-25; 161:2-4; 161:6-8; 161:10; 166:20-25; 167:2-6	R, 403, MIS, O V, H, BSD, PK
167:20-25	403, 602, 701, MIS, V, I, NBE	46:9-11; 48:25-49:1; 49:3; 49:5-9; 49:11-15; 156:11-24; 157:1; 157:2-17; 157:19-21; 157:23-159:6; 159:8-13; 159:15-24; 160:5-7; 160:9-12; 160:14-17; 160:19-21; 160:23-25; 161:2-4; 161:6-8; 161:10; 166:20-25; 167:2-6; 168:1-2; 168:4	R, 403, MIS, O V, H, BSD, PK
168:5-11		46:9-11; 48:25-49:1; 49:3; 49:5-9; 49:11-15; 156:11-24; 157:1; 157:2-17; 157:19-21; 157:23-159:6; 159:8-13; 159:15-24; 160:5-7; 160:9-12; 160:14-17; 160:19-21; 160:23-25; 161:2-4; 161:6-8; 161:10; 166:20-25; 167:2-6; 168:1-2; 168:4; 168:12-13; 168:15	R, 403, MIS, O V, H, BSD, PK

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168:16-24	403, 602, 701, MIS, V, I	46:9-11; 48:25-49:1; 49:3; 49:5-9; 49:11-15; 156:11-24; 157:1; 157:2-17; 157:19-21; 157:23-159:6; 159:8-13; 159:15-24; 160:5-7; 160:9-12; 160:14-17; 160:19-21; 160:23-25; 161:2-4; 161:6-8; 161:10; 166:20-25; 167:2-6; 168:1-2; 168:4; 168:12-13; 168:15; 169:6-8	R, 403, MIS, O V, H, BSD, PK
169:1-3	403, 602, 701, MIS, V, I	46:9-11; 48:25-49:1; 49:3; 49:5-9; 49:11-15; 156:11-24; 157:1; 157:2-17; 157:19-21; 157:23-159:6; 159:8-13; 159:15-24; 160:5-7; 160:9-12; 160:14-17; 160:19-21; 160:23-25; 161:2-4; 161:6-8; 161:10; 166:20-25; 167:2-6; 168:1-2; 168:4; 168:12-13; 168:15; 169:6-8	R, 403, MIS, O V, H, BSD, PK
169:5	403, 602, 701, MIS, V, I	46:9-11; 48:25-49:1; 49:3; 49:5-9; 49:11-15; 156:11-24; 157:1; 157:2-17; 157:19-21; 157:23-159:6; 159:8-13; 159:15-24; 160:5-7; 160:9-12; 160:14-17; 160:19-21; 160:23-25; 161:2-4; 161:6-8; 161:10; 166:20-25; 167:2-6; 168:1-2; 168:4; 168:12-13; 168:15; 169:6-8	R, 403, MIS, O V, H, BSD, PK
169:22-170:3	403, 602, 701, MIS, V, I		
170:5-8	403, 602, 701, MIS, V, I, S, Cmpd.		

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170:10-14	403, 602, 701, MIS, V, I, S, Cmpd.		
170:16-23	403, 602, 701, MIS, V, I, S		
170:25-171:7	403, 602, 701, MIS, V, I, S		
171:19	403, 602, 701, MIS, V, I, S		
171:21	403, 602, 701, MIS, V, I, S		
171:23	403, 602, 701, MIS, V, I, S		

EXHIBIT 9

AA	Asked and answered; Fed. R. Evid. 611(a).
ARG	Argumentative, or attorney argument; Fed. R. Evid. 611(a).
BTS	Beyond the scope of examination or of 30(b)(6) topic; Fed R. Evid. 611, Fed. R. Civ. P. 30(b)(6).
BSD	Counter-Designation Beyond the Scope of the Designation(s).
CP	Compound question.
F	No foundation or assumes facts not in evidence; Fed. R. Evid. 602, 703, 901.
FOW	An objection to form is waived if it was not timely made during the deposition, Fed. R. Civ. P. 32(d)(3)(B).
H	Hearsay if offered for the truth of the matter asserted; Fed. R. Evid. 801, 803, 805.
I	Incomplete designation; Fed. R. Evid. 106, 403.
IH	Incomplete Hypothetical.
L	Leading; Fed. R. Evid. 611(c).
LC	Calls for Legal Conclusion; Fed. R. Evid. 701.
LW	Witness will be testifying live at trial.
MIL	Subject to motion in limine
MIS	Mischaracterization of testimony or evidence.
NARR	Narrative.
NR	Not responsive; Fed. R. Evid. 611(a).
O	Unqualified Opinion; Calls for improper expert opinion from lay witness; Fed. R. Evid. 701, 702.
OB	Attorney Objection improperly designated/Improper designation.
P	Privileged; Fed. R. Evid. 501, Fed. R. Civ. P. 26(b)(3),(4).
PK	Lack of personal knowledge; Fed. R. Evid. 602.
R	Not relevant; Fed. R. Evid. 401, 402.
SPEC	Calls for Speculation; Fed. R. Evid. 602, 701, 702.
403	Unfairly prejudicial; cumulative, waste of time, Fed. R. Evid. 403.
V	Vague or ambiguous; Fed. R. Evid. 611(a).

AA	Asked and answered; Fed. R. Evid. 611(a).
ARG	Argumentative, or attorney argument; Fed. R. Evid. 611(a).
BTS	Beyond the scope of examination or of 30(b)(6) topic; Fed R. Evid. 611, Fed. R. Civ. P. 30(b)(6).
BSD	Counter-Designation Beyond the Scope of the Designation(s).
CP	Compound question.
F	No foundation or assumes facts not in evidence; Fed. R. Evid. 602, 703, 901.
FOW	An objection to form is waived if it was not timely made during the deposition, Fed. R. Civ. P. 32(d)(3)(B).
H	Hearsay if offered for the truth of the matter asserted; Fed. R. Evid. 801, 803, 805.
I	Incomplete designation; Fed. R. Evid. 106, 403.
IH	Incomplete Hypothetical.
L	Leading; Fed. R. Evid. 611(c).
LC	Calls for Legal Conclusion; Fed. R. Evid. 701.
LW	Witness will be testifying live at trial.
MIL	Subject to motion in limine.
MIS	Mischaracterization of testimony or evidence.
NARR	Narrative.
NR	Not responsive; Fed. R. Evid. 611(a).
O	Unqualified Opinion; Calls for improper expert opinion from lay witness; Fed. R. Evid. 701, 702.
OB	Attorney Objection improperly designated/Improper designation.
P	Privileged; Fed. R. Evid. 501, Fed. R. Civ. P. 26(b)(3),(4).
PK	Lack of personal knowledge; Fed. R. Evid. 602.
R	Not relevant; Fed. R. Evid. 401, 402.
SPEC	Calls for Speculation; Fed. R. Evid. 602, 701, 702.
403	Unfairly prejudicial; cumulative, waste of time, Fed. R. Evid. 403.
V	Vague or ambiguous; Fed. R. Evid. 611(a).

Freivogel, Mary
#: 12980

Witness	Natera Designations	Labcorp Objections	Labcorp Counter-Designations	Natera Objections
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Freivogel, Mary	008:13-009:25	R, 403, SPEC, PK, O, F		
Freivogel, Mary	010:02-010:09	R, 403, SPEC, PK, O, F		
Freivogel, Mary	010:11-010:25	R, 403, SPEC, PK, O, CP, V, F		
Freivogel, Mary	011:03-011:08	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	011:10-011:13	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	011:15-011:21	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	011:23-015:18	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	015:20-016:08	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	016:16-016:18	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	016:20-016:24	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	017:02-017:10	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	017:17-018:03	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	018:05-019:05	R, 403, SPEC, PK, O, F, V, MIS		
Freivogel, Mary	019:07-019:14	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	019:16-019:19	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	019:21-020:03	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	020:15-020:23	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	020:25-021:12	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	021:14-021:22	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	021:24-022:05	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	022:07-022:16	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	022:19-022:23	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	022:25-023:02	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	023:04-023:10	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	023:12-023:17	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	023:24-024:02	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	024:04-026:20	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	026:22-027:08	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	027:10-027:12	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	027:20-027:22	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	027:24-028:01	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	028:06-029:22	R, 403, SPEC, PK, O, F, V		
Freivogel, Mary	029:24-032:15	R, 403, SPEC, PK, O, F, V		
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Freivogel, Mary	034:03-035:01	R, 403, SPEC, PK, F, V		
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Freivogel, Mary	038:11-042:03	R, 403, SPEC, PK, V		
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Freivogel, Mary	045:20-046:22	R, 403, SPEC, V, PK	46:23-47:14	H
Freivogel, Mary	047:22-048:16	R, 403, SPEC, V, PK, F	46:23-47:14	H
Freivogel, Mary	048:18-049:25	R, 403, SPEC, V, PK, F	46:23-47:14; 51:15-17; 51:25-52:07; 52:09-20	BSD, H
Freivogel, Mary	050:02-050:06	R, 403, SPEC, V, PK, F, CP	46:23-47:14; 51:15-17; 51:25-52:07; 52:09-20	BSD, H
Freivogel, Mary	050:08-050:14	R, 403, SPEC, V, PK, F, CP	46:23-47:14; 51:15-17; 51:25-52:07; 52:09-20	BSD, H
Freivogel, Mary	050:16-050:23	R, 403, SPEC, V, PK, F, CP	46:23-47:14; 51:15-17; 51:25-52:07; 52:09-20	BSD, H
Freivogel, Mary	053:03-053:05	R, 403, SPEC, V, PK, F	53:24-54:1; 54:03-06; 54:10-12; 54:14-18	BSD, H
Freivogel, Mary	053:08-053:23	R, 403, SPEC, V, PK, F	53:24-54:1; 54:03-06; 54:10-12; 54:14-18	BSD, H
Freivogel, Mary	054:19-055:14	R, 403, SPEC, V, PK, F	53:24-54:1; 54:03-06; 54:10-12; 54:14-18	BSD, H
Freivogel, Mary	055:22-056:09	R, 403, V, SPEC, PK, F		
Freivogel, Mary	056:11-056:15	R, 403, V, SPEC, PK, F		
Freivogel, Mary	056:17-057:12	R, 403, SPEC, PK, F, V		
Freivogel, Mary	057:14-057:25	R, 403, SPEC, PK, F, V, I		

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Freivogel, Mary	058:02-058:03	R, 403, SPEC, PK, F, V, I		
Freivogel, Mary	058:05-058:10	R, 403, SPEC, PK, F, V		
Freivogel, Mary	058:12-059:20	R, 403, SPEC, PK, F, V		
Freivogel, Mary	059:22-059:22	R, 403, SPEC, PK, F, V		
Freivogel, Mary	059:24-059:25	R, 403, SPEC, PK, F, V, I		
Freivogel, Mary	060:02-060:04	R, 403, SPEC, PK, F, V, I		
Freivogel, Mary	060:10-061:04	R, 403, SPEC, PK, F, V		
Freivogel, Mary	061:06-062:09	R, 403, SPEC, PK, F, V		

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Lusk, Richard	008:07-009:19			
Lusk, Richard	011:10-011:13			
Lusk, Richard	011:20-012:17			
Lusk, Richard	012:20-013:24	CP, 403		
Lusk, Richard	014:02-014:05			
Lusk, Richard	015:24-017:06			
Lusk, Richard	018:07-018:11			
Lusk, Richard	019:05-019:09			
Lusk, Richard	020:05-021:15	I, R, 403	19:19-22	H, I, MIS, R, 403
Lusk, Richard	023:10-025:24	NARR	19:19-22; 127:23-128:16	BSD, H, I, MIS, R, L, 403
Lusk, Richard	026:05-026:18	NARR, CP	19:19-22; 127:23-128:16	BSD, H, I, MIS, R, L, 403
Lusk, Richard	026:20-027:09		19:19-22; 127:23-128:16	BSD, H, I, MIS, R, L, 403
Lusk, Richard	030:17-032:16			
Lusk, Richard	033:07-034:09	CP,V, R, 403		
Lusk, Richard	034:12-036:24	CP, V, R, 403		
Lusk, Richard	037:02-037:17	SPEC, PK V, R, 403		
Lusk, Richard	037:19-038:15	CP, I, MIS, NARR, PK, SPEC, PK V, R, 403		
Lusk, Richard	038:18-038:22	CP, I, MIS, NARR, PK, SPEC, PK V, R, 403		
Lusk, Richard	038:24-040:22	Withdrawn, BTS, CP, MIS, NARR, PK, SPEC, PK V, R, 403		
Lusk, Richard	041:07-041:13	BTS, MIS, NARR, R, 403, V		
Lusk, Richard	041:19-042:17	BTS, MIS, NARR, R, 403, V		
Lusk, Richard	042:19-045:10	F, MIS, NARR, SPEC, PK V, R, 403		
Lusk, Richard	045:12-045:14	MIS, NARR, SPEC, PK PK V, R, 403		
Lusk, Richard	045:22-047:03	MIS, NARR, V, R, 403	127:23-128:16	BSD, H, L
Lusk, Richard	047:10-049:10	MIS, NARR, SPEC, PK PK, V, R, 403	50:9-10; 127:23-128:16	BSD, H, L, I, V
Lusk, Richard	049:14-050:08	MIS, NARR, SPEC, PK PK, V, R, 403	50:9-10	
Lusk, Richard	050:11-050:14			
Lusk, Richard	051:14-054:23			
Lusk, Richard	055:07-059:21	MIS, NARR, SPEC, PK PK, V, R, 403	126:18-127:22	BSD, H, L
Lusk, Richard	059:23-061:02	MIS, NARR, SPEC, PK PK, V, R, 403	126:18-127:22	BSD, H, L
Lusk, Richard	061:04-061:16	MIS, NARR, SPEC, PK PK V, R, 403	126:18-127:22	BSD, H, L
Lusk, Richard	061:18-063:19	MIS, NARR, SPEC, PK PK, V, R, 403	126:18-127:22	BSD, H, L
Lusk, Richard	063:21-064:10	MIS, NARR, SPEC, PK PK, V, R, 403		
Lusk, Richard	064:12-065:05	MIS, NARR, SPEC, PK PK, V, R, 403		
Lusk, Richard	065:07-065:20	MIS, NARR, SPEC, PK PK, V, R, 403		
Lusk, Richard	065:22-066:02	MIS, NARR, SPEC, PK PK, V, R, 403		
Lusk, Richard	066:11-068:05	V		
Lusk, Richard	068:08-068:13			
Lusk, Richard	069:10-071:10	MIS, NARR, OB, SPEC, PK PK, V, R, 403	71:11-13	
Lusk, Richard	071:14-071:18		71:11-13	
Lusk, Richard	071:24-074:22	SPEC, PK PK, V, R, 403		
Lusk, Richard	074:24-075:12	SPEC, PK PK, V		
Lusk, Richard	078:06-079:06	SPEC, PK PK V, R, 403		
Lusk, Richard	079:08-079:20	SPEC, PK PK V, R, 403		
Lusk, Richard	079:22-080:04	SPEC, PK PK V, R, 403		
Lusk, Richard	080:06-081:12	SPEC, PK V, R, 403		
Lusk, Richard	081:20-081:22	OB, SPEC, PK V, R, 403		
Lusk, Richard	081:23-082:18	SPEC, PK V, R, 403		
Lusk, Richard	082:20-084:09	SPEC, PK V, R, 403		
Lusk, Richard	084:24-086:15			
Lusk, Richard	087:05-087:06	SPEC, PK V, R, 403	86:16-21	BSD, H
Lusk, Richard	087:08-087:19	SPEC, PK V, R, 403	86:16-21	BSD, H
Lusk, Richard	087:21-088:04	SPEC, PK V, R, 403	86:16-21	BSD, H
Lusk, Richard	088:06-088:24	SPEC, PK V, R, 403	86:16-21	BSD, H
Lusk, Richard	089:14-093:15	SPEC, PK V, R, 403		
Lusk, Richard	093:17-094:03	SPEC, PK V, R, 403		
Lusk, Richard	094:05-096:09	BTS, F, SPEC, PK V, R, 403		
Lusk, Richard	096:11-105:03	BTS, MIS, NARR, OB, R, 403, SPEC, PK V	106:17-20; 106:22-23; 106:25-107:7	BSD, H
Lusk, Richard	105:05-105:10	MIS, NARR, OB, R, 403, SPEC, PK V	106:17-20; 106:22-23; 106:25-107:7	BSD, H
Lusk, Richard	105:12-106:03	MIS, NARR, R, 403, SPEC, PK V	106:17-20; 106:22-23; 106:25-107:7	BSD, H
Lusk, Richard	106:05-106:06	BTS, V, R, 403	106:17-20; 106:22-23; 106:25-107:7	BSD, H
Lusk, Richard	107:08-107:11		106:17-20; 106:22-23; 106:25-107:7	BSD, H
Lusk, Richard	108:17-108:21			
Lusk, Richard	109:04-114:24	SPEC, PK V, R, 403		
Lusk, Richard	115:02-115:22	AA, SPEC, PK V, R, 403		
Lusk, Richard	116:02-119:10	AA, SPEC, PK V, R, 403		
Lusk, Richard	119:12-120:02	SPEC, PK V, R, 403, MIL		
Lusk, Richard	120:19-121:07	SPEC, PK V, R, 403, MIL		
Lusk, Richard	121:09-121:16	SPEC, PK V, R, 403, MIL		
Lusk, Richard	121:18-121:21	SPEC, PK V, R, 403, MIL		
Lusk, Richard	121:23-122:05	SPEC, PK V, R, 403, MIL		

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Lusk, Richard	122:16-123:03	SPEC, PK, V, R, 403, MIL		
Lusk, Richard	123:05-124:03	BTS, SPEC, PK V, R, 403, MIL		
Lusk, Richard	124:06-124:13	BTS, SPEC, PK V, R, 403, MIL		
Lusk, Richard	124:15-124:19	BTS, SPEC, PK V, R, 403, MIL		
Lusk, Richard	124:21-124:21	BTS, SPEC, PK V, R, 403, MIL		

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Malani, Nirav	006:12-008:02			
Malani, Nirav	010:07-013:15	R, 403		
Malani, Nirav	024:12-024:22			
Malani, Nirav	026:20-027:02			
Malani, Nirav	027:16-027:19	AA, V, R, 403		
Malani, Nirav	027:21-028:12	AA, V, R, 403		
Malani, Nirav	028:19-029:06			
Malani, Nirav	029:20-030:23			
Malani, Nirav	034:06-034:08	V, R, 403		
Malani, Nirav	034:12-036:05	MIS, NARR, V, R, 403		
Malani, Nirav	036:09-037:13	MIS, NARR, V, R, 403		
Malani, Nirav	037:16-037:19			
Malani, Nirav	038:14-038:19			
Malani, Nirav	044:14-044:15	F, V, R, 403		
Malani, Nirav	044:17-045:18	F, MIS, V, R, 403		
Malani, Nirav	045:20-046:06	F, V, R, 403		
Malani, Nirav	046:09-046:20	F, V, R, 403		
Malani, Nirav	054:18-055:16	R, 403		
Malani, Nirav	058:18-059:11	V, R, 403	64:21-67:21	BSD, H, 403
Malani, Nirav	059:18-060:03	O, PK, SPEC, V, R, 403	64:21-67:21	BSD, H, 403
Malani, Nirav	060:05-060:15	O, PK, SPEC, V, R, 403	64:21-67:21	BSD, H, 403
Malani, Nirav	061:12-061:17	MIS, SPEC, V, R, 403	64:21-67:21	BSD, H, 403
Malani, Nirav	061:19-063:05	MIS, SPEC, V, R, 403	64:21-67:21	BSD, H, 403
Malani, Nirav	063:14-063:19	F, V, R, 403	64:21-67:21	BSD, H, 403
Malani, Nirav	063:21-064:12	V, R, 403	64:21-67:21	BSD, H, 403
Malani, Nirav	069:05-069:11	CP, MIS, SPEC, V, R, 403		
Malani, Nirav	069:13-069:22	CP, MIS, SPEC, V, R, 403		
Malani, Nirav	070:14-070:18	CP, MIS, NARR, V, R, PK, 403		
Malani, Nirav	070:20-070:25	CP, MIS, NARR, V, R, PK, SPEC, 403		
Malani, Nirav	071:24-072:05	OB, CP, MIS, NARR, V, PK, R, 403		
Malani, Nirav	072:24-073:24	CP, MIS, NARR, R, 403, SPEC, V		
Malani, Nirav	074:02-074:14	O, CP, MIS, NARR, R, 403, SPEC, V		
Malani, Nirav	074:17-074:22	O, MIS, NARR, R, 403, SPEC, V		
Malani, Nirav	074:24-074:24	O, MIS, NARR, R, 403, SPEC, V		
Malani, Nirav	083:05-088:21	R, 403, V		
Malani, Nirav	088:23-089:11			
Malani, Nirav	090:25-092:08		92:9-93:15	H
Malani, Nirav	097:04-098:08	R, 403, V, PK	92:9-93:15	
Malani, Nirav	098:13-098:17	R, 403, V, PK	92:9-93:15	BSD, H
Malani, Nirav	099:08-099:13	R, 403, V, PK	92:9-93:15	BSD, H
Malani, Nirav	099:16-102:16	R, 403, V, PK	92:9-93:15	BSD, H
Malani, Nirav	105:03-108:18	R, 403, V, PK	92:9-93:15	BSD, H
Malani, Nirav	109:07-109:18	R, 403, V, PK, CP		
Malani, Nirav	112:08-112:15	R, 403, V, PK	109:25-111:10	BSD, H
Malani, Nirav	113:23-115:04	R, 403, V		
Malani, Nirav	126:03-126:14	R, 403, V, PK	121:3-5; 121:7-122:14; 124:10-128:2.	BSD, H, 403
Malani, Nirav	127:22-127:25			
Malani, Nirav	128:19-129:23			
Malani, Nirav	133:24-134:23	MIS, V, R, 403		
Malani, Nirav	134:25-136:13	MIS, V, R, 403		
Malani, Nirav	139:24-141:10	R, 403, V, PK, SPEC		
Malani, Nirav	142:03-142:06	MIS, NARR, SPEC, V, R, 403		
Malani, Nirav	142:08-142:12	MIS, NARR, SPEC, V, R, 403		
Malani, Nirav	144:25-145:11	R, 403, V, PK		
Malani, Nirav	148:02-148:08	R, 403, V, PK		
Malani, Nirav	149:18-149:21	MIS, NARR, SPEC, V, R, 403		
Malani, Nirav	159:13-161:07	MIS, NARR, SPEC, V, R, 403		
Malani, Nirav	162:17-162:18	F, MIS, SPEC, V, R, 403	161:8-23; 161:25-162:16; 183:22-25; 184:3-6	BSD, H, 403
Malani, Nirav	162:20-163:06	F, MIS, SPEC, V, R, 403	161:8-23; 161:25-162:16; 183:22-25; 184:3-6	BSD, H, 403
Malani, Nirav	163:08-163:09	F, MIS, SPEC, V, R, 403	161:8-23; 161:25-162:16; 183:22-25; 184:3-6	BSD, H, 403
Malani, Nirav	164:16-165:11	MIS, NARR, SPEC, V, R, 403, LC, O		
Malani, Nirav	165:13-166:06	MIS, NARR, SPEC, V, R, 403, LC, O		
Malani, Nirav	166:08-166:11	MIS, NARR, SPEC, V, R, 403, LC, O		
Malani, Nirav	167:06-167:08	MIS, NARR, SPEC, V, R, 403, LC, O		
Malani, Nirav	167:10-167:11	MIS, NARR, SPEC, V, R, 403, LC, O		

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Malani, Nirav	170:24-172:08			
Malani, Nirav	175:08-175:12			
Malani, Nirav	175:15-175:17			
Malani, Nirav	175:19-175:23			
Malani, Nirav	199:21-199:24	BTS, SPEC, PK, V, R, 403		
Malani, Nirav	200:03-200:10	BTS, SPEC, PK, V, R, 403		
Malani, Nirav	200:12-200:24	BTS, SPEC, PK, V, R, 403		
Malani, Nirav	201:03-201:10	BTS, SPEC, PK, V, R, 403		
Malani, Nirav	201:19-202:04	BTS, SPEC, PK, LC, O, V, R, 403		
Malani, Nirav	202:06-202:23	SPEC, V, R, 403, LC, O		
Malani, Nirav	202:25-203:12	SPEC, V, R, 403		
Malani, Nirav	203:14-204:10	O, SPEC, V, R, 403		
Malani, Nirav	204:13-204:19	O, SPEC, V, R, 403		
Malani, Nirav	204:22-205:13	O, SPEC, V, R, 403		
Malani, Nirav	205:15-206:08	O, SPEC, V, R, 403		
Malani, Nirav	207:04-207:07			
Malani, Nirav	207:14-207:16			
Malani, Nirav	209:05-209:07	NARR, PK, R, 403		
Malani, Nirav	209:09-209:09	NARR, PK, R, 403		
Malani, Nirav	212:10-212:20			
Malani, Nirav	212:25-213:04	LC, O, NARR, R, 403		
Malani, Nirav	213:06-213:25	LC, O, NARR, R, 403		
Malani, Nirav	220:22-220:25			
Malani, Nirav	221:08-221:19			
Malani, Nirav	222:10-222:12			
Malani, Nirav	222:15-222:18	O, SPEC, V, R, 403		
Malani, Nirav	222:21-223:06	O, SPEC, V, R, 403		
Malani, Nirav	223:10-223:14	I, O, SPEC, V, R, 403		
Malani, Nirav	223:16-223:18	I, O, SPEC, V, R, 403		
Malani, Nirav	223:21-234:04	OB, AA, ARG, CP, F, I, LC, MIS, NARR, O, R, SPEC, 403, V		
Malani, Nirav	225:12-225:15	O, SPEC, V, R, 403		
Malani, Nirav	225:18-225:25	O, SPEC, V, R, 403		
Malani, Nirav	226:20-226:22	O, SPEC, V, R, 403		
Malani, Nirav	226:25-227:02	O, SPEC, V, R, 403		
Malani, Nirav	234:12-234:14			
Malani, Nirav	234:22-236:08	O, PK, SPEC, V, R, 403		
Malani, Nirav	236:10-236:11	O, PK, SPEC, V, R, 403		
Malani, Nirav	236:20-236:22	I, OB, R, 403		
Malani, Nirav	237:04-237:15	PK, SPEC, V, R, 403		
Malani, Nirav	237:17-237:21	PK, SPEC, V, R, 403		
Malani, Nirav	237:23-238:13	PK, SPEC, V, R, 403		
Malani, Nirav	238:15-238:21	PK, SPEC, V, R, 403		
Malani, Nirav	238:23-238:23	PK, SPEC, V, R, 403		
Malani, Nirav	238:25-239:04			
Malani, Nirav	239:11-240:25	F, NARR, SPEC, V, R, 403		
Malani, Nirav	241:03-241:22	F, NARR, SPEC, V, R, 403	183:22-25; 184:3-6	H, BSD
Malani, Nirav	241:24-242:06	F, NARR, SPEC, V, R, 403	183:22-25; 184:3-6	H, BSD
Malani, Nirav	242:14-242:24			
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Malani, Nirav	248:21-249:13	NARR, SPEC, V, R, 403		
Malani, Nirav	249:15-249:20	NARR, SPEC, V, R, 403		
Malani, Nirav	249:22-250:10	NARR, SPEC, V, R, 403		
Malani, Nirav	250:12-250:21	NARR, SPEC, V, R, 403		
Malani, Nirav	269:19-269:21			
Malani, Nirav	270:05-270:06	R, 403, V, PK		

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Masukawa, Kevin	013:13-013:20			
Masukawa, Kevin	014:10-014:12			
Masukawa, Kevin	014:14-014:19			
Masukawa, Kevin	015:11-016:10			
Masukawa, Kevin	018:06-019:05	R, 403		
Masukawa, Kevin	021:04-022:14	R, 403		
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Masukawa, Kevin	030:21-031:01			
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Masukawa, Kevin	032:13-032:16		32:25-33:10	F, I
Masukawa, Kevin	032:22-032:24		32:25-33:10	F, I
Masukawa, Kevin	034:24-025:02			
Masukawa, Kevin	035:09-035:10		49:4-6; 49:9-19	MIS, F, I
Masukawa, Kevin	035:12-036:02		49:4-6; 49:9-19	MIS, F, I
Masukawa, Kevin	036:12-041:09	403, R	49:4-6; 49:9-19	MIS, F, I
Masukawa, Kevin	041:14-041:15			
Masukawa, Kevin	041:17-041:18			
Masukawa, Kevin	042:04-042:19			
Masukawa, Kevin	042:22-043:09			
Masukawa, Kevin	043:12-043:14			
Masukawa, Kevin	044:06-044:17			
Masukawa, Kevin	044:199-044:22			
Masukawa, Kevin	046:02-046:13			
Masukawa, Kevin	047:12-047:14			
Masukawa, Kevin	047:17-047:25			
Masukawa, Kevin	053:22-053:24		52:17-25; 53:3-18; 55:13-16	BSD, F, I, SPEC, V
Masukawa, Kevin	054:08-054:13		52:17-25; 53:3-18; 55:13-16	BSD, F, I, SPEC, V
Masukawa, Kevin	054:22-055:03		52:17-25; 53:3-18; 55:13-16	BSD, F, I, SPEC, V
Masukawa, Kevin	056:05-056:07		55:13-16	BSD, F, I, SPEC, V
Masukawa, Kevin	057:08-057:15		57:21-23; 59:9-15	BSD, F, I, V
Masukawa, Kevin	058:03-058:07		57:21-23; 59:9-15	BSD, F, I, V
Masukawa, Kevin	061:05-061:15	R, 403, V, SPEC	62:14-16; 62:19-20	BSD, F, I, V
Masukawa, Kevin	063:14-063:21		63:5-13	
Masukawa, Kevin	064:04-064:16		65:23-66:17	F, R, V
Masukawa, Kevin	064:21-065:16		65:23-66:17	BSD, F, R, V
Masukawa, Kevin	065:18-065:22		65:23-66:17	BSD, F, R, V
Masukawa, Kevin	068:23-069:04		68:4-7	BSD, F, R, V
Masukawa, Kevin	069:23-070:14			
Masukawa, Kevin	070:17-071:10		71:11-13; 71:15-24	BSD, F, I, R, V
Masukawa, Kevin	071:25-072:02			
Masukawa, Kevin	072:05-072:25			
Masukawa, Kevin	073:03-073:04			
Masukawa, Kevin	073:07-073:17			
Masukawa, Kevin	075:18-076:02		76:3-14; 77:10-12	BTS, BSD, F, I, SPEC, V
Masukawa, Kevin	076:15-077:09	O	76:3-14; 77:10-12	BTS, BSD, F, I, SPEC, V
Masukawa, Kevin	078:02-079:02		79:3-5; 79:7-13; 80:8-10; 80:19-81:13; 81:15-22	BTS, BSD, F, I, R, SPEC, V
Masukawa, Kevin	079:14-080:07	O, PK, SPEC	79:3-5; 79:7-13; 80:8-10; 80:19-81:13; 81:15-22	BTS, BSD, F, I, R, SPEC, V
Masukawa, Kevin	080:11-080:13		79:3-5; 79:7-13; 80:8-10; 80:19-81:13; 81:15-22	BTS, BSD, F, I, R, SPEC, V
Masukawa, Kevin	080:16-080:18		79:3-5; 79:7-13; 80:8-10; 80:19-81:13; 81:15-22	BTS, BSD, F, I, R, SPEC, V
Masukawa, Kevin	082:11-083:09			
Masukawa, Kevin	083:15-083:23	O	83:24-25; 84:3-7; 84:18-85:5; 85:11-86:10; 87:2-25	BTS, BSD, F, I, R, SPEC, 403, V
Masukawa, Kevin	084:08-084:17	O	83:24-25; 84:3-7; 84:18-85:5; 85:11-86:10; 87:2-25	BTS, BSD, F, I, R, SPEC, 403, V
Masukawa, Kevin	085:06-085:07		83:24-25; 84:3-7; 84:18-85:5; 85:11-86:10; 87:2-25	BTS, BSD, F, I, R, SPEC, 403, V
Masukawa, Kevin	085:10-085:10		83:24-25; 84:3-7; 84:18-85:5; 85:11-86:10; 87:2-25	BTS, BSD, F, I, R, SPEC, 403, V
Masukawa, Kevin	086:11-086:14		83:24-25; 84:3-7; 84:18-85:5; 85:11-86:10; 87:2-25	BTS, BSD, F, I, R, SPEC, 403, V
Masukawa, Kevin	086:17-087:01		83:24-25; 84:3-7; 84:18-85:5; 85:11-86:10; 87:2-25	BTS, BSD, F, I, R, SPEC, 403, V
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Masukawa, Kevin	089:16-090:09			
Masukawa, Kevin	090:11-091:15	R, 403	91:16-21; 92:1-2; 92:5	BTS, BSD, F, I, R, 403, V
Masukawa, Kevin	092:12-092:18	PK, SPEC	91:16-21; 92:1-2; 92:5	BTS, BSD, F, I, R, 403, V
Masukawa, Kevin	092:21-093:04		94:4-95:3; 96:8-17	BSD, F, I, R, 403, V
Masukawa, Kevin	093:07-093:22		94:4-95:3; 96:8-17	BSD, F, I, R, 403, V
Masukawa, Kevin	095:04-096:07	PK, SPEC	94:4-95:3; 96:8-17	BSD, F, I, R, 403, V

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Masukawa, Kevin	103:24-104:14	PK, SPEC, O	101:18-21; 102:10-103:16; 103:19-23	BSD, F, I, MIS, SPEC, V
Masukawa, Kevin	116:08-116:11			
Masukawa, Kevin	116:18-116:20		117:3-13; 118:11-15	BSD, F, I
Masukawa, Kevin	116:22-117:02		117:3-13; 118:11-15	BSD, F, I
Masukawa, Kevin	117:14-117:18		117:3-13; 118:11-15	BSD, F, I
Masukawa, Kevin	118:23-118:23	I		
Masukawa, Kevin	119:03-119:19		120:5-121:10; 121:15-19	BSD, F, I
Masukawa, Kevin	121:11-121:14		120:5-121:10; 121:15-19; 123:15-16; 123:21-124:10	BSD, AA, F, I, V
Masukawa, Kevin	121:21-122:14		120:5-121:10; 121:15-19; 123:15-16; 123:21-124:10	BSD, AA, F, I, V
Masukawa, Kevin	122:17-122:19		120:5-121:10; 121:15-19; 123:15-16; 123:21-124:10	BSD, AA, F, I, V
Masukawa, Kevin	130:24-131:03		129:19-23; 129:25-130:18; 130:24-131:5; 131:9-17; 131:19-20	BSD, F, MIS, SPEC, V
Masukawa, Kevin	137:17-137:22			
Masukawa, Kevin	138:06-138:07		138:19-21; 138:24-139:3; 139:11-13; 139:20-24; 139:25-140:15	BSD, F, R, SPEC
Masukawa, Kevin	138:09-138:18		138:19-21; 138:24-139:3; 139:11-13; 139:20-24; 139:25-140:15	BSD, F, R, SPEC
Masukawa, Kevin	143:16-143:23			
Masukawa, Kevin	143:23-144:14			
Masukawa, Kevin	145:15-145:18			
Masukawa, Kevin	146:01-146:12		146:13-147:03	BSD, F, I
Masukawa, Kevin	148:23-023:25	SPEC, PK, O	148:16-18; 148:21-22	BSD, F, I
Masukawa, Kevin	149:03-150:11	SPEC, PK, O, F	148:16-18; 148:21-22	BSD, F, I
Masukawa, Kevin	150:14-153:03	SPEC, PK, O, F		
Masukawa, Kevin	153:05-153:08		153:16-22; 154:1-6; 154:10-14; 154:18-155:11; 155:14-15	BSD, BTS, F, I, MIS, R, SPEC
Masukawa, Kevin	153:12-153:15		153:16-22; 154:1-6; 154:10-14; 154:18-155:11; 155:14-15	BSD, BTS, F, I, MIS, R, SPEC
Masukawa, Kevin	156:12-157:21			
Masukawa, Kevin	157:23-158:02			
Masukawa, Kevin	159:23-161:09	R, 403		
Masukawa, Kevin	161:12-165:03	R, 403		
Masukawa, Kevin	165:06-165:19	R, 403		

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Moyal, Hila	009:24-011:02			
Moyal, Hila	011:06-012:13			
Moyal, Hila	012:20-014:03			
Moyal, Hila	014:07-016:18	R, 403, BTS, PK, SPEC	249:2-251:7	BSD, H, L
Moyal, Hila	017:05-018:20	R, 403, BTS, PK, SPEC	249:2-251:7	BSD, H, L
Moyal, Hila	019:14-020:18	R, 403, V	249:2-251:7	BSD, H, L
Moyal, Hila	022:02-024:14	R, 403, BTS, PK, SPEC	249:2-251:7	BSD, H, L
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Moyal, Hila	025:25-027:01	R, 403, BTS, PK, SPEC	249:2-251:7	BSD, H, L
Moyal, Hila	027:03-027:10	R, 403, BTS, PK, SPEC	249:2-251:7	BSD, H, L
Moyal, Hila	027:12-030:08	R, 403, BTS, PK, SPEC	249:2-251:7	BSD, H, L
Moyal, Hila	030:11-031:10	R, 403, BTS, PK, SPEC		
Moyal, Hila	032:10-032:21	R, 403, BTS, PK, SPEC, F	249:2-251:7	BSD, H, L
Moyal, Hila	032:23-032:24	R, 403, BTS, PK, SPEC, F	249:2-251:7	BSD, H, L
Moyal, Hila	033:01-033:17	R, 403, BTS, PK, SPEC, F		
Moyal, Hila	033:19-034:16	R, 403, BTS, PK, SPEC, F		
Moyal, Hila	036:09-038:04	R, 403, BTS, PK, SPEC, F		
Moyal, Hila	038:05-038:18	R, 403, BTS, PK, SPEC		
Moyal, Hila	038:20-040:18	R, 403, BTS, PK, SPEC		
Moyal, Hila	042:05-043:04	R, 403, BTS, PK, SPEC		
Moyal, Hila	043:15-044:05	R, 403, BTS, PK, SPEC		
Moyal, Hila	044:07-045:15	R, 403, BTS, PK, SPEC		
Moyal, Hila	045:18-047:01	R, 403, BTS, PK, SPEC, NARR		
Moyal, Hila	047:03-047:05	R, 403, BTS, PK, SPEC, NARR		
Moyal, Hila	047:12-047:15	R, 403, BTS, PK, SPEC, NARR		
Moyal, Hila	047:17-048:18	R, 403, BTS, PK, SPEC, NARR		
Moyal, Hila	048:20-049:13	R, 403, BTS, PK, SPEC, NARR, AA, V, CP		
Moyal, Hila	049:16-049:25	R, 403, I		
Moyal, Hila	050:08-051:07	R, 403, BTS, PK, SPEC		
Moyal, Hila	051:10-052:01	R, 403, BTS, PK, SPEC		
Moyal, Hila	052:03-052:12	R, 403, BTS, PK, SPEC		
Moyal, Hila	052:14-053:05	R, 403, BTS, PK, SPEC		
Moyal, Hila	053:07-053:11	R, 403, BTS, PK, SPEC		
Moyal, Hila	053:13-054:24	R, 403, BTS, PK, SPEC		
Moyal, Hila	055:23-056:17	R, 403, BTS, PK, SPEC, F		
Moyal, Hila	056:19-057:07	R, 403, BTS, PK, SPEC, F, AA		
Moyal, Hila	057:10-057:23	R, 403, BTS, PK, SPEC, F, AA		
Moyal, Hila	057:25-058:15	R, 403, BTS, PK, SPEC, F, AA		
Moyal, Hila	058:18-059:01	R, 403, BTS, PK, SPEC, F, AA		
Moyal, Hila	059:03-059:03	R, 403, BTS, PK, SPEC, F, AA		
Moyal, Hila	060:01-061:10	R, 403, I		
Moyal, Hila	061:13-062:10			
Moyal, Hila	062:12-063:09			
Moyal, Hila	063:22-064:17			
Moyal, Hila	064:19-066:24	R, 403, BTS, PK, SPEC, O, F, V		
Moyal, Hila	067:01-067:12	R, 403, BTS, PK, SPEC, O, F, V		
Moyal, Hila	067:14-068:24	I		
Moyal, Hila	069:01-069:02	I		
Moyal, Hila	069:07-069:14			
Moyal, Hila	069:20-072:25	R, 403, BTS, PK, SPEC, V		
Moyal, Hila	073:02-075:10	R, 403, BTS, PK, SPEC, V, I		
Moyal, Hila	075:15-075:16	R, 403, BTS, PK, SPEC, V, F		
Moyal, Hila	075:18-075:21	R, 403, BTS, PK, SPEC, V, F		
Moyal, Hila	075:23-077:08	R, 403, BTS, PK, SPEC, V, F		
Moyal, Hila	077:10-077:19	R, 403, BTS, PK, SPEC, V, F		
Moyal, Hila	078:10-078:18	R, 403, BTS, PK, SPEC, V, F, I		
Moyal, Hila	079:07-079:24	R, 403, BTS, PK, SPEC, I		
Moyal, Hila	080:15-081:05	R, 403, BTS, PK, SPEC		
Moyal, Hila	081:21-081:23	R, 403, BTS, V, AA		
Moyal, Hila	081:25-083:17	R, 403, BTS, V, AA		
Moyal, Hila	083:22-086:03	R, 403, BTS, V, PK, SPEC		
Moyal, Hila	086:06-086:14	R, 403, BTS, V, PK, SPEC	45:18-46:14; 249:2-251:7	BSD, H, L
Moyal, Hila	086:16-086:16	R, 403, BTS, V, PK, SPEC, NARR	45:18-46:14; 249:2-251:7	BSD, H, L
Moyal, Hila	087:01-089:11	R, 403, BTS, V, PK, SPEC, NARR	249:2-251:7	BSD, H, L
Moyal, Hila	089:19-091:13	R, 403, BTS, V, PK, SPEC	249:2-251:7	BSD, H, L
Moyal, Hila	091:15-093:04	R, 403, BTS, V, PK, SPEC	249:2-251:7	BSD, H, L

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Moyal, Hila	093:22-095:02	R, 403, BTS, V, PK, SPEC, MIS	249:2-251:7	BSD, H, L
Moyal, Hila	095:04-097:08	R, 403, BTS, V, PK, SPEC, MIS	249:2-251:7	BSD, H, L
Moyal, Hila	097:16-098:10			
Moyal, Hila	098:17-098:24			
Moyal, Hila	099:07-100:10	I		
Moyal, Hila	100:13-100:22	R, 403, BTS, V, PK, SPEC		
Moyal, Hila	100:24-101:09	R, 403, BTS, V, PK, SPEC		
Moyal, Hila	101:16-101:23	R, 403, BTS, V, PK, SPEC, NARR		
Moyal, Hila	101:25-102:14	R, 403, BTS, V, PK, SPEC, NARR		
Moyal, Hila	102:16-102:17	R, 403, BTS, V, PK, SPEC, NARR		
Moyal, Hila	102:19-103:10	R, 403, BTS, V, PK, SPEC, NARR		
Moyal, Hila	103:12-103:16	R, 403, BTS, V, PK, SPEC, NARR		
Moyal, Hila	103:19-104:03	R, 403, BTS, V, PK, SPEC, NARR		
Moyal, Hila	104:05-104:07	R, 403, BTS, V, PK, SPEC, NARR		
Moyal, Hila	104:11-106:06	R, 403, V, CP		
Moyal, Hila	106:08-106:15	R, 403, V, CP		
Moyal, Hila	107:02-107:19			
Moyal, Hila	107:21-108:20	R, 403, AA		
Moyal, Hila	109:21-110:22	R, 403, BTS, PK, SPEC		
Moyal, Hila	112:16-112:23			
Moyal, Hila	112:25-113:18			
Moyal, Hila	114:11-115:03	R, 403, BTS, PK, SPEC, NARR, CP		
Moyal, Hila	115:05-116:03	R, 403, BTS, PK, SPEC, NARR, CP		
Moyal, Hila	116:06-116:23	R, 403, BTS, PK, SPEC		
Moyal, Hila	116:25-117:15	R, 403, BTS, PK, SPEC		
Moyal, Hila	117:17-118:20	R, 403, BTS, PK, SPEC		
Moyal, Hila	118:22-119:03	R, 403, BTS, PK, SPEC		
Moyal, Hila	119:05-119:05	R, 403, BTS, PK, SPEC, CP		
Moyal, Hila	119:17-121:01	R, 403, BTS, PK, SPEC, CP		
Moyal, Hila	121:03-122:15	R, 403, BTS, PK, SPEC		
Moyal, Hila	123:05-123:09			
Moyal, Hila	123:13-125:09			
Moyal, Hila	125:11-125:21			
Moyal, Hila	126:03-129:11			
Moyal, Hila	129:20-131:03	R, 403, BTS, PK, SPEC, V		
Moyal, Hila	131:05-131:24	R, 403, BTS, PK, SPEC, V	249:2-251:7	BSD, H, L
Moyal, Hila	132:17-137:19	R, 403, BTS, PK, SPEC, V	249:2-251:7	BSD, H, L
Moyal, Hila	137:23-140:09		249:2-251:7	BSD, H, L
Moyal, Hila	141:01-142:06			
Moyal, Hila	142:10-143:13		249:2-251:7	BSD, H, L
Moyal, Hila	143:17-144:05		249:2-251:7	BSD, H, L
Moyal, Hila	144:08-144:11		249:2-251:7	BSD, H, L
Moyal, Hila	144:13-146:07		249:2-251:7	BSD, H, L
Moyal, Hila	146:09-146:15		249:2-251:7	BSD, H, L
Moyal, Hila	146:21-147:16	R, 403, BTS, PK, SPEC, V	249:2-251:7	BSD, H, L
Moyal, Hila	150:01-151:13	R, 403, BTS, PK, SPEC, V, CP		
Moyal, Hila	151:15-151:17	R, 403, BTS, PK, SPEC, V, CP		
Moyal, Hila	152:05-153:09			
Moyal, Hila	153:19-154:24	R, 403, BTS, PK, SPEC, V, CP, NARR		
Moyal, Hila	155:01-155:17	R, 403, BTS, PK, SPEC, V, CP, NARR		
Moyal, Hila	155:24-156:12			
Moyal, Hila	157:05-157:18			
Moyal, Hila	157:23-158:07			
Moyal, Hila	158:09-158:13	R, 403, BTS, PK, SPEC, V, CP	249:2-251:7	BSD, H, L
Moyal, Hila	158:16-161:20	R, 403, BTS, PK, SPEC, V, CP	249:2-251:7	BSD, H, L
Moyal, Hila	161:23-162:23		249:2-251:7	BSD, H, L
Moyal, Hila	164:01-165:17		249:2-251:7	BSD, H, L
Moyal, Hila	165:19-166:15	R, 403, BTS, PK, SPEC, V, MIS	249:2-251:7	BSD, H, L
Moyal, Hila	166:17-167:06	R, 403, BTS, PK, SPEC, V, MIS	249:2-251:7	BSD, H, L
Moyal, Hila	167:14-172:08		249:2-251:7	BSD, H, L
Moyal, Hila	172:23-173:04		249:2-251:7	BSD, H, L
Moyal, Hila	173:08-173:16		249:2-251:7	BSD, H, L
Moyal, Hila	173:19-173:24	403, MIS, V	174:25-175:2; 175:4-176:18; 176:20-25; 249:2-251:7	BSD, H, L, NR
Moyal, Hila	174:08-174:24	R, 403, BTS, PK, SPEC, MIS	174:25-175:2; 175:4-176:18; 176:20-25; 249:2-251:7	BSD, H, L, NR
Moyal, Hila	177:04-177:15	R, 403, BTS, PK, SPEC, MIS	174:25-175:2; 175:4-176:18; 176:20-25; 249:2-251:7	BSD, H, L, NR
Moyal, Hila	177:17-177:17	R, 403, BTS, PK, SPEC, MIS	174:25-175:2; 175:4-176:18; 176:20-25; 249:2-251:7	BSD, H, L, NR
Moyal, Hila	177:23-178:11	R, 403, BTS, PK, SPEC, MIS	174:25-175:2; 175:4-176:18; 176:20-25; 249:2-251:7	BSD, H, L, NR

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Moyal, Hila	179:10-179:22	R, 403, BTS, PK, SPEC, MIS	174:25-175:2; 175:4-176:18; 176:20-25; 249:2-251:7	BSD, H, L, NR
Moyal, Hila	180:06-180:25	I		
Moyal, Hila	181:02-183:15		249:2-251:7	BSD, H, L
Moyal, Hila	183:23-188:11		249:2-251:7	BSD, H, L
Moyal, Hila	189:13-191:25	I		
Moyal, Hila	192:03-192:13			
Moyal, Hila	192:16-195:12		249:2-251:7	BSD, H, L
Moyal, Hila	196:02-197:25	I, ARG, MIS, SPEC, R, 403	249:2-251:7	BSD, H, L
Moyal, Hila	198:14-199:01		249:2-251:7	BSD, H, L
Moyal, Hila	199:12-200:10			
Moyal, Hila	200:13-201:02			
Moyal, Hila	201:12-203:12	R, 403, BTS, PK, SPEC	249:2-251:7	BSD, H, L
Moyal, Hila	203:13-203:16	R, 403, BTS, PK, SPEC, AA	249:2-251:7	BSD, H, L
Moyal, Hila	203:20-204:03	R, 403, BTS, PK, SPEC	249:2-251:7	BSD, H, L
Moyal, Hila	204:05-204:15	R, 403, BTS, PK, SPEC, ARG	249:2-251:7	BSD, H, L
Moyal, Hila	205:05-206:06	R, 403, BTS, PK, SPEC, IH, MIS	249:2-251:7	BSD, H, L
Moyal, Hila	206:13-207:05	R, 403, BTS, PK, SPEC, V, IH	249:2-251:7	BSD, H, L
Moyal, Hila	207:07-207:12	R, 403, BTS, PK, SPEC, V		
Moyal, Hila	207:14-207:23	R, 403, BTS, PK, SPEC, V		
Moyal, Hila	208:01-208:08	R, 403, BTS, PK, SPEC, V		
Moyal, Hila	208:10-209:01			
Moyal, Hila	209:19-210:19	R, 403, BTS, SPEC, MIS, V, AA		
Moyal, Hila	211:15-214:01			
Moyal, Hila	214:11-217:13			
Moyal, Hila	217:16-218:07	R, 403, BTS, PK, SPEC, V		
Moyal, Hila	218:09-218:19	R, 403, BTS, PK, SPEC, V		
Moyal, Hila	218:23-219:06	R, 403, BTS, PK, SPEC, V, MIS, AA		
Moyal, Hila	219:08-223:22		249:2-251:7	BSD, H, L
Moyal, Hila	223:24-228:17	R, 403, BTS, PK, SPEC, V, MIS	249:2-251:7	BSD, H, L
Moyal, Hila	228:19-229:08	R, 403, BTS, PK, SPEC, V, MIS, P		
Moyal, Hila	230:01-230:05			
Moyal, Hila	230:12-230:19			
Moyal, Hila	231:06-233:13		249:2-251:7	BSD, H, L
Moyal, Hila	234:06-237:09	R, 403, BTS, PK, SPEC, V	249:2-251:7	BSD, H, L
Moyal, Hila	237:17-238:08	R, 403, BTS, PK, SPEC, V, O	249:2-251:7	BSD, H, L
Moyal, Hila	238:20-239:17	R, 403, BTS, PK, SPEC, V, O	249:2-251:7	BSD, H, L
Moyal, Hila	239:22-240:04	R, 403, BTS, PK, SPEC, V, O	249:2-251:7	BSD, H, L
Moyal, Hila	240:06-240:15	R, 403, BTS, PK, SPEC, V, O, ARG, AA	249:2-251:7	BSD, H, L
Moyal, Hila	241:03-241:08	AA	249:2-251:7	BSD, H, L
Moyal, Hila	241:23-243:10		249:2-251:7	BSD, H, L
Moyal, Hila	244:04-244:24	R, 403, BTS, PK, SPEC, V		
Moyal, Hila	245:03-247:12	R, 403, BTS, PK, SPEC, V		
Moyal, Hila	247:19-247:24	R, 403		
Moyal, Hila	252:10-257:21	R, 403, BTS, PK, SPEC, V, AA, O, ARG	249:2-251:7	BSD, H, L

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Olivares, Eric	012:05-012:07			
Olivares, Eric	012:16-013:15			
Olivares, Eric	013:21-014:07			
Olivares, Eric	014:09-014:24			
Olivares, Eric	015:06-016:16			
Olivares, Eric	016:20-017:05			
Olivares, Eric	020:23-022:23			
Olivares, Eric	023:02-025:24			
Olivares, Eric	028:10-028:18			
Olivares, Eric	029:06-029:19			
Olivares, Eric	031:01-032:06	R, 403, PK, SPEC, CP, I, H		
Olivares, Eric	034:20-034:24			
Olivares, Eric	036:04-036:07	R, 403, PK, SPEC, CP, H		
Olivares, Eric	036:10-037:09	R, 403, PK, SPEC, CP, H		
Olivares, Eric	037:15-037:24	R, 403, PK, SPEC, CP, H, V		
Olivares, Eric	038:08-038:10	R, 403, PK, SPEC, CP, H, V		
Olivares, Eric	038:15-038:24	R, 403, CP, H, V		
Olivares, Eric	039:05-039:06	R, 403, CP, H, V		
Olivares, Eric	039:09-040:25	R, 403, CP, H, V, I		
Olivares, Eric	041:06-041:06	R, 403, CP, H, V, I		
Olivares, Eric	041:10-042:05	H		
Olivares, Eric	042:08-043:05	H		
Olivares, Eric	044:05-044:18	H		
Olivares, Eric	045:12-045:20	R, 403, F, V, H		
Olivares, Eric	046:12-046:17	R, 403, F, V, H		
Olivares, Eric	047:10-048:14	R, 403, V, H, PK, SPEC, CP	49:11-12; 49:14	BSD, H
Olivares, Eric	048:18-048:25	R, 403, V, H, PK, SPEC, CP	49:11-12; 49:14	BSD, H
Olivares, Eric	049:02-049:02	R, 403, V, H, PK, SPEC, CP	49:11-12; 49:14	BSD, H
Olivares, Eric	049:05-049:07	R, 403, V, H, PK, SPEC, CP	49:11-12; 49:14	BSD, H
Olivares, Eric	050:01-050:23	R, 403, V, H, PK, SPEC, CP		
Olivares, Eric	050:25-052:03	R, 403, V, H, PK, SPEC, CP, NARR		
Olivares, Eric	052:07-053:01	R, 403, V, H, PK, SPEC, CP, NARR		
Olivares, Eric	053:03-053:07	R, 403, V, H, PK, SPEC, O		
Olivares, Eric	053:10-053:19	H		
Olivares, Eric	054:02-054:03	R, 403, V, H, PK, SPEC		
Olivares, Eric	054:05-054:15	R, 403, V, H, PK, SPEC		
Olivares, Eric	054:17-055:19	R, 403, V, H, PK, SPEC, O		
Olivares, Eric	056:02-056:05	R, 403, V, H, PK, SPEC		
Olivares, Eric	056:07-056:09	R, 403, V, H, PK, SPEC		
Olivares, Eric	056:18-057:08	H		
Olivares, Eric	057:23-057:25	R, 403, V, H, PK, SPEC		
Olivares, Eric	058:02-058:05	R, 403, V, H, PK, SPEC		
Olivares, Eric	058:16-058:18	R, 403, V, H, PK, SPEC		
Olivares, Eric	058:20-060:06	R, 403, V, H, PK, SPEC		
Olivares, Eric	060:23-061:13	R, 403, V, H, PK, SPEC, NARR, MIS		
Olivares, Eric	061:15-061:20	R, 403, V, H, PK, SPEC, NARR, MIS		
Olivares, Eric	061:22-063:08	R, 403, V, H, PK, SPEC		
Olivares, Eric	063:11-063:17	R, 403, V, H, PK, SPEC		
Olivares, Eric	063:19-064:03	R, 403, V, H, PK, SPEC		
Olivares, Eric	064:06-065:14	R, 403, V, H, PK, SPEC, IH		
Olivares, Eric	065:16-066:10	R, 403, V, H, PK, SPEC, IH		
Olivares, Eric	066:24-066:25			
Olivares, Eric	067:10-067:11			
Olivares, Eric	067:15-068:06	R, 403, V, H, SPEC, PK, V		
Olivares, Eric	068:08-068:13	R, 403, V, H, SPEC, PK, V		
Olivares, Eric	068:15-068:15	R, 403, V, H, SPEC, PK, V		
Olivares, Eric	069:08-069:23			
Olivares, Eric	069:25-070:15	H, R, 403, V, SPEC, PK, CP	71:4-9	BSD, H
Olivares, Eric	070:17-070:19	H, R, 403, V, SPEC, PK, CP	71:4-9	BSD, H
Olivares, Eric	071:24-073:05	H		
Olivares, Eric	073:08-074:05	R, 403, V, IH, SPEC, PK, CP		

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Olivares, Eric	074:07-074:18	R, 403, V, IH, SPEC, PK, O		
Olivares, Eric	075:17-076:10	R, 403, V, IH, SPEC, PK, O		
Olivares, Eric	076:12-076:12	R, 403, V, IH, SPEC, PK, O	49:11-12; 49:14	BSD, H
Olivares, Eric	076:14-076:19	R, 403, V, IH, SPEC, PK, O	49:11-12; 49:14	BSD, H
Olivares, Eric	076:21-077:02	H	49:11-12; 49:14	BSD, H
Olivares, Eric	077:11-077:14	H	49:11-12; 49:14; 71:4-9; 77:15-17; 77:20-78:1	BSD, H
Olivares, Eric	078:02-078:10	R, 403, V, IH, SPEC, PK, O, NARR	77:15-17; 77:20-78:1	BSD, H
Olivares, Eric	078:12-079:21	R, 403, V, IH, SPEC, PK, O, NARR, CP		
Olivares, Eric	079:23-080:10	R, 403, V, IH, SPEC, PK, O, NARR, CP		
Olivares, Eric	082:06-082:10			
Olivares, Eric	082:21-084:11	H, OB		
Olivares, Eric	084:22-085:13	H		
Olivares, Eric	085:16-085:25	H		
Olivares, Eric	087:01-088:15	R, 403, V, IH, SPEC, PK, O, NARR, CP, H	49:11-12; 49:14	BSD, H
Olivares, Eric	088:17-089:07	R, 403, V, IH, SPEC, PK, O, NARR, CP, H	49:11-12; 49:14	BSD, H
Olivares, Eric	089:16-090:22	R, 403, SPEC, PK, H		
Olivares, Eric	090:24-091:24	R, 403, SPEC, PK, H		
Olivares, Eric	092:01-093:03	R, 403, SPEC, PK, H		
Olivares, Eric	093:16-093:21	H		
Olivares, Eric	094:09-094:17	R, 403, SPEC, PK, H	49:11-12; 49:14	BSD, H
Olivares, Eric	095:07-098:21	R, 403, SPEC, PK, H, O		
Olivares, Eric	098:23-099:08	R, 403, SPEC, PK, H, O		
Olivares, Eric	099:18-100:03	H		
Olivares, Eric	100:07-100:10	H		
Olivares, Eric	100:13-101:09	H		
Olivares, Eric	101:24-102:08	R, 403, SPEC, PK, O, H	49:11-12; 49:14	BSD, H
Olivares, Eric	102:25-105:19	R, 403, SPEC, PK, H	49:11-12; 49:14	BSD, H
Olivares, Eric	105:21-108:19	R, 403, SPEC, PK, H, V, IH	49:11-12; 49:14	BSD, H
Olivares, Eric	109:05-109:09	H		
Olivares, Eric	109:13-111:19	R, 403, SPEC, PK, H, V, AA	49:11-12; 49:14; 71:4-9	BSD, H
Olivares, Eric	111:22-112:05	R, 403, SPEC, PK, H, V, AA	49:11-12; 49:14; 71:4-9	BSD, H
Olivares, Eric	112:18-114:08	R, 403, SPEC, PK, H, V	49:11-12; 49:14	BSD, H
Olivares, Eric	114:10-114:10	R, 403, SPEC, PK, H, V	49:11-12; 49:14	BSD, H
Olivares, Eric	114:12-115:06	R, 403, SPEC, PK, H, CP, F	49:11-12; 49:14	BSD, H
Olivares, Eric	115:08-117:06	H	49:11-12; 49:14	BSD, H
Olivares, Eric	117:16-119:06	R, 403, SPEC, PK, H	49:11-12; 49:14	BSD, H
Olivares, Eric	119:08-119:14	R, 403, SPEC, PK, H, AA	49:11-12; 49:14	BSD, H
Olivares, Eric	119:24-122:18	H	49:11-12; 49:14	BSD, H
Olivares, Eric	122:21-123:03	R, 403, SPEC, PK, H, O, IH		
Olivares, Eric	123:05-125:14	R, 403, SPEC, PK, H, O, IH		
Olivares, Eric	125:22-126:25	H		
Olivares, Eric	127:06-129:13	H		
Olivares, Eric	129:23-131:05	R, 403, SPEC, PK, AA, H		
Olivares, Eric	131:08-131:10	R, 403, SPEC, PK, AA, H		
Olivares, Eric	132:03-132:19	H		
Olivares, Eric	132:23-133:06	H		
Olivares, Eric	133:08-133:18	H		
Olivares, Eric	133:25-134:25	H, I		
Olivares, Eric	135:02-135:17	R, 403, SPEC, PK, H		
Olivares, Eric	136:01-136:01	H, I		
Olivares, Eric	136:15-137:24	H	49:11-12; 49:14; 71:4-9	BSD, H
Olivares, Eric	138:01-138:08	H	49:11-12; 49:14; 71:4-9	BSD, H
Olivares, Eric	139:02-143:12	R, 403, SPEC, PK, H	49:11-12; 49:14; 71:4-9	BSD, H
Olivares, Eric	144:01-136:13	H		
Olivares, Eric	146:21-148:14	H		
Olivares, Eric	148:21-148:25	R, 403, SPEC, PK, V, H	149:25-150:9	H
Olivares, Eric	149:06-149:24	R, 403, SPEC, PK, V, H	149:25-150:9	H
Olivares, Eric	150:12-150:17	R, 403, SPEC, PK, V, H	149:25-150:9	H
Olivares, Eric	150:19-151:03	R, 403, SPEC, PK, V, H		
Olivares, Eric	151:08-152:14	H		
Olivares, Eric	152:23-153:10	H		
Olivares, Eric	153:21-154:02			
Olivares, Eric	154:13-154:18	H		

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Olivares, Eric	155:02-156:12	H		
Olivares, Eric	156:18-158:14	H		
Olivares, Eric	158:21-161:10	H		
Olivares, Eric	161:14-162:03	R, 403, PK, SPEC, H		
Olivares, Eric	162:11-163:18	R, 403, PK, SPEC, H		
Olivares, Eric	163:21-164:15	R, 403, V, H		
Olivares, Eric	164:17-165:20	R, 403, V, H		
Olivares, Eric	167:03-167:08	R, 403, V, H, SPEC, PK		
Olivares, Eric	167:10-170:18	R, 403, V, H, SPEC, PK		
Olivares, Eric	171:01-171:22			
Olivares, Eric	171:24-175:24	H		
Olivares, Eric	177:08-179:07	H		
Olivares, Eric	180:05-183:03	H		
Olivares, Eric	183:08-184:04	R, 403, H, SPEC, PK		
Olivares, Eric	184:07-184:14	R, 403, H, SPEC, PK		
Olivares, Eric	184:16-184:23	R, 403, H, SPEC, PK		
Olivares, Eric	185:09-186:15	R, 403, H, SPEC, PK		
Olivares, Eric	186:17-186:17	R, 403, H, SPEC, PK		
Olivares, Eric	186:22-187:05	H		
Olivares, Eric	188:09-190:01	H		
Olivares, Eric	190:11-190:21	H		
Olivares, Eric	191:12-192:23	H		
Olivares, Eric	192:25-195:09	R, 403, H, SPEC, PK		
Olivares, Eric	195:11-195:11	R, 403, H, SPEC, PK		
Olivares, Eric	195:24-196:14	R, 403, H, SPEC, PK		
Olivares, Eric	198:08-200:09	H		
Olivares, Eric	200:12-201:01	R, 403, H, SPEC, PK		
Olivares, Eric	201:03-201:16	R, 403, H, SPEC, PK		
Olivares, Eric	201:20-201:24	R, 403, H, SPEC, PK		
Olivares, Eric	202:01-202:10	R, 403, H, SPEC, PK		
Olivares, Eric	202:15-203:14	R, 403, H, SPEC, PK		
Olivares, Eric	203:22-205:09	R, 403, H, SPEC, PK		
Olivares, Eric	205:12-206:04	R, 403, H, SPEC, PK		
Olivares, Eric	206:19-208:07	H, PK		
Olivares, Eric	208:14-210:25	R, 403, H, SPEC, PK		
Olivares, Eric	211:05-211:19	R, 403, H, SPEC, PK		
Olivares, Eric	212:09-214:04	H		
Olivares, Eric	215:10-217:13	R, 403, H, SPEC, PK, MIS		
Olivares, Eric	217:15-218:04	R, 403, H, SPEC, PK, MIS		
Olivares, Eric	218:06-219:08	R, 403, H, SPEC, PK, V, CP		
Olivares, Eric	219:09-220:22	R, 403, H, SPEC, PK, V, CP		
Olivares, Eric	221:05-224:07	R, 403, H, SPEC, PK, V, CP		
Olivares, Eric	224:10-226:04	R, 403, H, SPEC, PK, V, CP		
Olivares, Eric	226:07-226:09	R, 403, H, SPEC, PK, V, CP		
Olivares, Eric	226:21-227:13	R, 403, H, SPEC, PK, V, CP		
Olivares, Eric	227:16-228:19	R, 403, H, SPEC, PK, V, CP		
Olivares, Eric	229:02-229:17	R, 403, H, SPEC, PK, V, CP		
Olivares, Eric	229:19-229:23	R, 403, H, SPEC, PK, V, CP		
Olivares, Eric	230:07-230:16			
Olivares, Eric	230:25-232:04	H		
Olivares, Eric	232:18-234:11	H		
Olivares, Eric	234:19-236:24	R, 403, H, SPEC, PK, V, CP, LC		
Olivares, Eric	237:01-237:20	R, 403, H, SPEC, PK, V, CP, LC		
Olivares, Eric	237:22-238:17	R, 403, H, SPEC, PK, V, CP, LC		
Olivares, Eric	238:19-239:06	R, 403, H, SPEC, PK, V, CP, LC		
Olivares, Eric	239:08-239:17	R, 403, H, SPEC, PK, V, CP, LC		
Olivares, Eric	239:19-242:01	R, 403, H, SPEC, PK, V, CP, LC		
Olivares, Eric	242:03-243:01	R, 403, H, SPEC, PK, V, CP, LC		
Olivares, Eric	243:05-243:21	R, 403, H, SPEC, PK, V, NARR		
Olivares, Eric	243:23-244:08	R, 403, H, SPEC, PK, V, NARR, ARG		
Olivares, Eric	244:11-244:21	R, 403, H, SPEC, PK, V, NARR, ARG		
Olivares, Eric	244:24-247:16	R, 403, H, SPEC, PK, V, CP		
Olivares, Eric	247:18-247:20	R, 403, H, SPEC, PK, V, CP		

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Olivares, Eric	248:09-249:05	H		
Olivares, Eric	249:13-249:21	H		
Olivares, Eric	249:23-253:13	H		
Olivares, Eric	253:19-255:05	H		
Olivares, Eric	255:13-256:10	H		
Olivares, Eric	256:18-257:13			
Olivares, Eric	258:09-259:20	R, 403, SPEC, PK, H		
Olivares, Eric	260:04-260:12	R, 403, H, SPEC, PK		
Olivares, Eric	260:15-260:17	R, 403, H, SPEC, PK		
Olivares, Eric	261:06-261:22	R, 403, H, SPEC, PK	49:11-12; 49:14	BSD, H
Olivares, Eric	261:24-262:03	R, 403, H, SPEC, PK	49:11-12; 49:14	BSD, H
Olivares, Eric	262:06-262:06	R, 403, H, SPEC, PK	49:11-12; 49:14	BSD, H
Olivares, Eric	263:04-263:09	R, 403, H, SPEC, PK	49:11-12; 49:14	BSD, H
Olivares, Eric	264:04-264:16	R, 403, H, SPEC, PK	49:11-12; 49:14	BSD, H
Olivares, Eric	267:05-268:10	R, 403, H, SPEC, PK	49:11-12; 49:14	BSD, H
Olivares, Eric	268:21-271:04	H		
Olivares, Eric	271:18-272:17	H		
Olivares, Eric	273:01-274:23	R, 403, H, NARR		
Olivares, Eric	275:05-275:13			
Olivares, Eric	276:01-276:14	I		
Olivares, Eric	277:10-279:12	H		
Olivares, Eric	279:17-279:25	R, 403, H, SPEC, PK		
Olivares, Eric	280:03-281:11			
Olivares, Eric	282:14-286:02	R, 403, H, SPEC, PK		
Olivares, Eric	286:05-286:19	R, 403, H, SPEC, PK		
Olivares, Eric	287:14-287:21	R, 403, H, SPEC, PK		
Olivares, Eric	288:03-288:03	R, 403, H, SPEC, PK		
Olivares, Eric	289:12-289:23	R, 403, H, PK		
Olivares, Eric	290:07-292:08			
Olivares, Eric	292:14-295:22	R, 403, H, SPEC, PK, O		
Olivares, Eric	295:24-297:04	R, 403, H, SPEC, PK, NARR, O		
Olivares, Eric	297:06-297:07	R, 403, H, SPEC, PK, NARR, O		
Olivares, Eric	297:11-297:24	R, 403, H, SPEC, PK, O		
Olivares, Eric	298:01-298:11	H		
Olivares, Eric	298:20-299:14	H		
Olivares, Eric	300:05-301:09	R, 403, H, MIS, SPEC, PK		
Olivares, Eric	301:15-302:02	R, 403, H, MIS, SPEC, PK		
Olivares, Eric	302:14-303:03			
Olivares, Eric	303:07-306:24	R, 403, H, MIS, SPEC, PK, O, LC, I, NARR		
Olivares, Eric	307:07-308:09	R, 403, H, MIS, SPEC, PK, O, LC, NARR		

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Paul, Joshua	010:11-010:18			
Paul, Joshua	015:12-015:13			
Paul, Joshua	015:18-015:19			
Paul, Joshua	015:23-015:23			
Paul, Joshua	016:03-017:02			
Paul, Joshua	022:13-023:11			
Paul, Joshua	023:24-024:20	R, 403, V, SPEC, PK, O	25:11-15	BSD, H
Paul, Joshua	025:19-026:11	R, 403, V, SPEC, PK	25:11-15	BSD, H
Paul, Joshua	028:12-028:21	R, 403, V, SPEC, PK	25:11-15	BSD, H
Paul, Joshua	028:23-028:24	R, 403, V, SPEC, PK	25:11-15	BSD, H
Paul, Joshua	029:02-029:16	R, 403, V, SPEC, BTS	25:11-15	BSD, H
Paul, Joshua	029:18-029:20	R, 403, V, SPEC, BTS	25:11-15	BSD, H
Paul, Joshua	029:22-030:03	R, 403, V, SPEC, BTS	25:11-15	BSD, H
Paul, Joshua	030:16-032:01			
Paul, Joshua	033:03-033:16			
Paul, Joshua	037:09-037:10	R, 403, V, SPEC, BTS, CP		
Paul, Joshua	037:23-037:20	R, 403, V, SPEC, BTS, CP, I		
Paul, Joshua	038:13-038:24		25:11-15	BSD, H
Paul, Joshua	039:02-040:12	R, 403, V, SPEC, BTS, CP, MIS	25:11-15; 40:18-41:11	BSD, H
Paul, Joshua	040:14-040:16	R, 403, V, SPEC, BTS, CP, MIS	25:11-15; 40:18-41:11	BSD, H
Paul, Joshua	043:12-043:17	R, 403, SPEC, BTS, CP, MIS, F		
Paul, Joshua	043:19-043:24	R, 403, SPEC, BTS, CP, MIS, F		
Paul, Joshua	044:16-044:17			
Paul, Joshua	044:20-045:04			
Paul, Joshua	045:10-045:19			
Paul, Joshua	046:01-046:10			
Paul, Joshua	047:12-047:14			
Paul, Joshua	047:22-047:23			
Paul, Joshua	048:06-048:13		48:22-25	H
Paul, Joshua	051:05-051:20			
Paul, Joshua	052:07-052:10	R, 403, V, PK, SPEC		
Paul, Joshua	052:17-052:22	R, 403, V, BTS		
Paul, Joshua	052:24-052:24	R, 403, V, BTS		
Paul, Joshua	053:02-053:03	R, 403, V, BTS, PK, SPEC		
Paul, Joshua	053:05-053:05	R, 403, V, BTS, PK, SPEC		
Paul, Joshua	053:07-053:08	R, 403, V, BTS, PK, SPEC		
Paul, Joshua	053:10-053:12	R, 403, V, BTS, PK, SPEC		
Paul, Joshua	053:14-053:16	R, 403, BTS		
Paul, Joshua	054:06-054:09	R, 403, BTS, V	54:14-25	BSD, H, I
Paul, Joshua	054:11-054:12	R, 403, BTS, V	54:14-25	BSD, H, I
Paul, Joshua	057:21-058:01	R, 403, BTS, PK, SPEC, F, O		
Paul, Joshua	058:03-058:08	R, 403, BTS, PK, SPEC, F, O		
Paul, Joshua	058:10-058:12	R, 403, BTS, PK, SPEC, F	58:17-59:14	BSD, H
Paul, Joshua	058:14-058:14	R, 403, BTS, PK, SPEC, F	58:17-59:14	BSD, H
Paul, Joshua	061:22-062:05			
Paul, Joshua	063:04-063:06			
Paul, Joshua	063:23-063:25	R, 403, BTS, PK, SPEC, F, O		
Paul, Joshua	064:02-064:03	R, 403, BTS, PK, SPEC, F, O		
Paul, Joshua	066:21-067:03	R, 403, BTS, PK, SPEC, F, O	25:11-15; 48:22-25; 65:21-23; 65:25-66:6; 68:5-8; 68:10-19	BSD, H
Paul, Joshua	067:06-067:10	R, 403, BTS, PK, SPEC, F, O	25:11-15; 48:22-25; 65:21-23; 65:25-66:6; 68:5-8; 68:10-19	BSD, H
Paul, Joshua	067:20-067:24	R, 403, BTS, PK, SPEC, F, O	25:11-15; 48:22-25; 65:21-23; 65:25-66:6; 68:5-8; 68:10-19	BSD, H
Paul, Joshua	068:01-068:03	R, 403, BTS, PK, SPEC, F, O	25:11-15; 48:22-25; 65:21-23; 65:25-66:6; 68:5-8; 68:10-19	BSD, H
Paul, Joshua	069:04-069:10	R, 403, BTS, PK, SPEC, F, O	25:11-15; 48:22-25; 65:21-23; 65:25-66:6; 68:5-8; 68:10-19; 69:17-20; 69:22-25	BSD, H
Paul, Joshua	069:13-069:15	R, 403, BTS, PK, SPEC, F, O	25:11-15; 48:22-25; 65:21-23; 65:25-66:6; 68:5-8; 68:10-19; 69:17-20; 69:22-25	BSD, H
Paul, Joshua	072:05-072:06	R, 403, BTS, PK, SPEC, F, O, LC, V, NARR	25:11-15; 48:22-25; 65:21-23; 65:25-66:6; 68:5-8; 68:10-19; 69:17-20; 69:22-25	BSD, H

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Paul, Joshua	072:12-072:14	R, 403, BTS, PK, SPEC, F, O, LC, V, NARR	25:11-15; 48:22-25; 65:21-23; 65:25-66:6; 68:5-8; 68:10-19; 69:17-20; 69:22-25	BSD, H
Paul, Joshua	076:05-076:11	R, 403, BTS, SPEC, LC, V		
Paul, Joshua	076:14-076:14	R, 403, BTS, SPEC, LC, V		
Paul, Joshua	076:17-076:23	R, 403, BTS, PK, SPEC, LC, V		
Paul, Joshua	076:25-076:25	R, 403, BTS, PK, SPEC, V		
Paul, Joshua	087:03-087:04	R, 403, BTS, PK, SPEC, V		
Paul, Joshua	087:06-087:07	R, 403, BTS, PK, SPEC, V		
Paul, Joshua	087:09-087:09	R, 403, BTS, PK, SPEC, V		
Paul, Joshua	087:11-087:15	R, 403, BTS, PK, SPEC, V, O		
Paul, Joshua	087:17-087:17	R, 403, BTS, PK, SPEC, V, O		
Paul, Joshua	087:19-087:21	R, 403, BTS, PK, SPEC, V, O		
Paul, Joshua	087:23-088:03			
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Paul, Joshua	088:20-088:20	R, 403, BTS, V, NARR, CP		
Paul, Joshua	088:22-088:23	R, 403, BTS, V, NARR, PK, SPEC, O, LC	25:11-15; 89:3-20	BSD, H
Paul, Joshua	089:01-089:02	R, 403, BTS, V, NARR, PK, SPEC, LC	25:11-15; 89:3-20	BSD, H
Paul, Joshua	089:21-091:04	R, 403, BTS, V, NARR, PK, SPEC, O, LC	25:11-15; 89:3-20	BSD, H
Paul, Joshua	091:06-091:08	R, 403, BTS, V, NARR, PK, SPEC, O, LC	25:11-15; 89:3-20	BSD, H
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Paul, Joshua	093:20-094:02	R, 403, V, BTS, PK, SPEC, F		
Paul, Joshua	094:04-094:04	R, 403, V, BTS, PK, SPEC, F		
Paul, Joshua	094:06-095:04	R, 403, V, BTS, PK, SPEC, F		
Paul, Joshua	096:03-096:04	R, 403, V, BTS, PK, SPEC, F	96:5-12	BSD, H
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Paul, Joshua	099:05-099:06	R, 403, V, BTS, PK, SPEC, F, LC, O	96:5-12; 99:8-9; 99:11-15; 99:17-18; 99:20-21	BSD, H
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Paul, Joshua	104:19-106:06	R, 403, V, BTS, SPEC, O	104:6-18	BSD, H
Paul, Joshua	106:23-107:14	R, 403, V, BTS, SPEC, O	25:11-15	BSD, H
Paul, Joshua	107:16-107:17	R, 403, V, BTS, SPEC, O	25:11-15; 108:19-21; 108:23-109:3	BSD, H
Paul, Joshua	107:19-107:21	R, 403, V, BTS, SPEC, O	25:11-15; 108:19-21; 108:23-109:3	BSD, H
Paul, Joshua	108:08-108:10	R, 403, V, BTS, SPEC, O	25:11-15; 108:19-21; 108:23-109:3	BSD, H
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Paul, Joshua	113:20-113:22	R, 403, V, BTS, SPEC, O	25:11-15; 108:19-21; 108:23-109:3; 112:15-113:08	BSD, H
Paul, Joshua	113:24-113:24	R, 403, V, BTS, SPEC, O, I	25:11-15; 108:19-21; 108:23-109:3; 112:15-113:08	BSD, H
Paul, Joshua	114:12-114:15	R, 403, V, BTS, SPEC, O	25:11-15; 108:19-21; 108:23-109:3; 112:15-113:08	BSD, H
Paul, Joshua	114:17-114:25	R, 403, V, BTS, SPEC, O	25:11-15; 108:19-21; 108:23-109:3; 112:15-113:08	BSD, H
Paul, Joshua	117:13-117:15	R, 403, V, BTS, SPEC, O, PK		
Paul, Joshua	117:18-117:25	R, 403, V, BTS, SPEC, O, PK		
Paul, Joshua	118:02-118:23	R, 403, V, BTS, SPEC, O, PK		
Paul, Joshua	119:22-120:15			
Paul, Joshua	121:17-122:08	R, 403, V, BTS, SPEC, O, PK		
Paul, Joshua	122:10-122:11	R, 403, V, BTS, SPEC, O, PK		
Paul, Joshua	122:13-122:21	R, 403, V, BTS, SPEC, O, PK		
Paul, Joshua	122:23-122:24	R, 403, V, BTS, SPEC, O, PK		
Paul, Joshua	123:02-123:12	R, 403, V, BTS, SPEC, O, PK		
Paul, Joshua	123:14-123:15	R, 403, V, BTS, SPEC, O, PK		
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Paul, Joshua	126:08-126:08	R, 403, V, BTS, SPEC, O, PK	125:12-15; 125:17-126:2	BSD, H
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Paul, Joshua	137:21-138:12	R, 403, BTS, SPEC, V, O	139:18-20; 139:22-140:6	BSD, H
Paul, Joshua	138:14-138:15	R, 403, BTS, SPEC, V, O	139:18-20; 139:22-140:6	BSD, H
Paul, Joshua	138:17-138:18	R, 403, BTS, SPEC, V, O	139:18-20; 139:22-140:6	BSD, H
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Paul, Joshua	141:02-142:09	R, 403, BTS, SPEC, V, O	139:18-20; 139:22-140:6	BSD, H
Paul, Joshua	142:20-143:02	R, 403, BTS, PK, SPEC, V, O, CP	139:18-20; 139:22-140:6	BSD, H
Paul, Joshua	143:04-143:10	R, 403, BTS, PK, SPEC, V, O, CP	139:18-20; 139:22-140:6	BSD, H
Paul, Joshua	143:12-143:16	R, 403, BTS, PK, SPEC, V, O, CP	139:18-20; 139:22-140:6	BSD, H
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Paul, Joshua	144:09-145:15	R, 403, BTS, PK, SPEC, V, O, CP		
Paul, Joshua	145:17-145:18	R, 403, BTS, PK, SPEC, V, O, CP		
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Paul, Joshua	145:22-146:02	R, 403, BTS, PK, SPEC, V, O, CP		
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Paul, Joshua	146:23-146:25	R, 403, BTS, PK, SPEC, V, O		
Paul, Joshua	151:14-151:15			
Paul, Joshua	152:01-155:01	R, 403, PK, SPEC		
Paul, Joshua	155:03-155:15	R, 403, BTS, PK, SPEC, V, MIS		
Paul, Joshua	155:17-155:21	R, 403, BTS, PK, SPEC, V, MIS		
Paul, Joshua	155:24-156:13	R, 403, PK, SPEC		
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Paul, Joshua	164:12-164:13	R, 403, BTS, PK, SPEC, V, O	162:5-10	BSD, H
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Paul, Joshua	166:02-167:01			
Paul, Joshua	167:11-167:16	R, 403, BTS, PK, SPEC, V		
Paul, Joshua	167:18-167:18			
Paul, Joshua	167:20-168:12	R, 403, BTS, PK, SPEC, V		
Paul, Joshua	168:21-169:04			
Paul, Joshua	175:25-176:03	R, 403, BTS, PK, SPEC, V, O, MIS		
Paul, Joshua	176:05-176:08	R, 403, BTS, PK, SPEC, V, O, MIS		
Paul, Joshua	176:10-176:18	R, 403, BTS, PK, SPEC, V, O		
Paul, Joshua	176:20-176:22	R, 403, BTS, PK, SPEC, V, O		
Paul, Joshua	176:24-177:08	R, 403, BTS, PK, SPEC, V, O, MIS		
Paul, Joshua	177:10-178:06	R, 403, BTS, PK, SPEC, V, O, MIS		
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Paul, Joshua	184:16-184:20	R, 403, BTS, PK, SPEC, V, O	185:6-7; 185:9-13	H
Paul, Joshua	184:22-184:24	R, 403, BTS, PK, SPEC, V, O	185:6-7; 185:9-13	H
Paul, Joshua	185:01-185:04	R, 403, BTS, PK, SPEC, V, O	185:6-7; 185:9-13	H
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Paul, Joshua	186:17-186:25	R, 403, BTS, PK, SPEC, V, O	185:6-7; 185:9-13	BSD, H
Paul, Joshua	189:13-189:15			
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Paul, Joshua	191:11-192:14	R, 403, BTS, PK, SPEC, V, O		
Paul, Joshua	193:23-193:25	R, 403, BTS, PK, SPEC, V, O		
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Paul, Joshua	194:05-194:05	R, 403, BTS, PK, SPEC, V, O		
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Paul, Joshua	195:15-195:18	R, 403, BTS, PK, SPEC, V, O		
Paul, Joshua	195:20-195:22	R, 403, BTS, PK, SPEC, V, O		
Paul, Joshua	195:24-195:24	R, 403, BTS, PK, SPEC, V, O		
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Paul, Joshua	198:02-200:02	R, 403, BTS, PK, SPEC, V, O, F		
Paul, Joshua	200:04-200:06	R, 403, BTS, PK, SPEC, V, O, F		
Paul, Joshua	200:08-200:10	R, 403, BTS, PK, SPEC, V, O, F		
Paul, Joshua	200:12-200:25	R, 403, BTS, PK, SPEC, V, O, F	202:6-8; 202:10; 202:12; 202:14-17	BSD, H
Paul, Joshua	201:02-201:03	R, 403, BTS, PK, SPEC, V, O, F	202:6-8; 202:10; 202:12; 202:14-17	BSD, H
Paul, Joshua	201:05-201:05	R, 403, BTS, PK, SPEC, V, O, F	202:6-8; 202:10; 202:12; 202:14-17	BSD, H
Paul, Joshua	201:07-201:09	R, 403, BTS, PK, SPEC, V, O, F	202:6-8; 202:10; 202:12; 202:14-17	BSD, H
Paul, Joshua	201:11-201:11	R, 403, BTS, PK, SPEC, V, O, F	202:6-8; 202:10; 202:12; 202:14-17	BSD, H
Paul, Joshua	201:13-201:14	R, 403, BTS, PK, SPEC, V, O, F	202:6-8; 202:10; 202:12; 202:14-17	BSD, H
Paul, Joshua	201:16-201:20	R, 403, BTS, PK, SPEC, V, O, F	202:6-8; 202:10; 202:12; 202:14-17	BSD, H
Paul, Joshua	201:22-202:01	R, 403, BTS, PK, SPEC, V, O, F, MIS	202:6-8; 202:10; 202:12; 202:14-17	BSD, H
Paul, Joshua	202:03-202:04	R, 403, BTS, PK, SPEC, V, O, F, MIS	202:6-8; 202:10; 202:12; 202:14-17	BSD, H
Paul, Joshua	202:19-204:11	R, 403, BTS, PK, SPEC, V, O, F, MIS	202:6-8; 202:10; 202:12; 202:14-17	BSD, H
Paul, Joshua	204:13-203:13	R, 403, BTS, PK, SPEC, V, O, F, MIS	202:6-8; 202:10; 202:12; 202:14-17	BSD, H
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Paul, Joshua	209:01-210:25	R, 403, BTS, PK, SPEC, V, O	211:8-9; 211:11-13	BSD, H
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Paul, Joshua	212:04-212:20	R, 403, BTS, PK, SPEC, V, O	211:8-9; 211:11-13	H
Paul, Joshua	212:25-214:01	R, 403, BTS, PK, SPEC, V, I		
Paul, Joshua	214:08-214:21	R, 403, BTS, PK, SPEC, V		
Paul, Joshua	215:15-215:21	R, 403, BTS, PK, SPEC, V, O		
Paul, Joshua	216:12-216:22			
Paul, Joshua	217:18-217:20	R, 403, BTS, V, O, NARR		
Paul, Joshua	217:22-217:25	R, 403, BTS, V, O, NARR		
Paul, Joshua	218:02-218:03			
Paul, Joshua	218:10-218:13	R, 403, BTS, V, O, NARR		
Paul, Joshua	218:15-218:15	R, 403, BTS, V, O, NARR		
Paul, Joshua	218:17-219:16	R, 403, BTS, V, O, NARR, PK, SPEC		
Paul, Joshua	219:18-219:18	R, 403, BTS, V, O, NARR, PK, SPEC		
Paul, Joshua	219:20-220:25	R, 403, BTS, V, O, NARR, PK, SPEC		
Paul, Joshua	221:02-221:07	R, 403, BTS, V, O, NARR, PK, SPEC		
Paul, Joshua	221:18-222:05	R, 403, BTS, V, O, PK, SPEC		
Paul, Joshua	222:07-222:13	R, 403, BTS, V, O, PK, SPEC		
Paul, Joshua	222:15-222:16	R, 403, BTS, V, O, PK, SPEC		
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Paul, Joshua	223:04-224:11	R, 403, BTS, V, O, PK, SPEC	224:12-14; 224:16-19; 226:5-16; 226:18-227:2	BSD, H
Paul, Joshua	225:10-225:11	R, 403, BTS, V, O, PK, SPEC	224:12-14; 224:16-19; 226:5-16; 226:18-227:2	BSD, H
Paul, Joshua	225:13-225:15	R, 403, BTS, V, O, PK, SPEC	224:12-14; 224:16-19; 226:5-16; 226:18-227:2	BSD, H
Paul, Joshua	227:04-227:07	R, 403, BTS, V, O, PK, SPEC	224:12-14; 224:16-19; 226:5-16; 226:18-227:2	BSD, H
Paul, Joshua	227:09-227:18	R, 403, BTS, V, O, PK, SPEC	224:12-14; 224:16-19; 226:5-16; 226:18-227:2	BSD, H
Paul, Joshua	227:20-228:02	R, 403, BTS, V, O, PK, SPEC	224:12-14; 224:16-19; 226:5-16; 226:18-227:2	BSD, H
Paul, Joshua	228:04-228:05	R, 403, BTS, V, O, PK, SPEC	224:12-14; 224:16-19; 226:5-16; 226:18-227:2	BSD, H
Paul, Joshua	228:07-228:12	R, 403, BTS, V, O, PK, SPEC, I	224:12-14; 224:16-19; 226:5-16; 226:18-227:2; 228:13-21	BSD, H
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Paul, Joshua	230:15-231:07	R, 403, BTS, F, V, PK, SPEC	230:8-11	H
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Porreca, Gregory	030:01-030:02	I		
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Porreca, Gregory	316:04-316:13	AA, ARG, MIS, NARR, PK, R, SPEC, 403, V	308:1-6; 308:8-13; 311:4-5; 311:7-8; 314:8-11	BSD, H
Porreca, Gregory	316:15-316:16			
Porreca, Gregory	317:05-317:09			
Porreca, Gregory	317:12-320:09	AA, ARG, MIS, NARR, PK, R, SPEC, 403, V		
Porreca, Gregory	320:16-321:02	AA, ARG, MIS, NARR, PK, R, SPEC, 403, V		

Witness	Natera Designations	Labcorp Objections	Labcorp Counter-Designations	Natera Objections
Porreca, Gregory	321:04-322:03	AA, ARG, MIS, NARR, PK, R, SPEC, 403, V		
Porreca, Gregory	322:05-322:05	AA, ARG, MIS, NARR, PK, R, SPEC, 403, V		

Stuart, Jim
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Witness	Natera Designations	Labcorp Objections	Labcorp Counter-Designations	Natera Objections
Stuart, Jim	005:21-006:02			
Stuart, Jim	006:15-010:20	R, 403		
Stuart, Jim	012:11-013:24	R, 403, BTS, PK, SPEC, V, O		
Stuart, Jim	014:01-014:14	R, 403, BTS, PK, SPEC, V, O		
Stuart, Jim	014:16-015:02	R, 403, BTS, PK, SPEC, V, O		
Stuart, Jim	015:04-017:11	R, 403, BTS, PK, SPEC, V, O		
Stuart, Jim	018:06-018:24	R, 403, BTS, V		
Stuart, Jim	019:01-019:23	R, 403, BTS, V		
Stuart, Jim	020:16-021:14	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	021:21-023:25	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	024:02-025:12	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	025:14-026:21	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	026:23-029:03	R, 403, BTS, V, PK, SPEC, CP		
Stuart, Jim	029:05-029:25	R, 403, BTS, V, PK, SPEC, CP		
Stuart, Jim	030:02-030:25	R, 403, BTS, V, PK, SPEC, CP		
Stuart, Jim	032:02-034:05	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	034:07-035:05	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	035:07-037:14	R, 403, BTS, V, PK, SPEC, CP		
Stuart, Jim	037:16-037:17	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	037:24-038:03	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	038:05-039:23	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	040:17-041:19	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	041:21-043:02	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	043:15-045:14	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	045:22-046:05	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	046:07-047:08	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	047:10-047:19	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	047:21-049:25	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	052:05-054:13	R, 403, BTS, V, PK, SPEC, F		
Stuart, Jim	055:12-056:20	R, 403, BTS, V, F		
Stuart, Jim	056:22-057:07	R, 403, BTS, V, F	56:21; 57:08-16	OB, H
Stuart, Jim	058:03-058:15	R, 403, BTS, V, F	58:16-19; 58:21-24; 59:1-2; 59:4-8	BSD, H
Stuart, Jim	059:09-059:11	R, 403, BTS, V, F	58:16-19; 58:21-24; 59:1-2; 59:4-8	BSD, H
Stuart, Jim	059:13-059:16	R, 403, BTS, V, F	58:16-19; 58:21-24; 59:1-2; 59:4-8	BSD, H
Stuart, Jim	059:25-061:12	R, 403, BTS, V, F, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	061:14-063:15	R, 403, BTS, V, F, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	063:17-063:20	R, 403, BTS, V, F, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	064:05-064:21	R, 403, BTS, V, F, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	064:24-065:05	R, 403, BTS, V, F, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	065:12-065:23	R, 403, BTS, V, F, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	065:25-066:20	R, 403, BTS, V, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	066:22-067:02	R, 403, BTS, V, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	068:03-068:04	R, 403, BTS, V, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	068:06-069:21	R, 403, BTS, V, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	070:01-074:01	R, 403, BTS, V, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	074:12-074:19	R, 403, BTS, V, PK, SPEC, F	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	074:21-076:06	R, 403, BTS, V, PK, SPEC, F	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	076:08-076:12	R, 403, BTS, V, PK, SPEC, F	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	077:04-077:12	R, 403, BTS, V, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	077:14-078:17	R, 403, BTS, V, PK, SPEC	65:06-07; 65:09-11; 67:11-68:02	BSD, H
Stuart, Jim	080:15-084:15	R, 403, BTS, V, PK, SPEC, O	80:2-14; 84:16-86:24; 89:08-11; 90:18-91:08	BSD, H
Stuart, Jim	087:09-088:13	R, 403, BTS, V, PK, SPEC	80:2-14; 84:16-86:24; 89:08-11; 90:18-91:08	BSD, H
Stuart, Jim	091:13-091:25	R, 403, BTS, V, PK, SPEC, I	80:2-14; 84:16-86:24; 89:08-11; 90:18-91:08	BSD, H
Stuart, Jim	093:09-095:14	R, 403, BTS, V, PK, SPEC	99:14-23	BSD, H
Stuart, Jim	095:16-095:25	R, 403, BTS, V, PK, SPEC	99:14-23	BSD, H
Stuart, Jim	096:07-099:13	R, 403, BTS, V, PK, SPEC	99:14-23	BSD, H
Stuart, Jim	100:08-100:14	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	100:20-101:19	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	103:06-103:09	R, 403, BTS, V, PK, SPEC, F	103:02-05; 104:16-19; 104:21-105:07; 105:09-13	BSD, H
Stuart, Jim	103:11-104:15	R, 403, BTS, V, PK, SPEC, F	103:02-05; 104:16-19; 104:21-105:07; 105:09-13	BSD, H
Stuart, Jim	105:14-106:02	R, 403, BTS, V, PK, SPEC, F	103:02-05; 104:16-19; 104:21-105:07; 105:09-13	BSD, H
Stuart, Jim	106:04-106:15	R, 403, BTS, V, PK, SPEC, F, I	103:02-05; 104:16-19; 104:21-105:07; 105:09-13; 67:11-68:02	BSD, H
Stuart, Jim	107:07-107:12	R, 403, BTS, V, PK, SPEC, F	103:02-05; 104:16-19; 104:21-105:07; 105:09-13; 67:11-68:02	BSD, H
Stuart, Jim	107:14-108:05	R, 403, BTS, V, PK, SPEC, F	103:02-05; 104:16-19; 104:21-105:07; 105:09-13; 67:11-68:02	BSD, H
Stuart, Jim	108:07-108:25	R, 403, BTS, V, PK, SPEC, F	103:02-05; 104:16-19; 104:21-105:07; 105:09-13; 67:11-68:02	BSD, H
Stuart, Jim	109:07-111:01	R, 403, BTS, V, PK, SPEC, F	103:02-05; 104:16-19; 104:21-105:07; 105:09-13; 67:11-68:02; 111:02-03; 111:14-25; 112:11-19; 112: 21-23	BSD, H
Stuart, Jim	112:01-112:10	R, 403, BTS, V, PK, SPEC, F	103:02-05; 104:16-19; 104:21-105:07; 105:09-13; 67:11-68:02; 111:02-03; 111:14-25; 112:11-19; 112: 21-23	BSD, H
Stuart, Jim	112:06-123:15	Not Designated		
Stuart, Jim	114:06-115:10	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	115:14-115:18	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	117:13-119:16	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	120:04-122:04	R, 403, V, F		
Stuart, Jim	124:18-126:17	R, 403, V, F		
Stuart, Jim	126:21-131:22	R, 403, BTS, V, PK, SPEC, O		
Stuart, Jim	131:24-132:19	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	132:21-132:25	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	133:02-133:23	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	135:08-137:08	R, 403, BTS, V, PK, SPEC, LC	137:25-138:03; 141:13-17; 141:19	BSD, H
Stuart, Jim	137:10-137:19	R, 403, BTS, V, PK, SPEC, LC	137:25-138:03; 141:13-17; 141:19	BSD, H
Stuart, Jim	137:21-137:23	R, 403, BTS, V, PK, SPEC, LC	137:25-138:03; 141:13-17; 141:19	BSD, H
Stuart, Jim	138:04-138:06	R, 403, BTS, V, PK, SPEC, LC	137:25-138:03; 141:13-17; 141:19	BSD, H
Stuart, Jim	138:08-140:23	R, 403, BTS, V, PK, SPEC, LC	137:25-138:03; 141:13-17; 141:19	BSD, H
Stuart, Jim	140:25-141:12	R, 403, BTS, V, PK, SPEC, LC	137:25-138:03; 141:13-17; 141:19	BSD, H
Stuart, Jim	141:20-141:23	R, 403, BTS, V, PK, SPEC, LC	137:25-138:03; 141:13-17; 141:19	BSD, H
Stuart, Jim	142:01-142:15	R, 403, BTS, V, PK, SPEC, LC	137:25-138:03; 141:13-17; 141:19	BSD, H

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Stuart, Jim	142:22-143:09	R, 403, BTS, V, PK, SPEC, LC	137:25-138:03; 141:13-17; 141:19	BSD, H
Stuart, Jim	143:22-144:21	R, 403, BTS, V, PK, SPEC		
Stuart, Jim	144:23-146:09	R, 403, V, SPEC, BTS, PK, LC, O	67:11-68:02; 103:2-5	BSD, H
Stuart, Jim	146:11-147:21	R, 403, V, SPEC, BTS, PK, LC, O	67:11-68:02; 103:2-5	BSD, H
Stuart, Jim	147:23-151:06	R, 403, V, SPEC, BTS, PK	67:11-68:02; 103:2-5	BSD, H
Stuart, Jim	151:17-152:05	R, 403, V, I	67:11-68:02; 103:2-5	BSD, H
Stuart, Jim	152:07-152:14	R, 403, V	67:11-68:02; 103:2-5	BSD, H

Salari, Raheleh
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Witness	Natera Designations	Labcorp Objections	Labcorp Counter-Designations	Natera Objections
Salari, Raheleh	008:04-008:20			
Salari, Raheleh	015:15-015:17			
Salari, Raheleh	015:22-015:23			
Salari, Raheleh	016:13-016:17			
Salari, Raheleh	017:09-018:14			
Salari, Raheleh	019:13-020:16			
Salari, Raheleh	020:19-020:19			
Salari, Raheleh	023:24-024:12			
Salari, Raheleh	024:21-026:07			
Salari, Raheleh	027:05-027:10			
Salari, Raheleh	028:09-028:21	H		
Salari, Raheleh	029:11-030:12	H		
Salari, Raheleh	032:14-033:21	H, O		
Salari, Raheleh	033:25-034:22	H, O		
Salari, Raheleh	34:3-22	H, O		
Salari, Raheleh	036:18-037:23		39:25-40:3; 42:14-43:4	F, SPEC
Salari, Raheleh	038:09-038:16		39:25-40:3; 42:14-43:4	F, SPEC
Salari, Raheleh	039:05-039:09	H	39:25-40:3; 42:14-43:4	F, SPEC
Salari, Raheleh	054:03-054:10	H, O	56:7-12	I
Salari, Raheleh	054:24-055:08	H		
Salari, Raheleh	056:13-056:15	H		
Salari, Raheleh	057:06-057:20	H		
Salari, Raheleh	058:06-058:08	H		
Salari, Raheleh	068:09-068:11	H	69:2-4	BSD
Salari, Raheleh	068:13-068:17	H	69:2-4	BSD
Salari, Raheleh	069:23-070:14	H		
Salari, Raheleh	071:05-071:09	H	71:10-12	
Salari, Raheleh	071:22-072:05	H	71:10-12	
Salari, Raheleh	072:21-073:09	H		
Salari, Raheleh	074:06-074:18	OB, H		
Salari, Raheleh	074:23-075:07	H		
Salari, Raheleh	075:11-076:11	H		
Salari, Raheleh	076:14-076:15	H		
Salari, Raheleh	076:23-077:04	H	77:5-10; 77:19-22, 78:8-13	
Salari, Raheleh	079:22-080:25	H		
Salari, Raheleh	081:06-083:09	H, OB		
Salari, Raheleh	083:11-083:14	H		
Salari, Raheleh	084:14-084:25	H	83:23-84:2	
Salari, Raheleh	085:16-085:23	H		
Salari, Raheleh	086:15-086:20	H		
Salari, Raheleh	089:14-090:02	H		
Salari, Raheleh	091:22-091:24	H	93:1-9	BSD
Salari, Raheleh	092:02-092:02	H	93:1-9	BSD
Salari, Raheleh	092:23-092:25	H	93:1-9	BSD
Salari, Raheleh	094:09-094:12	H		
Salari, Raheleh	094:15-095:14	H		
Salari, Raheleh	095:17-095:22	H		
Salari, Raheleh	095:25-096:05	H		
Salari, Raheleh	097:16-098:03	H	98:12-16	
Salari, Raheleh	098:06-098:11	H	98:12-16	
Salari, Raheleh	101:10-101:16	H	109:10-17	CP, I
Salari, Raheleh	101:19-101:19	H	109:10-17	
Salari, Raheleh	103:04-103:09	H		
Salari, Raheleh	103:12-103:13	H		

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Witness	Natera Designations	Labcorp Objections	Labcorp Counter-Designations	Natera Objections
Salari, Raheleh	103:16-103:16	H		
Salari, Raheleh	103:19-104:02	H	104:23-25	
Salari, Raheleh	104:06-104:12	H	104:23-25	
Salari, Raheleh	104:17-107:20	H	104:23-25	
Salari, Raheleh	106:04-106:23	H	64:6-13, 115:20-117:5, 117:10-11, 118:6-23	BSD, F, I, SPEC
Salari, Raheleh	107:14-107:25	H	108:1-15	
Salari, Raheleh	109:18-110:12	H		
Salari, Raheleh	110:22-110:25	H		
Salari, Raheleh	111:09-111:11	H, O	109:10-17	CP, I, MIS
Salari, Raheleh	111:16-112:08	H, O	109:10-17	CP, I, MIS
Salari, Raheleh	112:11-112:11	H, O	109:10-17	CP, I, MIS
Salari, Raheleh	112:20-113:08	H, O	109:10-17	CP, I, MIS
Salari, Raheleh	113:13-113:19	H	109:10-17	CP, I, MIS
Salari, Raheleh	114:11-114:18	H		
Salari, Raheleh	115:08-115:19	H		
Salari, Raheleh	122:10-122:23	H		
Salari, Raheleh	124:10-124:20	H		
Salari, Raheleh	125:10-125:14	H		
Salari, Raheleh	125:18-125:24	H		
Salari, Raheleh	127:03-127:05	H		
Salari, Raheleh	127:07-127:11	H		
Salari, Raheleh	127:15-127:16	H		
Salari, Raheleh	130:11-132:02	H	64:6-13, 115:20-117:5, 117:10-11, 118:6-23, 132:8-9, 132:13	BSD, F, I, SPEC

Witness	Natera Designations	Labcorp Objections	Labcorp Counter-Designations	Natera Objections
Swamy, Sajani	008:09-008:17			
Swamy, Sajani	012:03-015:02	R, 403, V		
Swamy, Sajani	015:05-015:09	V		
Swamy, Sajani	015:05-015:09	V		
Swamy, Sajani	015:25-016:25	R, 403, V, SPEC		
Swamy, Sajani	018:21-020:02	R, 403, V	21:19-22:8; 22:12-23:5	BSD, H
Swamy, Sajani	020:18-021:08	R, 403, V, F	21:19-22:8; 22:12-23:5	BSD, H
Swamy, Sajani	021:10-021:18	R, 403, V, F	21:19-22:8; 22:12-23:5	BSD, H
Swamy, Sajani	023:12-023:14	R, 403, V, F, MIS	24:9-24:23	BSD, H
Swamy, Sajani	023:18-024:07	R, 403, V, F, MIS	24:9-24:23	BSD, H
Swamy, Sajani	031:12-032:01			
Swamy, Sajani	032:08-032:11			
Swamy, Sajani	032:13-032:13			
Swamy, Sajani	032:15-032:16			
Swamy, Sajani	032:19-032:19			
Swamy, Sajani	032:21-033:03			
Swamy, Sajani	033:12-033:16	R, 403, V, F		
Swamy, Sajani	033:18-033:21	R, 403, V, F		
Swamy, Sajani	037:03-037:09	R, 403, V, F, MIS	37:10-15; 41:6-8	H
Swamy, Sajani	037:16-038:05	R, 403, V	37:10-15; 41:6-8	H
Swamy, Sajani	038:11-038:16	R, 403, V, SPEC, PK, F	37:10-15	H
Swamy, Sajani	038:20-038:21	R, 403, V, SPEC, PK, F	37:10-15	H
Swamy, Sajani	039:18-040:11	R, 403, V, SPEC, PK, F	37:10-15; 41:6-8	H
Swamy, Sajani	040:13-040:17	R, 403, V, SPEC, PK, F	37:10-15; 41:6-8	H
Swamy, Sajani	040:19-040:24	R, 403, SPEC, PK, F, O	37:10-15; 41:6-8	H
Swamy, Sajani	041:02-041:04	R, 403, SPEC, PK, F, O	37:10-15; 41:6-8	H
Swamy, Sajani	041:22-042:03	R, 403, SPEC, PK, F	37:10-15; 41:6-8	H
Swamy, Sajani	043:05-044:03	R, 403, V, SPEC, PK, F, LC, O	37:10-15; 41:6-8	H
Swamy, Sajani	044:05-044:05	R, 403, V, SPEC, PK, F, LC, O	37:10-15; 41:6-8	H
Swamy, Sajani	044:07-044:08	R, 403, V, SPEC, PK, F, LC, O	37:10-15; 41:6-8	H
Swamy, Sajani	044:10-044:11	R, 403, V, SPEC, PK, F, LC, O	37:10-15; 41:6-8	H
Swamy, Sajani	044:13-044:16	R, 403, V, SPEC, PK, F, LC, O	37:10-15; 41:6-8	H
Swamy, Sajani	044:20-044:21	R, 403, V, SPEC, PK, F, LC, O	37:10-15; 41:6-8	H
Swamy, Sajani	044:23-045:05	R, 403, V, SPEC, PK, F, LC, O	37:10-15; 41:6-8	H
Swamy, Sajani	045:09-045:17	R, 403, V, SPEC, PK, F, LC, O	37:10-15; 41:6-8	H
Swamy, Sajani	045:24-046:02	R, 403, V, SPEC, PK, F, LC, O	37:10-15; 41:6-8; 46:19-47:4	BSD, H
Swamy, Sajani	046:04-046:05	R, 403, V, SPEC, PK, F, LC, O	37:10-15; 41:6-8; 46:19-47:4	BSD, H
Swamy, Sajani	048:16-049:15	R, 403, V, SPEC, PK, F, LC	37:10-15; 41:6-8; 46:19-47:4	BSD, H
Swamy, Sajani	049:17-049:18	R, 403, V, SPEC, PK, F, LC	37:10-15; 41:6-8; 46:19-47:4	BSD, H
Swamy, Sajani	049:20-049:23	R, 403, V, SPEC, PK, F, LC	37:10-15; 41:6-8; 46:19-47:4	BSD, H
Swamy, Sajani	049:25-050:02	R, 403, V, SPEC, PK, F, LC	37:10-15; 41:6-8; 46:19-47:4	BSD, H
Swamy, Sajani	050:04-050:10	R, 403, V SPEC, PK, F, LC, AA	37:10-15; 41:6-8; 46:19-47:4	BSD, H
Swamy, Sajani	050:12-050:15	R, 403, V SPEC, PK, F, LC	37:10-15; 41:6-8; 46:19-47:4	BSD, H
Swamy, Sajani	050:17-050:18	R, 403		
Swamy, Sajani	050:23-050:24	R, 403		
Swamy, Sajani	052:22-052:25	R, 403, V, PK, F, LC		
Swamy, Sajani	053:02-053:03	R, 403, V, PK, F, LC		
Swamy, Sajani	053:05-053:08	R, 403, V, PK, F, LC		
Swamy, Sajani	053:10-053:12	R, 403, V, PK, F, LC		
Swamy, Sajani	053:14-053:22	R, 403, V, F, LC		
Swamy, Sajani	054:16-055:01			
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Swamy, Sajani	214:20-214:20	R, 403, V, PK, SPEC, O		
Swamy, Sajani	214:22-215:01	R, 403, V, PK, SPEC, O	215:10-12; 215:14-16	BSD, H
Swamy, Sajani	215:03-215:05	R, 403, V, PK, SPEC, O	215:10-12; 215:14-16	BSD, H
Swamy, Sajani	215:07-215:09	R, 403, V, PK, SPEC, O	215:10-12; 215:14-16	BSD, H
Swamy, Sajani	215:18-216:05	R, 403, V, PK, SPEC, O	215:10-12; 215:14-16	H
Swamy, Sajani	216:07-216:08	R, 403, V, SPEC, O	215:10-12; 215:14-16	H
Swamy, Sajani	216:13-216:18	R, 403, V, SPEC, O	215:10-12; 215:14-16	H
Swamy, Sajani	216:20-216:21	R, 403, V, SPEC, PK	215:10-12; 215:14-16	H
Swamy, Sajani	224:14-224:22	R, 403, V, SPEC, PK	215:10-12; 215:14-16	H
Swamy, Sajani	224:24-224:25	R, 403, V, SPEC, F		
Swamy, Sajani	225:08-225:11	R, 403, V, SPEC, PK		
Swamy, Sajani	225:13-225:16	R, 403, V, SPEC, PK		
Swamy, Sajani	225:18-225:19	R, 403, V, SPEC, PK		
Swamy, Sajani	225:21-225:22	R, 403, V, SPEC, PK		
Swamy, Sajani	225:24-226:01	R, 403, V, SPEC, PK		
Swamy, Sajani	226:03-226:05	R, 403, V, SPEC, PK		
Swamy, Sajani	226:15-226:20	R, 403, V, SPEC, PK		
Swamy, Sajani	227:02-227:06			
Swamy, Sajani	228:10-228:14	R, 403, V, SPEC, PK, MIS, O	228:21-25	BSD, H
Swamy, Sajani	228:17-228:20	R, 403, V, SPEC, PK, MIS, O	228:21-25	BSD, H
Swamy, Sajani	230:01-230:08	R, 403, V, SPEC, PK, MIS, O	228:21-25	BSD, H
Swamy, Sajani	230:10-230:10	R, 403, V, MIS, O	228:21-25	BSD, H
Swamy, Sajani	232:20-232:21	R, 403, V, MIS, O	232:6-11; 232:13-18	BSD, H
Swamy, Sajani	232:23-233:02	R, 403, SPEC, PK, V	232:6-11; 232:13-18	BSD, H
Swamy, Sajani	233:04-233:11	R, 403, SPEC, PK, V	232:6-11; 232:13-18	BSD, H
Swamy, Sajani	233:13-233:14	R, 403, SPEC, PK, V	232:6-11; 232:13-18	BSD, H
Swamy, Sajani	233:16-234:06	R, 403, SPEC, PK, V	232:6-11; 232:13-18	BSD, H

Velenich, Andrea
#: 13019

Witness	Natera Designations	Labcorp Objections	Labcorp Counter-Designations	Natera Objections
Velenich, Andrea	006:24-008:18			
Velenich, Andrea	018:03-018:10			
Velenich, Andrea	021:01-022:04	V, 403		
Velenich, Andrea	023:05-023:08	CP, V, R, 403	24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	023:10-023:12	CP, V, R, 403	24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	024:07-024:11		24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	024:22-025:04	CP, PK, V, R, 403	24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	025:06-025:09	CP, PK, V, R, 403	24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	025:15-025:21		24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	027:10-027:16	V, R, LC, 403		
Velenich, Andrea	028:20-028:21	V, R, 403	24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	028:23-029:07	V, R, 403	24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	029:09-029:10	V, R, 403	24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	029:12-029:19	V, R, 403	24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	030:07-030:13	V, 403		
Velenich, Andrea	030:15-030:16	V, 403		
Velenich, Andrea	030:18-030:24	V, 403		
Velenich, Andrea	032:06-032:08	F, V, R, 403	24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	032:10-032:10	F, V, R, 403	24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	032:12-032:19	F, SPEC, V, R, 403	24:12-17, 29:21-30:1, 32:23-33:1, 33:4-8	BSD, H
Velenich, Andrea	032:21-032:21	F, SPEC, V, R, 403	24:12-17, 29:21-30:1, 32:23-33:1, 33:4-8	BSD, H
Velenich, Andrea	034:05-034:09			
Velenich, Andrea	034:23-035:01	O, SPEC, V, R, 403		
Velenich, Andrea	035:03-035:04	O, SPEC, V, R, 403		
Velenich, Andrea	035:06-035:09	F, NARR, O, SPEC, V, R, 403		
Velenich, Andrea	035:12-035:14	F, NARR, O, SPEC, V, R, 403		
Velenich, Andrea	035:16-035:16	F, NARR, O, SPEC, V, R, 403		
Velenich, Andrea	035:18-035:20	F, NARR, O, SPEC, V, R, 403		
Velenich, Andrea	035:22-035:22	F, NARR, O, SPEC, V, R, 403		
Velenich, Andrea	035:24-036:01	F, I, NARR, O, SPEC, V, R, 403		
Velenich, Andrea	036:04-036:07	F, NARR, O, SPEC, V, R, 403		
Velenich, Andrea	036:09-036:12	F, NARR, O, SPEC, V, R, 403		
Velenich, Andrea	036:15-036:20	F, NARR, O, SPEC, V, R, 403		
Velenich, Andrea	036:22-037:01	F, NARR, O, SPEC, V, R, 403		
Velenich, Andrea	037:03-037:12	R, 403		
Velenich, Andrea	037:19-040:01	AA, ARG, CP, F, MIS, NARR, O, OB, R, SPEC, 403, V		
Velenich, Andrea	040:03-040:03	AA, ARG, CP, F, MIS, NARR, O, OB, R, SPEC, 403, V		
Velenich, Andrea	041:06-042:03	V, 403		
Velenich, Andrea	042:05-042:07	SPEC, V, R, 403		
Velenich, Andrea	042:09-042:17	SPEC, V, R, 403		
Velenich, Andrea	042:19-042:21	MIS, NARR, R, 403	43:3-7, 43:9-17	H
Velenich, Andrea	042:23-043:01	MIS, NARR, R, 403	43:3-7, 43:9-17	H
Velenich, Andrea	047:01-047:05	V	47:6-8, 47:10-15; 104:4-5, 104:7-10	BSD, H
Velenich, Andrea	047:24-048:02			
Velenich, Andrea	048:17-049:04			
Velenich, Andrea	049:06-049:09	V, R, 403		
Velenich, Andrea	049:11-049:13	V, R, 403		
Velenich, Andrea	049:15-050:05	O, SPEC, V, R, 403		
Velenich, Andrea	050:08-050:13	O, SPEC, V, R, 403		
Velenich, Andrea	061:06-061:15			
Velenich, Andrea	065:12-065:12	I, R, 403		
Velenich, Andrea	065:18-065:08			
Velenich, Andrea	068:14-069:18	OB, F, CP, V, R, 403		
Velenich, Andrea	069:20-070:12	V, R, 403	47:6-8, 47:10-15; 104:4-5, 104:7-10	BSD, H
Velenich, Andrea	073:08-073:13			
Velenich, Andrea	073:18-073:20	PK, SPEC, V, R, 403		
Velenich, Andrea	073:22-075:10	PK, SPEC, V, R, 403		
Velenich, Andrea	077:01-077:04			
Velenich, Andrea	077:13-077:19			
Velenich, Andrea	077:21-078:05			
Velenich, Andrea	078:07-079:13	R, 403		
Velenich, Andrea	080:01-080:07	SPEC, V, R, 403		
Velenich, Andrea	080:09-080:15	SPEC, V, R, 403		
Velenich, Andrea	080:17-080:22	SPEC, V, R, 403		
Velenich, Andrea	080:24-080:24	SPEC, V, R, 403		
Velenich, Andrea	087:14-087:17	PK, V, R, 403	24:12-17, 29:21-30:1	BSD, H

Velenich, Andrea
#. 13020

Witness	Natera Designations	Labcorp Objections	Labcorp Counter-Designations	Natera Objections
Velenich, Andrea	087:19-087:19	PK, V, R, 403	24:12-17, 29:21-30:1	BSD, H
Velenich, Andrea	090:10-090:12			
Velenich, Andrea	090:21-091:03			
Velenich, Andrea	092:13-092:17			
Velenich, Andrea	094:13-094:15	LC, MIS, PK, R, SPEC, 403, V	139:24-140:3, 140:6-9	BSD, H
Velenich, Andrea	094:17-095:06	LC, MIS, PK, R, SPEC, 403, V	139:24-140:3, 140:6-9	BSD, H
Velenich, Andrea	095:08-095:15	LC, MIS, PK, R, SPEC, 403, V	139:24-140:3, 140:6-9	BSD, H
Velenich, Andrea	096:01-096:03			
Velenich, Andrea	096:12-097:01			
Velenich, Andrea	097:03-097:04			
Velenich, Andrea	097:12-097:17			
Velenich, Andrea	099:12-099:17			
Velenich, Andrea	100:01-100:17	SPEC, V, R, 403		
Velenich, Andrea	100:20-101:04	O, SPEC, V, R, 403	47:6-8, 47:10-15	BSD, H
Velenich, Andrea	101:07-101:16	O, SPEC, V, R, 403	47:6-8, 47:10-15	BSD, H
Velenich, Andrea	101:18-101:20	SPEC, V, R, 403		
Velenich, Andrea	102:01-102:05	SPEC, V, R, 403		
Velenich, Andrea	102:07-102:22		102:23-103:2, 103:4-7, 104:4-5, 104:7-10	BSD, H
Velenich, Andrea	112:24-113:04	O, PK, 403		
Velenich, Andrea	113:17-113:18	O, SPEC, V, R, 403		
Velenich, Andrea	113:20-113:23	O, SPEC, V, R, 403		
Velenich, Andrea	114:01-114:06	O, SPEC, V, R, 403		
Velenich, Andrea	114:08-114:11	PK, SPEC, V, R, 403		
Velenich, Andrea	114:20-116:15	ARG, LC, R, 403		
Velenich, Andrea	116:17-117:08	ARG, LC, R, 403		
Velenich, Andrea	119:01-119:04			
Velenich, Andrea	121:04-121:09	LC, PK, SPEC, V, R, 403		
Velenich, Andrea	121:11-122:17	LC, PK, SPEC, V, R, 403		
Velenich, Andrea	123:05-123:10	LC, PK, SPEC, V, R, 403		
Velenich, Andrea	123:12-123:16	LC, PK, SPEC, V, R, 403		
Velenich, Andrea	125:10-125:20	LC, PK, SPEC, V, R, 403		
Velenich, Andrea	125:22-125:24	LC, PK, SPEC, V, R, 403		
Velenich, Andrea	126:13-126:15	LC, PK, SPEC, V, R, 403		
Velenich, Andrea	126:17-126:20	LC, PK, SPEC, V, R, 403		
Velenich, Andrea	127:01-127:02			
Velenich, Andrea	127:09-127:20			
Velenich, Andrea	127:24-127:24	I, R, 403		

EXHIBIT 10 -
REDACTED IN
ITS ENTIRETY

EXHIBIT 11 -
REDACTED IN
ITS ENTIRETY

EXHIBIT 12

JTX Exhibit No.	Date	Description	Bates Beg No.	Bates End No.	Witness
1	3/31/2020	U.S. Patent No. 10,604,799 (Porreca et al.)	Invitae0000007800	Invitae0000007822	
2	4/11/2014	U.S. Patent No. 10,604,799 File History (Application No. 14/250,891	Invitae0000000001	Invitae0000002508	
3	10/19/2021	U.S. Patent No. 11,149,308 (Porreca et al.)	Invitae0000007823	Invitae0000007850	
4	5/17/2021	U.S. Patent No. 11,149,308 File History (Application No. 17/322,610	Invitae0000002509	Invitae0000002794	
5	10/26/2021	U.S. Patent No. 11,155,863 (Porreca et al.)	Invitae0000007851	Invitae0000007877	
6	5/17/2021	U.S. Patent No. 11,155,863 File History (Application No. 17/322,587	Invitae0000002795	Invitae0000003098	

EXHIBIT 13

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.

Defendant.

C.A. No. 21-669 (GBW)

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.

Defendant.

C.A. No. 21-1635 (GBW)

EXHIBIT 13: PLAINTIFF'S STATEMENT OF INTENDED PROOFS

Pursuant to Delaware Local Rule 16.3(c)(8), Plaintiff Laboratory Corporation of America Holdings (“Labcorp”) hereby submits the following brief statement of what Labcorp intends to prove in support of its claims at trial, including the details of the damages claimed or of other relief sought. This statement is not intended to be exhaustive, and Labcorp reserve the right to prove any matters identified in the pleadings, fact and expert discovery, and any of the accompanying statements of facts and legal issues to be litigated at trial. With respect to proof to be presented by expert testimony, Labcorp incorporates by reference the reports and depositions of Labcorp’s expert witnesses addressing the issues identified below.

Labcorp further reserve the right to amend and/or supplement this statement to the extent necessary to respond to issues raised by Defendant Natera, Inc. (“Natera”) and to rebut any alleged proof(s) offered by Natera before and during trial, in response to rulings by the Court, or for any other reason.

I. INFRINGEMENT OF THE PATENTS-IN-SUIT

A. Infringement of the ’799 Patent

1. Labcorp will prove by a preponderance of the evidence that Natera directly infringes, literally and/or under the doctrine of equivalents, the ’799 Asserted Claims under 35 U.S.C. § 271(a) by performing the claimed process of the ’799 Asserted Claims using the Signatera test.

B. Infringement of the ’308 Patent

2. Labcorp will prove by a preponderance of the evidence that Natera directly infringes, literally and/or under the doctrine of equivalents, the ’308 Asserted Claims under 35 U.S.C. § 271(a) by performing the claimed process of the ’308 Asserted Claims using the Signatera test.

C. Infringement of the '863 Patent

3. Labcorp will prove by a preponderance of the evidence that Natera directly infringes, literally and/or under the doctrine of equivalents, the '863 Asserted Claims under 35 U.S.C. § 271(a) by performing the claimed process of the '863 Asserted Claims using the Signatera test.

II. REMEDIES

4. Labcorp will prove by a preponderance of the evidence that it is entitled to lost profits related to Natera's use of the Signatera test.

5. Labcorp will prove by a preponderance of the evidence that it is entitled to reasonable royalties related to Natera's use of the Signatera test.

6. Labcorp will prove by a preponderance of the evidence that it is entitled to attorneys' fees and costs pursuant to 35 U.S.C. § 285 as a result of Natera's infringement of one or more of the Asserted Claims of the '799 Patent, the '308 Patent, and/or the '863 Patent.

7. Natera bears the burden of proving that they are entitled to any remedies, including that this is an exceptional case and/or attorneys' fees and costs pursuant to 35 U.S.C. § 285 in the event one or more of the Asserted Claims of the Asserted Patents are found not infringed and invalid. Labcorp, to the extent necessary, will introduce evidence to rebut Natera's assertion that it is entitled to any remedies, including that this is an exceptional case and/or attorneys' fees and costs pursuant to 35 U.S.C. § 285.

8. Labcorp will prove by a preponderance of the evidence that it is entitled to a permanent injunction enjoining Natera, its officers, agents, servants, employees, and those persons acting in active concert or participation with all or any of them from using Natera's Signatera test prior to the expiration of the Asserted Patents, pursuant to 35 U.S.C. § 283.

III. VALIDITY

9. Natera bears the burden of establishing by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid under 35 U.S.C. § 101. Labcorp, to the extent necessary, will introduce evidence to rebut Natera's assertion that the Asserted Claims of the Asserted Patents are invalid under 35 U.S.C. § 101.

10. Natera bears the burden of establishing by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid as anticipated under 35 U.S.C. § 102. Labcorp, to the extent necessary, will introduce evidence to rebut Natera's assertion that the Asserted Claims of the Asserted Patents are anticipated under 35 U.S.C. § 102.

11. Natera bears the burden of establishing by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid as obvious under 35 U.S.C. § 103. Labcorp, to the extent necessary, will introduce evidence to rebut Natera's assertion that the Asserted Claims of the Asserted Patents are obvious under 35 U.S.C. § 103, such as evidence of objective indicia of non-obviousness.

12. Natera bears the burden of establishing by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid for failure to satisfy the written description requirement of 35 U.S.C. § 112. Labcorp, to the extent necessary, will introduce evidence to rebut Defendants' assertion that the Asserted Claims of the Asserted Patents are invalid for failure to satisfy the written description requirement of 35 U.S.C. § 112.

13. Natera bears the burden of establishing by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid for failure to satisfy the enablement requirement of 35 U.S.C. § 112. Labcorp, to the extent necessary, will introduce evidence to rebut

Natera's assertion that the Asserted Claims of the Asserted Patents are invalid for failure to satisfy the enablement requirement of 35 U.S.C. § 112.

14. Natera bears the burden of establishing by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid for failure to satisfy the definiteness requirement of 35 U.S.C. § 112. Labcorp objects to Defendants' inclusion of this invalidity ground as an intended proof for the jury trial. Labcorp, to the extent necessary, will introduce evidence to rebut Natera's assertion that the Asserted Claims of the Asserted Patents are invalid for failure to satisfy the definiteness requirement of 35 U.S.C. § 112.

EXHIBIT 14

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

EXHIBIT 14: DEFENDANT'S BRIEF STATEMENT OF INTENDED PROOFS

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Natera respectfully submits the following statement of intended proofs. Further details regarding these intended proofs have been explained at length in Natera's pleadings and discovery responses, including in its contentions, interrogatory responses, expert reports, by experts at depositions, and by fact witnesses at depositions. Natera reserves the right to revise, modify, supplement, or change its statement of intended proofs in response to subsequent Court rulings and/or to rebut Labcorp's identification of issues of law and fact to be litigated and any alleged intended proof(s) or any new issues Labcorp may raise, or for other good cause. The following Statement of Intended Proofs is not exhaustive and Natera reserves the right to prove any matters identified in the pleadings and discovery responses, including in its contentions, expert reports, by experts at depositions, and by fact witnesses at depositions.

Natera will rebut any assertions by Labcorp regarding the intended proofs that Labcorp has set forth in Exhibit 13. Further details regarding Natera's intended proofs are available in Natera's Answer and Counterclaims (D.I. 31); and Natera's discovery responses, including its contentions, interrogatories (including any supplemental responses), and expert reports, as well as statements of experts at depositions, as well as the intended proofs set forth in the parties' Statement of Uncontested Facts, Natera's Statement of Contested Issues of Fact That Remain to Be Litigated, and Natera's Statement of Contested Issues of Law That Remain to Be Litigated, submitted herewith.

I. THE ASSERTED PATENTS ARE INVALID

1. Natera will prove that it is entitled to a judgment that the Asserted Claims of the Asserted Patents are invalid.
2. Natera will prove by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid under 35 U.S.C. §§ 101, 102, 103, and/or 112.

A. Non-Patentable Subject Matter¹

3. Natera will prove by clear and convincing evidence that the Asserted Claims of the Asserted Patents claim non-patentable subject matter under 35 U.S.C. § 101.

B. Anticipation

4. Natera will prove by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid as anticipated under 35 U.S.C. § 102.

C. Obviousness

5. Natera will prove by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid as obvious under 35 U.S.C. § 103.

6. To the extent Labcorp attempts to rely upon any secondary considerations of non-obviousness, and to the extent Labcorp comes forward with evidence of any such secondary considerations and evidence purporting to show nexus, Natera will introduce evidence to rebut Labcorp's assertions of both nexus and any such secondary considerations.

D. Enablement

7. Natera will prove by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid for failure to satisfy the enablement requirement of 35 U.S.C. § 112.

E. Written Description

8. Natera will prove by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid for failure to satisfy the written description requirement of 35 U.S.C. § 112.

¹ Natera refers the Court to its Statement of Additional Matters concerning the presentation and adjudication of the subject-matter-eligibility challenge to the Asserted Claims.

F. Indefiniteness

9. Natera will prove by clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid as indefinite under 35 U.S.C. § 112.

G. Priority Date

10. Natera will rebut any evidence presented by Labcorp to show that the Asserted Claims of the '799, '308, and '863 Patents are entitled to priority dates earlier than their respective application filing dates.

II. NATERA DOES NOT INFRINGE THE ASSERTED PATENTS

11. Natera will show that Labcorp has failed to meet its burden to prove by a preponderance of the evidence that Natera infringes any of the Asserted Claims of the Asserted Patents by using Signatera in violation of 35 U.S.C. § 271(a). For example, Natera will show that the accused functionality of the Signatera test does not satisfy each limitation of the Asserted Claims of the '799, '308, and '863 Patents, either literally or under the doctrine of equivalents. Natera will also show that the claim vitiation doctrine and the doctrine of ensnarement foreclose Labcorp's theory of equivalence.

12. Natera will thus establish that it is entitled to a judgment that Natera does not infringe any of the Asserted Claims of the Asserted Patents.

III. REMEDIES

A. Lost Profits

13. Natera will show that Labcorp has failed to meet its burden to prove by a preponderance of the evidence that, to the extent any of the Asserted Claims of the Asserted Patents are found to be not invalid and infringed, Labcorp is entitled to lost profits damages for the time

period through November 2023.² Natera will also present evidence to rebut Labcorp's claim as to the amount of lost profits damages Labcorp is entitled to.

B. Reasonable Royalty

14. Natera will show that Labcorp has failed to meet its burden to prove by a preponderance of the evidence that, to the extent the Asserted Claims are found to be infringed and not invalid, Labcorp is entitled to the amount of reasonable royalty damages it seeks. Natera will present evidence to rebut Labcorp's asserted reasonable royalty damages amount, royalty base, and royalty rate.

C. Pre-Judgment and Post-Judgment Interest

15. To the extent any of the Asserted Claims of the Asserted Patents are found to be infringed and not invalid, and any damages are awarded, Natera will show that Labcorp has failed to meet its burden to prove by a preponderance of the evidence that it is entitled to pre-judgment and post-judgment interest. To the extent any additional damages are sought by Labcorp post-verdict, Natera will present evidence to rebut Labcorp's asserted damages amount, royalty base, and royalty rate.

D. Permanent Injunction

16. To the extent any of the Asserted Claims of the Asserted Patents are found to be infringed and not invalid, and Labcorp seeks a permanent injunction, Natera will show that Labcorp has failed to meet its burden to prove that Labcorp is entitled to a permanent injunction enjoining Natera's use of the accused functionality in Signatera until the expiration of the Asserted Patents.

² Labcorp has confirmed that it does not seek lost profits for the period after November 2023.

E. Exceptional Case

17. Natera will show that Labcorp has failed to meet its burden to prove that the case is exceptional under 35 U.S.C. § 285.

18. To the extent one or more of the Asserted Claims of the Asserted Patents is found to be not infringed and/or invalid, Natera will prove that this is an exceptional case under 35 U.S.C. § 285.

F. Attorneys' Fees, Costs, and Litigation Expenses

19. To the extent one or more of the Asserted Claims of the Asserted Patents is found to be not infringed and/or invalid, Natera will prove that Natera is entitled to attorneys' fees, costs, and litigation expenses under 35 U.S.C. § 285 and will prove the amount.

20. Natera will prove that it is entitled to any other relief as this Court deems just and proper.

EXHIBIT 15

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.

Defendant.

C.A. No. 21-669 (GBW)

**HIGHLY CONFIDENTIAL –
ATTORNEY’S EYES ONLY**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.

Defendant.

C.A. No. 21-1635 (GBW)

EXHIBIT 15: PLAINTIFF’S STATEMENT OF ADDITIONAL MATTERS

Pursuant to Delaware Local Rule 16.3(c)(13), Plaintiff Laboratory Corporation of America Holdings (“Plaintiff” or “Labcorp”) hereby submit the following additional matters:

1. Natera’s 101 Challenges

As Plaintiff describes in its first motion *in limine*, Plaintiff seeks the Court’s ruling that Judge Stark’s Order on November 30, 2021 (D.I. 28¹ at 5), bars Natera from re-litigating the patent eligibility of the ’799 Patent pursuant to 35 U.S.C. § 101 because of the law of the case. *See Kove IO, Inc. v. Amazon Web Services, Inc.*, 2024 WL 450028, *16–*18 (N.D. Ill. 2024) (ruling that the law of the case applied to the court’s finding on a motion to dismiss and dismissing an accused infringer’s § 101 challenge). Judge Stark’s eligibility ruling should apply with equal force to the ’863 and ’308 Patents, which, as is evident from the claim language, have claims with *narrower* scope than those of the ’799 Patent.

2. Invitae’s Bankruptcy

Natera should be precluded from introducing evidence, testimony, or argument related to Invitae’s bankruptcy proceedings, including Invitae’s financial health leading up to its bankruptcy, the circumstances that may have led to Invitae’s bankruptcy, and the other suit between Natera and Invitae (Case No. 20-125-GBW). As explained in Plaintiff’s second and third motions *in limine*, evidence of the prior litigation between Invitae and Natera and Invitae’s financial health are highly prejudicial to Plaintiff and may mislead the jury when deciding upon issues of infringement invalidity in this case.

¹ Citations are to Case No. 21-669-GBW.

3. Asserted Patents' Critical Dates

Natera should be precluded from introducing evidence, testimony, or argument that contest the asserted patents' priority dates or when the invention was conceived and reduced to practice. None of Natera's experts have proffered opinions on these issues. Yet, Natera includes them in its Statement of Contested Issues of Fact and Statement of Contested Issues of Law. Plaintiff seeks the Court's clarification that that Natera is precluded from eliciting evidence on these issues.

4. Natera's Patents That Signatera Embody

Natera should be precluded from introducing evidence, testimony, or argument that Natera's accused product Signatera does not infringe the asserted patents because it embodies or practices other Natera patents. Whether other Natera patents cover Signatera is irrelevant in this case to the issue of infringement of the asserted patents. *See Atlas Powder Co. v. E.I. du Pont De Nemours & Co.*, 750 F.2d 1569, 1581 (Fed. Cir. 1984) ("Patentable difference does not of itself tend to negative infringement. It may just as well be based upon infringement, plus improvement; and improvement may lie in addition, simplification, or variance."); *Temco Elec. Motor Co. v. Apco Mfg. Co.*, 275 U.S. 319, 328 (1928) ("It is well established that an improver cannot appropriate the basic patent of another, and that the improver without a license is an infringer, and may be sued as such."). Discussion of Natera patents is more like to confuse than help the jury.

5. The Court's Claim Construction Order

Natera should be precluded from introducing evidence, testimony, or argument relating to the Court's Claim Construction Order (D.I. 85) other than the Court's actual adopted constructions. Any attempt by Natera to introduce additional language outside of the claim construction order such as the Court's reasoning, the parties' arguments, and Plaintiff's motion for reconsideration

are more likely to confuse than help the jury and should therefore be excluded under Rule 403. Claim construction “falls ‘exclusively within the province of the court’” and the claim construction order “dictate[s] how *the court* will instruct the jury regarding a claim’s scope.” *Astellas Pharma Inc. v. Zydus, Inc.*, No. 1:20CV1589, 2025 WL 1650497, at *3 (D. Del. June 10, 2025) (quoting *O2 Micro Int’l Ltd. v. Beyond Innovation Tech. Co.*, 521 F.3d 1351, 1359 (Fed. Cir. 2008)) (emphasis added). Presenting lengthy portions of the Court’s Claim Construction Memorandum Opinion (D.I. 85) to the jury is inappropriate and would create a sideshow wherein *the parties* seek to debate before the jury the meaning of various aspects of this opinion. Each side attempting to influence the jury regarding the scope and interpretation of the claims impedes on the Court’s exclusive authority over claim construction and will confuse the jury as to the actual claim scope.

Presenting the Court’s actual adopted constructions from the Court’s Claim Construction Order properly instructs the jury regarding the scope of the claims. *See Sunny Fresh Foods, Inc. v. Michael Foods, Inc.*, 130 F. App’x 459, 464-65 (Fed. Cir. 2005) (“Lastly, Michael Foods argues that the district court erred by providing the jury with ‘a short synopsis’ of the claim construction order. The district court, in fact, provided a copy of the district court’s claim constructions with the jury instructions. Stated more accurately, Michael Foods’s complaint is that the district court provided the jury with merely the disputed claims and their respective definitions but excluded the dicta in the district court’s claim construction order setting forth the reasoning accompanying the actual definitions. This court finds no error in this practice. The district court clearly instructed the jury on the meaning of the disputed claim terms. The law requires no more.”); *MercExchange, LLC v. eBay, Inc.*, 401 F.3d 1323, 1329 (Fed. Cir. 2005), *vacated on other grounds and remanded*, 547 U.S. 388 (2006) (“We also agree with the district court that it was not necessary for the court

to include excerpts from its *Markman* order in the jury instructions. A district court's *Markman* order is an explanation to the parties of the reasoning behind its claim construction. The court's analysis need not be part of the jury instructions."); *Hillman Group, Inc. v. KeyMe, LLC*, 2021 WL 1248180, *4 (E.D. Tex. 2021) (refusing to permit either party presenting to the jury any claim construction materials, including tutorials presented to the court during the claim construction hearing—"Neither party is permitted to present claim construction materials (including tutorials) in a jury trial. The parties are expected to comply with the Court's previous order as stated in the July 2, 2020 claim construction opinion: 'The parties are ordered that they may not refer, directly or indirectly, to each other's claim construction positions in the presence of the jury. Likewise, the parties are ordered to refrain from mentioning any portion of this opinion, other than the actual definitions adopted by the Court, in the presence of the jury. Any reference to claim construction proceedings is limited to informing the jury of the definitions adopted by the Court.'"); *Boston Scientific Corp. v. Cook Medical LLC*, No. 1:17-cv-03448-JRS-MJD, 2023 WL 3604030, at *3 (S.D. Ind. May 22, 2023) ("For the following reasons, the Court precludes Plaintiffs from presenting 'dicta' from the claim construction order to the jury . . . and the jury should only be presented with the final construction adopted by the Court"); *Schwendimann v. Arkwright Advanced Coating, Inc.*, No. CV 11-820 (JRT/HB), 2018 WL 1064556, at *6 (D. Minn. Feb. 26, 2018) ("The Court's Claim Construction Order is a lengthy order that contains a significant amount of discussion and analysis. Both parties sought to include dicta from the Claim Construction Order in the jury instructions. . . . Consistent with the Court's practice, the Court refused to include the additional discussion that accompanied the construction of 'mix' and 'melt.'").

6. Case Narrowing

There is an outstanding issue as to case narrowing. Labcorp proposed narrowing the claims it would assert at trial to ten total claims with no more than four claims per patent in exchange for

Natera narrowing its invalidity grounds to no more than two prior art grounds per patent (each of which is specifically tethered to properly disclosed prior art) and no more than two § 112 defenses per patent. Labcorp based its proposal for the narrowing of the prior art grounds on the case narrowing order from the parties' prior litigation. *See Natera, Inc. v. ArcherDX, Inc.*, C.A. No. 20-125-GBW, D.I. 589, Oral Order (5/5/2023) (Defendants shall specifically identify, as it relates to each patent, up to two prior art defenses (i.e., § 102, § 103) and tether each defense to properly disclosed prior art references. By way of example only, for the '220 patent, Defendants may choose to assert (1) § 102 in view of Iafrate, and (2) § 102 in view of Faham, but as a result, Defendants could not then assert either § 103 in view of Faham OR § 103 in view of Faham and Broude").

Natera has thus far not agreed to Labcorp's proposal. Natera's most recent counterproposal was that Natera would narrow to three prior art grounds per patent, but that Natera would count both an anticipation and a single-reference obviousness defense based on the same prior art as one ground, not two. Natera also did not agree to three § 112 defenses per patent. Natera's counterproposal, is unreasonable and not in line with this Court's order in the prior litigation between the parties. Most troubling, Natera's experts rely upon 11 different primary prior art references in their reports, and for each of them Natera advances both anticipation and single-reference obviousness. Thus, Natera's proposal, if adopted, would allow it to effectively *double* the number of invalidity grounds. Natera's refusal to the number of § 112 defenses is similarly unreasonable.

EXHIBIT 16

**IN THE UNITED STATES DISTRICT COURT
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LABORATORY CORPORATION OF
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Plaintiff,

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C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

**EXHIBIT 16: DEFENDANT'S BRIEF STATEMENT OF
ADDITIONAL MATTERS**

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Natera respectfully submits the following statement of additional matters. Based on the current state of this action and the Court's rulings to date, Natera presents the following list of issues that it would like to address at the Pretrial Conference scheduled for September 3, 2025. Natera reserves the right to revise, modify, supplement, or amend this list based on issues raised by Labcorp, orders by the Court, negotiations between the parties, and/or for other good cause.

I. SUMMARY JUDGMENT AND *DAUBERT* MOTIONS

On September 29, 2023, Natera filed its Motions for Summary Judgment and to Preclude Certain Expert Testimony and accompanying materials. D.I. 214–227.¹ On October 20, 2023, Labcorp (then, Invitae) filed its opposition and accompanying materials. D.I. 246–250. On November 13, 2023, Natera filed its reply and accompanying materials. D.I. 260, 262, 264, 266, 267.

On September 29, 2023, Labcorp (then Invitae) filed its Motions for Summary Judgment and *Daubert* Motion to Exclude Expert Testimony and accompanying materials. D.I. 210. On October 20, 2023, Natera filed its opposition and accompanying materials. D.I. 242–245. On November 13, 2023, Labcorp filed its reply and accompanying materials. D.I. 261, 263, 265.

The Court has not yet ruled on Natera's summary judgment motions, and has not yet ruled on all of the parties' *Daubert* motions. Resolution of Natera's summary judgment motions may entirely resolve the issues for trial, as some of Natera's motions are entirely case dispositive: Natera has moved for summary judgment that Natera does not infringe the Asserted Patents literally or under the doctrine of equivalents, D.I. 218–223, and that certain of the Asserted Claims are invalid as anticipated under 35 U.S.C. §§ 102(a) and 102(g). D.I. 224–226. At a minimum,

¹ Docket cites are to C.A. No. 21-669 unless otherwise specified.

resolution of the motions may streamline the jury trial by resolving certain issues and disposing of a number of evidentiary disputes.

II. THE COURT’S CONSTRUCTION OF “SEQUENCE READS”

The Court construed the term “sequence reads” as “raw reads as generated by the sequencing instrument.” D.I. 84 at 5. Twice, the Court has explained that raw reads, as construed, “do not include any pre-processing or pre-alignment steps performed between sequencing and the claimed manipulation of those reads.” D.I. 84 at 5–6; *see also* D.I. 184 at 3. Labcorp has made clear that it opposes the jury ever being told, in any way, that raw reads do not include pre-processing or pre-alignment steps. Labcorp wants the ability to argue that pre-aligned reads, or pre-processed reads, or pre-aligned **and** pre-processed reads, are somehow “raw,” despite the Court twice having held otherwise. Labcorp’s asserted basis is that the language excluding pre-alignment and pre-processing is in the Court’s opinion, not in its construction. To that end, Labcorp has refused to include in the Cover Pleading and the Statement of Undisputed Facts that the Court’s construction means that the claimed “sequence reads” are unaligned and unprocessed.

Labcorp is incorrect. The Court made clear—both in its *Markman* decision and its decision denying Labcorp’s motion for reconsideration or clarification of its construction of “sequence reads”—that its construction of “raw reads” excludes any pre-aligned and pre-processed reads: “The Court’s Opinion about ‘sequence reads’ is unambiguous... the Court wrote, Defendant Natera, Inc. (‘Natera’) ‘asserts that the claim term “sequence reads” do not include any pre-processing or pre-alignment steps performed between sequencing and the claimed manipulation of those reads. The Court agrees with Natera....’” D.I. 184 at 3. The Court further explained “[t]hat ‘pre-aligned’ reads are not ‘raw reads’ and thus are excluded from the Court’s construction of ‘sequence reads’ is clear from the opinion itself.” *Id.*

Natera respectfully requests that the Court address this issue at the Pretrial Conference, and hold that the jury should be informed that the Court has construed “sequence reads” to mean “raw reads as generated by the sequencing instrument,” which “do not include any pre-processing or pre-alignment steps performed between sequencing and the claimed manipulation of those reads.” D.I. 184 at 3. Natera is not wedded to any particular form by which the jury is so informed; whether that definition comes in as a jury instruction, an agreed-upon statement to be read to the jury, or through the Court’s opinion itself is not itself material. What matters is that the jury learn what the Court has said the construction means, and that Labcorp not be allowed to suggest, argue, or imply otherwise. Misleading the jury should not be Labcorp’s next gambit to seek reconsideration of the Court’s claim construction. *Exergen Corp. v. Wal-Mart Stores, Inc.*, 575 F.3d 1312, 1321 (Fed. Cir. 2009) (“No party may contradict the court’s construction to a jury.”); *Kangaroo Media, Inc. v. YinzCam, Inc.*, C.A. No. 12-0382, 2014 WL 3378692, at *2 (W.D. Pa. July 9, 2014) (“No party will be permitted to argue its rejected claim construction position to the jury.”); *EMC Corp. v. Pure Storage, Inc.*, C.A. No. 13-1985, 2016 WL 775742, at *4 (D. Del. Feb. 25, 2016) (“[Party] is precluded from arguing a meaning to the jury through its expert that it already argued to the Court in the context of claim construction, as that truly would be ‘arguing claim construction to the jury.’”); *Mobile Telecommunications Techs., LLC v. Zte (USA) Inc.*, C.A. No. 13-946, 2016 WL 8260584, at *3 (E.D. Tex. July 22, 2016) (“The parties SHALL NOT introduce any references, evidence, testimony (including expert testimony), or argument that is inconsistent with the Court’s Claim Construction Memorandum and Order”); *LifeNet Health v. LifeCell Corp.*, C.A. No. 13-486, 2014 WL 5529679, at *6–7 (E.D. Va. Oct. 31, 2014) (excluding “arguments contrary to the Court’s claim construction... Plaintiff cannot argue that prior to transplantation actually means prior to packaging.”); *see also Schuyleman v. Barnhart Crane & Rigging Co.*, No.

23-562, 2025 WL 1414087, at *19–20 (W.D. Wash. May 15, 2025) (“Once a district court has construed the relevant claim terms, and unless altered by the district court, then that legal determination governs for purposes of trial. Thus, any expert testimony must adhere to the court’s claim constructions and must not apply alternative claim constructions.” (cleaned up)); *BMC Software, Inc. v. Servicenow, Inc.*, C.A. No. 14-903, 2016 WL 367251, at *2 (E.D. Tex. Jan. 29, 2016) (“no experts are to render any conclusions regarding the scope of the patents-in-suit or particular claim limitations that contradict or deviate from this Court’s Claim Construction Memorandum and Order”); *EVM Sys., LLC v. Rex Med., L.P.*, C.A. No. 13-184, 2015 WL 11089476, at *2 (E.D. Tex. June 10, 2015) (granting motion to exclude “claim construction issues or arguments contradicting the Court’s Claim Construction Order.”).

III. WITNESS IMPEACHMENT WITH PRIOR STATEMENT

Natera proposed in the draft Cover Pleading that where a party seeks to impeach a witness by prior testimony, “The allegedly impeaching testimony must be identified to the Court and opposing counsel and shown to the witness before it is read or displayed to any jury.”

Labcorp rejected this proposal, suggesting that the Court and the parties should address the mechanism for prior-statement impeachment during trial.

Natera respectfully submits that the rules should be set before trial, and should prohibit trial by ambush. Confronting a witness with a prior statement that is not, in fact, inconsistent with the witness’s in-court testimony sows jury confusion and creates unwarranted tension and the baseless impression of dishonesty. Natera submits that before a witness is impeached with a putatively inconsistent prior statement, the testimony should be shown to opposing counsel and the Court for determination whether the in-court and out-of-court statements are actually inconsistent and then, if so, to the witness so that the witness can see the prior testimony and be ready to answer questions about it. *See Jazz Pharm. Inc. v. Avadel CNS Pharm., LLC*, C.A. No.

21-691-GBW, D.I. 545 (Oral Order) (D. Del. Feb. 20, 2024) (holding that deposition testimony of a witness testifying live at trial may be used for impeachment purposes only and “[o]nly if the witness answers a question inconsistent with the prior deposition testimony may Avadel use video excerpts of the prior deposition testimony for impeachment purposes.”); *see also United States v. Hale*, 422 U.S. 171, 176 (1975) (“A basic rule of evidence provides that prior inconsistent statements may be used to impeach the credibility of a witness. As a preliminary matter, however, the court must be persuaded that the statements are indeed inconsistent.”); F.R.E. 613(a) (“When examining a witness about the witness’s prior statement... the party must, on request, show it or disclose its contents to an adverse party’s attorney.”).

IV. REFERENCE TO UNRELATED LITIGATION

Natera recently lost a jury trial in California brought by Guardant Health, Inc., in which Natera was found by the jury to have engaged in false advertising. The damages award was \$292.5 million, of which \$175.5 million represented punitive damages. *See Guardant Health, Inc. v. Natera, Inc.*, C.A. No. 21-04062, D.I. 847 (Verdict Form) (N.D. Cal. Nov. 25, 2024). There has also been press coverage of sanctions proceedings against Natera and its counsel in that case.

Natera asked Labcorp whether it intends to try to introduce anything having to do with the *Guardant* litigation during the trial of this case, expecting that the answer would be “no,” given that the lawsuits are unrelated and reference to the *Guardant* case would unfairly prejudice the jury. Labcorp’s answer was not an unqualified “no.” Instead, Labcorp asserted that it was considering introducing not only the *Guardant* litigation but also other, unspecified prior litigation results involving Natera, but not in Labcorp’s case-in-chief. Labcorp said it would seek to introduce that evidence only if Natera “opened the door” by describing its—to use Labcorp’s counsel’s phrase—“good hygiene.” Labcorp declined to explain that phrase further, identify any specifics as to what it thinks might constitute opening the door, list what evidence it would seek

to admit, or agree in advance to any procedures by which it would warn Natera or the Court that it believed that evidence had become fair game.

There is nothing about the *Guardant* litigation that could be relevant here at all. That Labcorp does not want to identify what other such evidence it might seek to admit suggests that none of that evidence is relevant either, whatever it is. But if Labcorp intends, under any circumstances, to introduce what is essentially bad character evidence against Natera, Natera requests that the parties and the Court discuss this at the pretrial conference to hear exactly what evidence Labcorp would try to admit, and under exactly what circumstances, so the ground rules can be clear for all parties before the trial. To allow Labcorp itself to decide when, in its view, a door has been opened, and then to seek to admit bad-acts evidence in open Court with no warning, risks jury confusion and prejudice at best, and a mistrial at worst.

V. GEORGE GEMELOS AS A TRIAL WITNESS

George Gemelos, Natera's Senior Vice President of Research and Development, will be one of Natera's trial witnesses. The R&D witnesses at Natera who were deposed—Dr. Raheleh Salari and Dr. Hsin-Ta Wu—both left Natera not long after the end of the discovery period. Dr. Gemelos's testimony would address the accused product, Signatera™, its research and development, and its functionality, including the specific portions of Signatera™ that Labcorp accuses of infringement. Dr. Gemelos will address the subject matter that would have been addressed by Drs. Salari and Wu but for their departures from Natera, including the subject matter for which Dr. Salari was designated to testify as Natera's corporate witness under Rule 30(b)(6). Both Drs. Salari and Wu live in California, outside of the Court's trial subpoena power. As a result, Natera promptly added Dr. Gemelos to its Rule 26(a)(1) disclosure and put him on Natera's witness list in January 2024, before Invitae's bankruptcy caused a trial adjournment. At the time, Natera offered to produce Dr. Gemelos for deposition.

In the twenty (20) months since then, Labcorp declined to request a deposition or further press its objection to Dr. Gemelos's inclusion in Natera's Rule 26(a)(1) disclosure. It did not identify any information it needed in any way. (Dr. Gemelos was not one of the parties' agreed-upon document custodians, and Labcorp never identified anything additional it claims to have needed.) To be clear, at then-Invitae's request, the case had not been stayed; if Invitae or Labcorp felt they needed something, they had over a year to ask for it. Indeed, in meet and confers this week, Labcorp declined Natera's offer to depose Dr. Gemelos in Wilmington the week before trial.

Instead, Labcorp seeks to capitalize on its own inaction by seeking to preclude Natera from calling, and to deprive the jury of the chance to hear from, a live Natera witness on a core issue in the case. That is baseless. Deponents leave companies sometimes. The right thing to do when that happens is promptly identify a replacement. That is exactly what Natera did with Dr. Gemelos.

VI. ISSUES FOR THE COURT

Certain issues before the Court, including certain issues presented in Natera's summary judgment motions, are issues of law for the Court to resolve, either before or after the jury trial. Natera wishes to discuss with the Court how the Court prefers to address these issues.

A. Natera's Section 101 Argument

Natera has asserted that the Asserted Claims of the Asserted Patents do not meet the requirements of 35 U.S.C. § 101. *See, e.g.*, C.A. No. 1:21-cv-699, D.I. 31 at ¶ 33; *see generally* C.A. No. 1:21-cv-1635, D.I. 8 at ¶ 45. Satisfaction of this requirement is "ultimately an issue of law" to be decided by the Court. *Berkheimer v. HP Inc.*, 881 F.3d 1360, 1365 (Fed. Cir. 2018), *cert. denied*, 140 S. Ct. 911 (2020). The Court previously denied Natera's motion to dismiss under Fed. R. Civ. P. 12(b)(6), in which Natera argued that all claims of the '799 patent are directed to an abstract idea and unpatentable under Section 101. C.A. No. 1:21-cv-699, D.I. 28 at 3–7. The Court held that Natera failed at Step One of the *Alice* test, finding that representative Claim 1 of

the '799 patent is, as Labcorp (then, Invitae) had argued, “directed to a ‘technological solution to the technological problem of how to better assemble DNA sequences [...] in a more computationally efficient and overall improved way.’” *Id.* at 4–5. But the record that developed subsequently, including inventor testimony and arguments made by Labcorp, shows that the Asserted Claims are not directed to “a specific solution to a technological problem in the field of sequence assembly,” as the Court previously found at the motion-to-dismiss stage. Labcorp has moved in *limine* to preclude Natera from advancing this defense, despite not having sought summary judgment on the issue. *See* Labcorp Motion in *Limine* No. 1. Natera would like to discuss with the Court the manner and timing of the presentation of evidence, and a ruling thereon, concerning its challenge to the subject matter eligibility of the Asserted Claims during the Pretrial Conference.

B. Natera’s Claim Vitiating Argument

Natera has asserted that Labcorp’s theory of infringement under the doctrine of equivalents fails because Labcorp’s equivalence theory would vitiate one or more claim elements of the Asserted Claims of the Asserted Patents. Whether a patentee’s theory of equivalence, in light of the claim language and alleged evidence of infringement, would vitiate the claim limitations is a legal conclusion to be resolved by the Court. *See Bio-Rad Lab’s, Inc. v. 10X Genomics Inc.*, 967 F.3d 1353, 1367, 1371–72 (Fed. Cir. 2020); *see also, e.g., Warner-Jenkinson Co. v. Hilton Davis Chem. Co.*, 520 U.S. 17, 39 n.8 (1997) (“[I]f a theory of equivalence would entirely vitiate a particular claim element, partial or complete judgment should be rendered by the court, as there would be no further material issue for the jury to resolve.”). Natera’s motion for summary judgment on this issue is pending before the Court. *See* D.I. 222, 223, 227, 227-1, 246, 248, 250, 262, 266, 267.

C. Natera's Ensnarement Argument

Natera has asserted that Labcorp's equivalence theory also fails because it would encompass or "ensnare" the prior art. *DePuy Spine, Inc. v. Medtronic Sofamor Danek, Inc.*, 567 F.3d 1314, 1322–23 (Fed. Cir. 2009). "This limitation is imposed even if a jury has found equivalence as to each claim element." *Id.* (citing *Wilson Sporting Goods Co. v. David Geoffrey & Assocs.*, 904 F.2d 677, 683, 687 (Fed. Cir. 1990), *overruled in part on other grounds*, *Cardinal Chem. Co. v. Morton Int'l, Inc.*, 508 U.S. 83, 92 n.12 (1993)). "[E]nsnarement is a legal question for the district court to decide." *G. David Jang, M.D. v. Bos. Sci. Corp.*, 872 F.3d 1275, 1288 (Fed. Cir. 2017); *see also DePuy Spine*, 567 F.3d at 1324 (holding ensnarement is "to be determined by the court, either on a pretrial motion for partial summary judgment or on a motion for judgment as a matter of law at the close of the evidence and after the jury verdict") (quoting *Warner-Jenkinson*, 520 U.S. at 39 n.8). To the extent there is any finding of infringement under the doctrine of equivalents, Natera asks that the issue be addressed in connection with post-trial briefing, supported by expert declarations, and an evidentiary hearing.

VII. CASE NARROWING

Natera responds briefly to Labcorp's discussion of this issue in its Statement of Additional Matters.

The parties have engaged in substantial back-and-forth in an effort to reach agreement on case narrowing. Thus far, the parties have agreed that Labcorp will narrow its number of asserted claims to ten. The parties have also agreed that Natera will narrow its invalidity defenses to three prior-art grounds and three non-prior-art grounds,

One remaining area of disagreement is whether Natera's narrowing of its invalidity defenses should be on a per-claim or per-patent basis. Natera's position is that its defense-narrowing should be on a per-claim basis because, as it has explained to Labcorp, some of the

dependent claims add limitations that may require or give rise to additional invalidity defenses, separate and apart from the claims from which they depend.

The parties also disagree about whether asserting that the same prior-art reference both anticipates a claim and renders that claim obvious (without being read in combination with any other references) should count as one or two prior-art defenses. Natera's position is that anticipation and single-reference obviousness based on the same reference should count as one ground for purposes of narrowing, because the evidence and arguments for anticipation and single-reference obviousness are almost entirely overlapping. Labcorp has refused to agree, but has not explained why beyond stating that "single-reference obviousness and anticipation are two different theories of invalidity that require different proofs."

To the extent that the Court issues any order regarding case narrowing, Natera respectfully requests that Labcorp be ordered to narrow to no more than 10 asserted claims and that Natera be ordered to narrow to no more than three prior art grounds per claim, where anticipation and single-reference obviousness based on the same reference count as one ground, and three non-prior art grounds per claim.

VIII. LABCORP'S UPDATED FINANCIAL INFORMATION

Natera has requested that Labcorp produce updated financial information, through November 2023, for its PCM product, which is the product that Labcorp contends competes with Signatera™ and forms the basis for Labcorp's lost profits claim. Labcorp has not yet responded to Natera's request, but from the parties' recent meet and confer sessions, Natera expects that Labcorp will agree to this request. Out of an abundance of caution Natera is including this issue here, so that if Labcorp refuses to provide updated financial information, the parties and the Court may address this issue at the Pretrial Conference.

IX. IDENTIFICATION OF EXHIBIT NUMBERS USED IN DEMONSTRATIVES

Natera proposed in the draft Cover Pleading that the parties identify by number any exhibits that they rely on in their demonstratives. Specifically, Natera proposed that “[e]ach demonstrative exhibit shall identify by exhibit number all trial exhibits that form the basis of the demonstrative exhibit. Such identified trial exhibits referenced in the demonstrative exhibit and shown to a witness may be offered into evidence during or at the conclusion of the examination for the witness with whom the demonstratives were used.” Natera’s proposal aimed to streamline the presentation of issues at trial and limit confusion by requiring that the parties specify what exhibits are excerpted, cited, or summarized in their demonstratives. Labcorp did not agree with Natera’s proposal, because it was concerned that it would not be able to tell whether and when exhibits would need to be cited for demonstratives that disclose generic concepts. Natera respectfully requests that the Court address this issue at the Pretrial Conference, and hold that, to the extent that a party’s demonstrative quotes, excerpts, summarizes, or depicts one or more exhibits, the party is required to identify by exhibit number all trial exhibits that form the basis of the demonstrative exhibit.

EXHIBIT 17A



OCEAN TOMO®

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ALEXANDER L. CLEMONS CURRICULUM VITAE

January 23, 2024

Alexander L. Clemons is a Managing Director at Ocean Tomo, LLC, a part of J.S. Held. Ocean Tomo provides Financial Expert, Management Consulting, and Advisory services related to intellectual property (“IP”) and other intangible assets, corporate accounting investigations, regulatory and reporting obligations, solvency and restructuring, and contractual or competition disputes. Practice offerings address economic damage calculations and testimony, accounting investigations and financial forensics, technology and intangible asset valuation, strategy and risk management consulting, mergers and acquisitions, debt and equity private placement, and IP brokerage. Subsidiaries of Ocean Tomo include Ocean Tomo Investments Group, LLC, a registered broker dealer. With more than 100 offices globally, J.S. Held assists clients—corporations, insurers, law firms, governments, and institutional investors—on complex technical, scientific, and financial matters across all assets and value at risk.

Mr. Clemons works in Ocean Tomo’s Intellectual Property Disputes Financial Expert Testimony practice. This practice area quantifies economic damages arising from intellectual property disputes and provides general litigation support. Mr. Clemons has extensive experience related to the assessment of economic damages in litigation matters involving intellectual property, breach of contract, and other claims. He has been retained as a damages expert on many engagements, providing written, deposition, arbitration, and trial testimony. Outside of a litigation context, Mr. Clemons has experience with intellectual property valuation and has provided analytical support to clients engaged in licensing negotiations and other transactions.

Mr. Clemons has assisted clients in numerous engagements involving the valuation of intellectual property and the determination of economic damages in commercial suits, including patent infringement, trademark infringement, copyright infringement, trade secret misappropriation, technology misappropriation, and breach of contract litigation. He possesses a solid understanding of the financial issues and theories related to the quantification of damages in litigation. While specific issues vary by engagement, most have included evaluation and analysis of financial and strategic data to support or rebut quantification of lost profits, reasonable royalties, price erosion, unjust enrichment, commercial success, and/or business valuation. Mr. Clemons has supported counsel in all phases of the litigation process from discovery to trial, and his experience spans a wide variety of industries, including pharmaceuticals, medical devices, medical diagnostics, laboratory instruments and reagents, healthcare services, healthcare data, telecommunications, semiconductors, consumer electronics, smart phones, software, gaming, VR/AR, e-commerce, consumer goods, food products, dietary supplements, chemical products, automotive, entertainment, financial services, insurance, firearms, military and aviation technologies, airport security, and ventilation products, among others.

Mr. Clemons graduated with Academic Excellence from the University of Illinois, Urbana-Champaign, with an MBA concentrated in Finance. He graduated *cum laude* from DePaul University, College of Law, with a JD. He also holds a Bachelor of Arts in Rhetoric from the University of Illinois, Urbana-Champaign.

200 West Madison Street
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EDUCATION

University of Illinois, MBA, Concentration in Finance, Graduated with
MBA Academic Excellence Award

DePaul University College of Law, JD, Graduated *cum laude*

University of Illinois, BA, Rhetoric

BAR ADMISSION

State of Illinois
November 2010

EXPERIENCE

Managing Director, Ocean Tomo
January 2022 to Present

Senior Director, Ocean Tomo
January 2021 to December 2021

Director, Ocean Tomo
July 2016 to December 2020

Associate, Ocean Tomo
January 2014 to June 2016

Analyst, Ocean Tomo
March 2013 to December 2013

Attorney, Dodd & Maatuka, LLC
May 2011 to March 2013

Law Clerk, Jeffrey M. Goldberg Law Offices
June 2008 to May 2010

MEMBERSHIPS

American Bar Association
Illinois State Bar Association
Intellectual Property Law Association of Chicago

PUBLICATIONS

“Role of Patent Expert in Antitrust Litigation.” *Lexology*, January 19, 2022.

“Uncertainty in Awarding Defendant’s Profits in Lanham Act Cases after
Romag.” *Landslide*, June 2020. With Cate Elsten.



“Separating ‘Pay’ from ‘Delay’: Fairness Opinions of Reverse Payment Settlements under *Actavis* and Its Progeny.” *Landslide*, July 2015.

“Apportionment in Reasonable Royalty Damages.” *ABA 30th Intellectual Property Law Conference*, March 2015. With Andrew Carter.

“Beyond the Smallest Salable Unit: How Surveys Provide a Path from Recent Case Law to an Appropriate Royalty Base.” *Landslide*, May 2014.

**ENGAGEMENTS
SERVING AS
EXPERT
(client in italics)**

Invitae Corporation v. Natera, Inc.

Civil Action Nos. 1:21-cv-00669 & 1:21-cv-01635
Cases Filed: 05/07/2021 & 11/21/2021
U.S. District Court for the District of Delaware
Claim(s): Patent Infringement
Testimony: Expert Report, Deposition

Photography By Frank Diaz LLC v. Friends of David Schweikert, et al.

Civil Action No. 2:22-cv-01170
Case Filed: 07/13/2022
U.S. District Court for the District of Arizona
Claim(s): Copyright Infringement
Testimony: Expert Report

Fortress Iron L.P. v. Digger Specialties, Inc.

Civil Action No. 3:21-cv-00014
Case Filed: 01/08/2021
U.S. District Court for the Northern District of Indiana
Claim(s): Patent Infringement
Testimony: Expert Report, Deposition

SecurityPoint Holdings, Inc., v. The United States

Civil Action No. 1:11-cv-00268
Case Filed: 05/02/2011
U.S. Court of Federal Claims
Claim(s): Patent Infringement Under 28 U.S.C. § 1498
Testimony: Expert Report, Deposition

Lyft, Inc., v. Quartz Auto Technologies LLC

Civil Case No. 4:21-cv-01871
Case Filed: 03/17/2021
U.S. District Court for the Northern District of California
Claim(s): Patent Infringement, Declaratory Judgment
Testimony: N/A



W. R. Grace & Co.-Conn. v. *Elysium Health, Inc.*

Civil Case No. 1:20-cv-01098

Case Filed: 08/21/2020

U.S. District Court for the District of Delaware

Claim(s): Patent Infringement

Testimony: Expert Report, Deposition, Trial

Central Texas Pain Center PLLC, et al., v. *Eric J. Miller, M.D., et al.*

Arbitration No. 01-21-0018-0513

American Arbitration Association

Claim(s): Breach of Contract

Testimony: Expert Report

DuraSystems Barriers, Inc. v. *Van-Packer Co. and Jeremias, Inc.*

Civil Case No. 1:19-cv-01388

Case Filed: 12/03/2019

U.S. District Court for the Central District of Illinois

Claim(s): Patent Infringement

Testimony: Expert Report, Deposition

***Makina ve Kimya Endustrisi Kurumu* v. Kutlay Kaya, et al.**

Civil Action No. 3:20-cv-00072

Case Filed: 11/24/2020

U.S. District Court for the Western District of Virginia

Claim(s): Trademark Infringement, False Advertising, Unfair

Competition, Breach of Contract

Testimony: Expert Report, Deposition, Trial

***Combined Insurance Company of America* v. Family Heritage Life Insurance Company of America, et al.**

Arbitration No. 01-20-0010-8869

American Arbitration Association

Claim(s): Breach of Contract, Tortious Interference, and Breach of

Fiduciary Duty

Testimony: Expert Report, Deposition, Arbitration

ChromaDex, Inc., et al., v. *Elysium Health, Inc.*

Civil Action No. 1:18-cv-01434

Case Filed: 09/17/2018

U.S. District Court for the District of Delaware

Claim(s): Patent Infringement

Testimony: Expert Report, Deposition



American River Nutrition, LLC, v. Kyäni, Inc.

Civil Action No. 4:19-cv-00255

Case Filed: 07/08/2019

U.S. District Court for the District of Idaho

Claim(s): Patent Infringement

Testimony: Expert Report, Deposition (single deposition for both American River Nutrition matters)

American River Nutrition, LLC, v. Beijing Gingko Group Biological Technology Co., Ltd. et al.

Civil Action No. 8:18-cv-02201

Case Filed: 12/12/2018

U.S. District Court for the Central District of California

Claim(s): Patent Infringement

Testimony: Expert Report, Deposition (single deposition for both American River Nutrition matters)

Otto Brands, LLC, et al., v. Otto's Express Car Wash, LLC, et al.

Civil Action No. 3:19-cv-00572

Case Filed: 04/11/2019

U.S. District Court for the Northern District of Florida

Claim(s): Trademark Infringement, Unfair Competition, False Designation of Origin, Anti-Cybersquatting, and False Advertising

Testimony: Expert Report

Auto Konnect, LLC, v. BMW of North America, LLC, et al.

Civil Action No. 2:18-cv-14019

Case Filed: 12/21/2018

U.S. District Court for the Eastern District of Michigan

Claims(s): Breach of Contract and Breach of the Implied Covenant of Good Faith and Fair Dealing

Testimony: Expert Report, Deposition, Trial

Halosil International, Inc., et al., v. Eco-Evolutions, LLC, et al.

Civil Action No. 1:18-cv-01375

Case Filed: 09/05/2018

U.S. District Court for the District of Delaware

Claims(s): Breach of Contract and False Advertising

Testimony: Expert Report, Deposition

Virginia Vallejo v. Narcos Productions LLC, et al.

Civil Action No. 1:18-cv-23462

Case Filed: 08/24/2018

U.S. District Court for the Southern District of Florida

Claims(s): Copyright Infringement

Testimony: Expert Report



Palm Partners, LLC, v. National Association of Addiction Treatment Providers

Civil Action No. 9:18-cv-81638

Case Filed: 11/30/2018

U.S. District Court for the Southern District of Florida

Claim(s): Defamation, Trade Libel, and Tortious Interference with Prospective Economic Advantage

Testimony: Expert Report

Gary James v. OneUnited Bank, N.A., et al.

Civil Action No. 1:17-cv-24415

Case Filed: 12/06/2017

U.S. District Court for the Southern District of Florida

Claim(s): Copyright Infringement

Testimony: Expert Report, Deposition

Genedics, LLC, v. Leap Motion, Inc.

Civil Action No. 1:18-cv-00265

Case Filed: 02/15/2018

U.S. District Court for the District of Delaware

Claim(s): Patent Infringement

Testimony: N/A

Umbanet, Inc., v. Epsilon Data Management, LLC

Civil Action No. 2:16-cv-00682

Case Filed: 06/23/2016

U.S. District Court for the Eastern District of Texas

Claim(s): Patent Infringement

Testimony: N/A

**ENGAGEMENTS
ASSISTING OTHER
OCEAN TOMO
EXPERTS
(client in italics)**

Novartis Pharma AG, et al., v. Regeneron Pharmaceuticals, Inc.

Civil Action No. 1:20-cv-00690

U.S. District Court for the Northern District of New York

Claim(s): Patent Infringement

hiQ Labs, Inc. v. LinkedIn Corporation

Civil Action No. 3:17-cv-03301

U.S. District Court for the Northern District of California

Claim(s): Declaratory Judgment, Intentional Interference with Contract and Prospective Economic Advantage, Unfair Competition, Computer Fraud and Abuse Act, California Comprehensive Computer Access and Fraud Act, Breach of Contract, Misappropriation, Trespass to Chattels



Mexichem Amanco Holding, S.A. de C.V. v. The Chemours Company, et al.

Civil Action No. 4:20-cv-01960

U.S. District Court for the Southern District of Texas

Claim(s): Patent Infringement

Roche Diabetes Care, Inc., v. Insulet Corporation

Civil Action No. 1:20-cv-00825

U.S. District Court for the District of Delaware

Claim(s): Patent Infringement

Regeneron Pharmaceuticals, Inc., v. Novartis Pharma AG, et al.

Case IPR2021-00816

United States Patent and Trademark Office

Claim(s): Patent Invalidity

Baxter International Inc., et al., v. CyDex Pharmaceuticals, Inc., et al.

Arbitration No. 01-21-0002-6106

American Arbitration Association

Claim(s): Breach of Contract, Declaratory Judgment, Breach of Implied Covenant of Good Faith and Fair Dealing

PureCircle USA Inc., et al., v. SweeGen, Inc., et al.

Civil Action No. 8:18-cv-01679

U.S. District Court for the Central District of California

Claim(s): Patent Infringement

Crocs, Inc., v. Effervescent, Inc., et al.

Civil Action No. 1:06-cv-00605

U.S. District Court for the District of Colorado

Claim(s): False Advertising, Patent Infringement

Cisco Systems, Inc., et al., v. Jedd Williams

Arbitration No. 1310025030

JAMS Arbitration

Claim(s): Misappropriation of Trade Secrets, Breach of Contract, Breach of Fiduciary Duty, Breach of the Implied Covenant of Good Faith and Fair Dealing

Align Activation Wear, LLC, v. lululemon usa inc., et al.

Civil Action No. 2:20-cv-03339

U.S. District Court for the Central District of California

Claim(s): Trademark Infringement, False Designation of Origin, and Unfair Competition



Huawei Technologies Co. Ltd., v. Verizon Communications, Inc., et al.

Civil Action No. 2:20-cv-00030

U.S. District Court for the Eastern District of Texas

Claim(s): Patent Infringement, RAND Obligations

Bio-Rad Laboratories, Inc., et al., v. 10X Genomics, Inc.

Civil Action No. 1:19-cv-12533

U.S. District Court for the District of Massachusetts

Claim(s): Patent Infringement and Antitrust Violation of Section 2 of the Sherman Act and Section 7 of the Clayton Act

Bio-Rad Laboratories, Inc., et al., v. Stilla Technologies, Inc., et al.

Civil Action No. 1:19-cv-11587

U.S. District Court for the District of Massachusetts

Claim(s): Patent Infringement

In the Matter of Certain Pre-filled Syringes for Intravitreal Injection and Components Thereof

Investigation No. 337-TA-1207

U.S. International Trade Commission

Claims(s): Patent Infringement

ICON Health & Fitness, Inc., v. Peloton Interactive, Inc.

Civil Action No. 1:20-cv-01386

U.S. District Court for the District of Delaware

Claim(s): Patent Infringement

CareDx, Inc., v. Natera, Inc.

Civil Action No. 1:19-cv-00662

U.S. District Court for the District of Delaware

Claim(s): False Advertising, Unfair Competition, and Unfair or Deceptive Trade Practices

Match Group, LLC, v. Bumble Trading Inc., et al.

Civil Action No. 6:18-cv-00080

U.S. District Court for the Western District of Texas

Claim(s): Patent Infringement, Trademark Infringement, Trade Dress Infringement, Trademark Dilution, Unfair Competition, and Misappropriation of Trade Secrets

Sanyo Electric Co., Ltd., v. Intel Corporation

Civil Action No. 2018-0723

Court of Chancery of the State of Delaware

Claim(s): Declaratory Judgment of Parties' Contractual Rights, Request for Contract Reformation, and Breach of Contract



Allscripts Healthcare, LLC, v. DR/Decision Resources, LLC
d/b/a Decision Resources Group

Civil Action No. 1:19-cv-11038

U.S. District Court for the District of Massachusetts

Claim(s): Misappropriation of Trade Secrets, Breach of Contract, Unfair and Deceptive Trade Practices, and Fraudulent Inducement

Illumina, Inc., v. Natera, Inc.

Civil Action No. 3:18-cv-01662

U.S. District Court for the Northern District of California

Claim(s): Patent Infringement

In the Matter of Certain Botulinum Toxin Products, Processes for Manufacturing or Relating to Same and Certain Products Containing Same

Investigation No. 337-TA-1145

U.S. International Trade Commission

Claims(s): Misappropriation of Trade Secrets

SecurityPoint Holdings, Inc., v. The United States

Civil Action No. 1:11-cv-00268

U.S. Court of Federal Claims

Claim(s): Patent Infringement Under 28 U.S.C. § 1498

Plexxikon, Inc., v. Novartis Pharmaceuticals Corporation

Civil Action No. 4:17-cv-04405

U.S. District Court for the Northern District of California

Claim(s): Patent Infringement

The Gillette Company v. Dollar Shave Club, Inc. et al.

Civil Action No. 1:15-cv-01158

U.S. District Court for the District of Delaware

Claim(s): Patent Infringement

Inguran, LLC, d/b/a STGenetics, et al., v. ABS Global, Inc., et al.

Civil Action No. 3:17-cv-00446

U.S. District Court for the Western District of Wisconsin

Claim(s): Patent Infringement

Masterbuilt Manufacturing, LLC, v. Wal-Mart Stores, Inc.

Civil Action No. 4:17-cv-00213

U.S. District Court for the Middle District of Georgia

Claim(s): Patent Infringement

Gilead Sciences, Inc., v. Roche Molecular Systems, Inc.

Arbitration No. 01-16-0004-7625

American Arbitration Association

Claim(s): Breach of Contract



Optical Air Data Systems, LLC, v. *L-3 Communications Corp., Display Systems Division, et al.*

Civil Action No. N17C-05-619

Superior Court of the State of Delaware

Claim(s): Breach of Contract

Acantha LLC* v. *DuPuy Orthopaedics Inc., et al.

Civil Action No. 1:15-cv-01257

U.S. District Court for the Eastern District of Wisconsin

Claim(s): Patent Infringement

Verinata Health, Inc., et al.,* v. *Ariosa Diagnostics, Inc., et al.

Civil Action No. 3:12-cv-05501

U.S. District Court for the Northern District of California

Claim(s): Patent Infringement

Lotes Co., Ltd.,* v. *Hon Hai Precision Industry Co., Ltd., et al.

Civil Action No. 3:11-cv-01036

U.S. District Court for the Northern District of California

Claim(s): Patent Infringement, Breach of Contract, and Underpayment of Royalties

RainDance Technologies, Inc., et al.,* v. *10X Genomics, Inc.

Civil Action No. 1:15-cv-00152

U.S. District Court for the District of Delaware

Claim(s): Patent Infringement

Shuffle Tech International LLC, et al.,* v. *Scientific Games Corporation, et al.

Civil Action No. 1:15-cv-03702

U.S. District Court for the Northern District of Illinois

Claim(s): Antitrust Violation of Section 2 of the Sherman Act and Section 7 of the Clayton Act

Idenix Pharmaceuticals LLC, et al.,* v. *Gilead Sciences, Inc.

Civil Action No. 1:14-cv-00846

U.S. District Court for the District of Delaware

Claim(s): Patent Infringement

Gilead Sciences, Inc.,* v. *Merck & Co., Inc., et al.

Civil Action No. 5:13-cv-40572

U.S. District Court for the Northern District of California

Claim(s): Patent Infringement

Actavis Laboratories UT, Inc.* v. *UCB, Inc.

Civil Action No. 2:15-CV-01001

U.S. District Court for the Eastern District of Texas

Claim(s): Patent Infringement

***Sanofi-Aventis U.S. LLC, et al., v. Genentech, Inc., et al.***

Civil Action No. 2:15-cv-05685

U.S. District Court for the Central District of California

Claim(s): Patent Infringement

Advanced Aerospace Technologies, Inc., v. The United States, et al.

Civil Action No. 1:12-cv-00085

U.S. Court of Federal Claims

Claim(s): Patent Infringement Under 28 U.S.C. § 1498

Fujitsu Limited v. Tellabs, Inc., et al.

Civil Action No. 1:09-cv-04530

U.S. District Court for the Northern District of Illinois

Claim(s): Patent Infringement, RAND Obligations

Mitsubishi Electric Corp., et al., v. Sceptre, Inc.

Civil Action No. 2:14-cv-04994

U.S. District Court for the Central District of California

Claim(s): Patent Infringement of Standard Essential Patents

Zenith Electronics LLC, et al., v. Sceptre, Inc.

Civil Action No. 2:14-cv-05150

U.S. District Court for the Central District of California

Claim(s): Patent Infringement of Standard Essential Patents

Rembrandt Social Media, LP, v. Facebook, Inc., et al.

Civil Action No. 1:13-cv-00158

U.S. District Court for the Eastern District of Virginia

Claim(s): Patent Infringement

Zecotek Imaging Systems Pte. Ltd. v. Saint-Gobain Ceramics & Plastics, Inc., et al.

Civil Action No. 5:12-cv-01533

U.S. District Court for the Northern District of Ohio

Claim(s): Patent Infringement

GSI Technology, Inc., v. United Memories, Inc., et al.

Civil Action No. 5:13-cv-01081

U.S. District Court for the Northern District of California

Claim(s): Breach of Contract, Unfair Competition, Fraud, Misappropriation of Trade Secrets, and Intentional Interference with Prospective Economic Advantage



Dalmatia Import Group, Inc., et al., v. FoodMatch, Inc., et al.

Civil Action No. 2:16-cv-02767

U.S. District Court for the Eastern District of Pennsylvania

Claim(s): Misappropriation of Trade Secrets, Breach of Contract, Unfair Competition, Tortious Interference with Contract, Trademark Infringement, Trademark Counterfeiting, and Conversion

Kuryakyn Holdings, LLC, v. Ciro, LLC, et al.

Civil Action No. 3:15-cv-00703

U.S. District Court for the Western District of Wisconsin

Claim(s): Misappropriation of Trade Secrets, Copyright Infringement, Unfair Competition and False Advertising, Breach of Contract, Breach of Fiduciary Duty, Unfair Competition, and Conversion

CONTACT

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Ocean Tomo, LLC

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EXHIBIT 17B

Curriculum Vitae

A. NAME

Joshua P. Earl

B. PROFESSIONAL MAILING ADDRESS

Professional Address:

Department of Microbiology and Immunology Center for Genomic Sciences
Drexel University College of Medicine
245 N. 15th Street
Philadelphia, PA 19102

C. EDUCATION

2014-2018

PhD in Biomedical Sciences, Concentration in Bioinformatics
Drexel University, Philadelphia PA 19102

2007-2009

MS in Computational Biology
Carnegie Mellon University, Pittsburgh PA 15213
Completed: Dec 2009

2001-2004

BS Major: Environmental Studies/Biology, Minor: Philosophy
St. Lawrence University, Canton NY 13617
Awarded: May 16, 2004 Honors: Cum Laude

2000-2001

A.A.S. Computer Information Technology
SUNY Canton, Canton NY 13617

1998-1999

Computer Science
Clarkson University, Potsdam NY

D. EMPLOYMENT HISTORY

2022-Present

Assistant Professor, Director of Clinical and Translational Bioinformatics

Drexel University College of Medicine, 245 N Broad St. Philadelphia PA 19102. All previous responsibilities at this institution. Additionally, increased management responsibility for new laboratory information management system (LIMS) design, implementation, and management, including overseeing new database administrator and additional bioinformatics programming personnel. Further development of bioinformatics pipelines to be used by the new Clinical Laboratory Improvements Amendments (CLIA) and College of American Pathologists (CAP) certified Drexel Medicine Diagnostics Laboratory, including novel new tests such as Lyme Disease infection, full-length 16S-based microbiome test, and 18S ribosomal region human-associated fungal species test.

2020-2022

Assistant Professor, Director of Bioinformatics

Drexel University College of Medicine, 245 N Broad St. Philadelphia PA 19102 Primarily the same responsibilities of the previous Research Instructor position, however new added responsibilities include overseeing the technical computer hardware/software development of a new COVID-19 testing lab. This included creating software to automatically interpret output of high throughput PCR Quantstudio machine tests, and workflow to integrate data into multiple health system and laboratory information systems. I also wrote and implemented standard operating procedure (SOP) creation and validation for laboratory information management systems (LIMS) for CLIA certification. Workflow development for all sequencers to final datasets and reports, which includes whole genome (bacterial) sequencing on Pacific Biosciences Sequel and Illumina Miseq/Nextseq assembly pipelines, a novel highly accurate microbiome sequencing to organism identification using Pacbio Sequel, pipeline implementation of COVID-19 strain identification using Pacbio Sequel, and currently developing a new novel fungal microbiome identification pipeline to match the same degree of granularity as our bacterial microbiome identification pipeline. In addition to doing lectures for multiple graduate level courses (phylogenetics, database information mining), I also run two weekly education clubs teaching statistical analysis in the R framework and using the Linux operating system for scientific research.

2013-2020

Research Instructor, Director of Bioinformatics

Drexel University College of Medicine, 245 N Broad St. Philadelphia PA 19102 Responsible for bioinformatics software and hardware development to support new Genomic Sequencing Center. Oversee bioinformatics programming group (2 bioinformatics programmers), graduate student mentorship in bioinformatics and assist teaching bioinformatics graduate classes. Continuing management, support and independent development of all bioinformatics research and analysis in prokaryote and eukaryote sequencing efforts. DNA sequencing technologies overseen include Pacific Biosciences RSII, Pacific Biosciences Sequel, Illumina Nextseq, and Roche Life Sciences 454. Management and system administration of Centos 6 Linux cluster computing system for DNA sequencing analysis and support for department. Development of multiple analysis pipelines for NGS (next generation sequencing) data analysis, including a novel 16S whole gene sequencing and clustering analysis pipeline in Ruby and R, whole genome assembly and annotation, and comparative genomic analysis pipelines for bacterial genomes using statistical techniques, transcriptome analysis with RNAseq.

2010-2013

Assistant Professor, Director of Bioinformatics:

Center for Genomic Sciences, Allegheny-Singer Research Institute, Pittsburgh, PA Responsible for the setup and continued maintenance of over 10 Windows/Linux servers for genomic analysis/data storage (including virtualized environments for specific analyses using both Hyper-V and VirtualBox). Oversaw installation and implementation of current generation sequencing technology of the Pacific Biosciences RS sequencer, both software and hardware. Developed pipelines for whole genome assembly and comparative genome analysis using current computational algorithms tailored for two sequencing methodologies (Roche 454 and Pacific Biosciences RSII). Developed programs to automate and facilitate genomic/genetic analysis for various data types. Implemented user friendly SQL database backed online tools with Ruby on Rails web application design, and database management protocol.

2008-2009

Computational Biology/Bioinformatics Programmer:

Center for Genomic Science, Allegheny-Singer Research Institute, Pittsburgh PA, Bioinformatics group. Responsible for development/maintenance of genomic analysis pipeline. Consulted/developed novel techniques for identifying horizontal gene transfer events. Developed statistical analysis of genomic data analysis for both prokaryotic/eukaryotic DNA sequence. Developed Java/Perl/R/VBA programs to automate various genomic analysis tasks, consulted on server hardware setup/use. Consulted/designed/implemented computer algorithms for sequence analysis of 2nd gen high-throughput genomics, including 454 Roche Lifesciences and Illumina sequence

2007-2008

Departmental Fellowship: Carnegie Mellon University, Pittsburgh, PA

2006-2007

Metrology Chemist, Pfizer/Johnson and Johnson:

Lititz, PA Quality Control Department. Responsible for calibration, maintenance, and repair of laboratory equipment on a monthly/yearly basis in microbiology, and chemistry labs. Repaired equipment ranging from relatively simple (water baths, electronic pipettes) to complex (computers, highly accurate measurement machinery). Dealt directly with vendors troubleshooting equipment, ordering parts, and scheduling vendor required calibrations.

2004-2006

Pharmaceutical Microbiology Analyst:

Lancaster Labs Inc. Performed FDA quality control testing on a variety of pharmaceutical products, including DEA controlled substances, and highly toxic compounds. Proficient in all SOP microbiological analyses ranging from total colony forming unit tests, to specific organism identification procedures (including Salmonella, Enteric, Staphylococcus, Pseudomonas, and Clostridia spp.) and helped adapt client methods to in-house testing. Responsible for environmental monitoring of BSL2 GLP compliant laboratory space, and the equipment therein. Given increased responsibility regularly during employment. Volunteered on large projects out of my department.

2004

Web Design Consultant

Town of Lisbon, N.Y. Collected information, designed, implemented and provided technical assistance for the Town of Lisbon's web site. Spring

Curriculum vitae

2003-2004

Forest Ecology T.A. (Teaching Assistant)

Biology Department St. Lawrence University

General Biology T.A.

Biology Department St Lawrence University (awarded 4.0/4.0 grade)

1999-2000

Warehouse Manager Targray Inc. Responsible for all incoming/outgoing shipping for warehouse in Northern NY, including invoices, bills of lading, Material Safety Data Sheets, inventory counts, and database management.

E. HONORS AND AWARDS

Travel Award Spring 2019 International Society for Otitis Media, Hollywood CA

Departmental Fellowship: Fall 2007 Carnegie Mellon University, Pittsburgh, PA

Beta Beta Beta Honors Society for Biology, Spring 2003-present

- Awarded for maintaining a 3.5/4.0 GPA in all Biology classes

Latin Honors: Cum Laude upon graduation from St. Lawrence University

Dean's List: St. Lawrence University Fall 2001 (Awarded for GPA > 3.62/4.0)

Phi Theta Kappa: Honors society for two year Colleges, SUNY Canton

F. Expert Witness Consulting Experience

1. Investigation No. 337-TA-1032 CERTAIN SINGLE-MOLECULE NUCLEIC ACID SEQUENCING SYSTEMS AND REAGENTS, CONSUMABLES, AND SOFTWARE FOR USE WITH SAME. 2016-2017
 - a. Source code review, patent review, report writing, deposition.
2. C. A. No. 17-cv-275-LPS-CJB & C. A. No. 17-cv-1353-LPS-CJB Pacific Biosciences of California, Inc. v. Oxford Nanopore Technologies, Inc., No. 1:2017cv00275 - Document 152 (D. Del. 2019)
 - a. Source code review, patent review, report writing, deposition, and trial testimony.
3. Case No. IPR2022-01158 Guardant Health Inc. v. University of Washington IPR of '951
 - a. Source code review, patent review, report writing
4. Case Nos: 21-cv-669-GBW and 21-cv-1635-GBW. Invitae Corporation v. Natera, Inc.
 - a. Source code review, patent review, report writing

G. EDUCATIONAL ACTIVITIES

Teaching Experience

Classes taught on bioinformatics concepts including Linux command line usage for bioinformatics analysis, bacterial genomics and phylogenetics, omics, and usage of the R statistical package in analysis of bioinformatics. Classes include **MIIM 555S Molecular Mechanisms of Microbial Pathogenesis**, **MIIM-620S OMICS**, **MIIM-542S-900 Mycology and Fungal Infections**, and **MIIM 513S MOLECULAR PATHOGENESIS II** in the Department of Microbiology and Immunology in the Institute for Molecular Medicine and Infectious Disease. Mentoring PhD students in comparative genomics, Linux operating system command line usage, R, programming, bioinformatics programs and analysis on two pangenomics projects (*Gardnerella vaginalis*, and *Porphyromonas gingivalis*), and an investigation of HPV integration into the human genome.

H. BIBLIOGRAPHY

Published full-length papers

1. Su, Y.-P., Lin, S. Y., Su, I.-J., Kao, Y.-L., Shen, S.-C., **Earl, J. P.**, Ehrlich, G. D., Chen, C.-Y., Huang, W., Su, Y.-H., & Tsai, H.-W. (2024). Characterization of integrated hepatitis B virus DNA harboring pre-S mutations in hepatocellular carcinoma patients with ground glass hepatocytes. *Journal of Medical Virology*, 96(1), e29348.
2. Moné, Y., **Earl, J. P.**, Król, J. E., Ahmed, A., Sen, B., Ehrlich, G. D., & Lapedes, J. R. (2023). Evidence supportive of a bacterial component in the etiology for Alzheimer's disease and for a temporal-spatial development of a pathogenic microbiome in the brain. *Frontiers in Cellular and Infection Microbiology*, 13, 1123228.
3. Dampier, W., Link, R. W., **Earl, J. P.**, Collins, M., De Souza, D. R., Koser, K., Nonnemacher, M. R., & Wigdahl, B. (2022). HIV- Bidirectional Encoder Representations From Transformers: A Set of Pretrained Transformers for Accelerating HIV Deep Learning Tasks. *Frontiers in Virology*, 2. <https://doi.org/10.3389/fviro.2022.880618>
4. Nickel, J. C., Ehrlich, G. D., Krol, J. E., Ahmed, A., Sen, B., Bhat, A., Mell, J. C., Doiron, R. C., Kelly, K.-L., & **Earl, J. P.** (2022). The bacterial microbiota of Hunner lesion interstitial cystitis/bladder pain syndrome. *BJU International*.
5. Xu, L., **Earl, J.**, & Pichichero, M. E. (2021). Nasopharyngeal microbiome composition associated with Streptococcus pneumoniae colonization suggests a protective role of Corynebacterium in young children. *PloS One*, 16(9), e0257207.
6. Socarras, K. M., **Earl, J. P.**, Krol, J. E., Bhat, A., Pabilonia, M., Harrison, M. H., Lang, S. P., Sen, B., Ahmed, A., Hester, M., Mell, J. C., Vandegrift, K., & Ehrlich, G. D. (2021). Species-Level Profiling of Ixodes pacificus Bacterial Microbiomes Reveals High Variability Across Short Spatial Scales at Different Taxonomic Resolutions. *Genetic Testing and Molecular Biomarkers*, 25(8), 551–562.

7. Xu, L., **Earl, J.**, Bajorski, P., Gonzalez, E., & Pichichero, M. E. (2021). Nasopharyngeal microbiome analyses in otitis-prone and otitis-free children. *International Journal of Pediatric Otorhinolaryngology*, 143, 110629.
8. Majer, H. M., Ehrlich, R. L., Ahmed, A., **Earl, J. P.**, Ehrlich, G. D., & Beld, J. (2021). Whole genome sequencing of *Streptomyces actuosus* ISP-5337, *Streptomyces sioyaensis* B-5408, and *Actinospica acidiphila* B-2296 reveals secondary metabolomes with antibiotic potential. *Biotechnology Reports (Amsterdam, Netherlands)*, 29, e00596.
9. Nickel*, J. C., Ehrlich, G., Doiron, R. C., Kelly, K.-L., & **Earl, J.** (2020). Mp77-03 the microbiome of Hunner lesions in interstitial cystitis/bladder pain syndrome (ic/bps). *The Journal of Urology*, 203(Supplement 4), e1163–e1164.
10. Santos-Cortez, R. L. P., Bhutta, M. F., **Earl, J. P.**, Hafren, L., Jennings, M., Mell, J. C., Pichichero, M. E., Ryan, A. F., Tateossian, H., & Ehrlich, G. D. (2020). Panel 3: Genomics, precision medicine and targeted therapies. *International Journal of Pediatric Otorhinolaryngology*, 130 Suppl 1, 109835.
11. Innamorati, K. A., **Earl, J. P.**, Aggarwal, S. D., Ehrlich, G. D., & Hiller, N. L. (2020). The Bacterial Guide to Designing a Diversified Gene Portfolio. In H. Tettelin & D. Medini (Eds.), *The Pangenome: Diversity, Dynamics and Evolution of Genomes*. Springer.
12. Król, J. E., Hall, D. C., Balashov, S., Pastor, S., & Sibert, J. (2019). Genome rearrangements induce biofilm formation in *Escherichia coli* C—an old model organism with a new application in biofilm research. *BMC Genomics*. <https://link.springer.com/article/10.1186/s12864-019-6165-4>
13. **Earl, J. P.**, Adappa, N. D., Krol, J., Bhat, A. S., Balashov, S., Ehrlich, R. L., ... Mell, J. C. (2018). Species-level bacterial community profiling of the healthy sinonasal microbiome using Pacific Biosciences sequencing of full-length 16S rRNA genes. *Microbiome*, 6(1), 190.
14. Greathouse, K. Leigh, James R. White, Ashely J. Vargas, Valery V. Bliskovsky, Jessica A. Beck, Natalia von Muhlinen, Eric C. Polley, Bowman ED, Khan MA, Robles AI, Cooks T, Ryan BM, Padgett N, Dzutsev AH, Trinchieri G, Pineda MA, Bilke S, Meltzer PS, Hokenstad AN, Stickrod TM, Walther-Antonio MR, **Earl JP** et al. 2018. Interaction between the Microbiome and TP53 in Human Lung Cancer. *Genome Biology* 19 (1): 123.
15. **Earl, J.P.**, de Vries, S.P.W., Ahmed, A., Powell, E., Schultz, M.P., Hermans, P.W.M., Hill, D.J., Constantinouds, C.I., Hu, F.Z., Bootsma, H.J. and Ehrlich, G.D. Comparative Genomic Analyses of the *Moraxella Catarrhalis* Serosensitive and Seroresistant Lineages Demonstrates Their Independent Evolution. *Genome Biology and Evolution* 8(4)955-974, 2016.
16. Rudkjøbing, V.B., Thomsen, T.R., Xu, Y., Melton-Kreft, R., Ahmed, A., Eickhardt-Sørensen, S.R., Bjarnsholt, T., Nielsen, P.H., **Earl, J.P.**, Ehrlich, G.D., and Moser, C. Comparing culture and molecular methods for the identification of microorganisms involved in necrotizing soft tissue infections. *BMC Infectious Diseases* 16:652-664. 2016 DOI 10.1186/s12879-016-1976-2
17. Dampier, W., Nonnemacher, M.R., Mell, J.C., **Earl, J.**, Ehrlich, G.D., Pirrone, V., Aiamkitsumrit, B., Zhong, W., Kercher, K., Passic, S., Williams, J.W., Jacobson, J.M., , and Wigdahl, B. HIV-1 genetic variation resulting in the development of new quasiespecies continues to be encountered in the peripheral blood of well-suppressed patients. *PLoS ONE* 11(5):e015538, 2016.
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19. Long KB, Li Z, Burgwin CM, Choe SG, Martyanov V, Sassi-Gaha S, **Earl J**, Eutsey R, Ahmed A, Ehrlich GD, Artlett CM, Whitfield ML, Blankenhorn EP. The Tsk2/+Mouse Fibrotic Phenotype is Due to a Gain-of-Function Mutation in the PIINP Segment of the Col3a1 Gene. *J Invest Dermatol*. 2014 Oct 20.
20. Janto, B., Hiller, N.L., Eutsey, R., Dahlgren, M., **Earl, J.**, Powell, E., Ahmed, A., Hu, F.Z. and Ehrlich, G.D. Development and validation of an *Haemophilus influenzae* supragenome hybridization (SGH) array for transcriptomic analyses. *PLoS One* Oct 7;9(10):e105493. 2014
21. Frazão, N., Hiller, N.L., Powell, E., **Earl, J.P.**, Ahmed, A., Sá-Leão, R., de Lencastre I, H., Ehrlich, G.D., and Tomasz, A. Virulence potential and genome-wide characterization of drug resistant *Streptococcus pneumoniae* clones selected in vivo by the 7-valent pneumococcal conjugate vaccine. *PLoS One* 2013 Sep 19;8(9):e74867.
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23. Janto, B., Ahmed, A., Ito, M., Liu, J., Hicks, D.B., Pagni, S., Fackelmayer, O., Smith, T-A., **Earl, J.**, Elbourne, L., Paulsen, I., Kolstø, A-B., Tourasse, N.J., Ehrlich, G.D., Boissy, R., Ivey, D.M., Li, G., Xue, Y., Ma, Y., Hu, H.Z.,* and Krulwich, T.A.* The genome of alkaliphilic *Bacillus pseudofirmus* OF4 reveals adaptations that support the ability to grow in an external pH range from 7.5 to 11.4 *Environmental Microbiology*. 13(12):3289-3309, 2011
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25. Zhang L, Xie J, Patel M, Bakhtyar A, Ehrlich GD, Ahmed A, **Earl J**, Marrs CF, Clemans D, Murphy TF, Gilsdorf JR. Nontypeable *Haemophilus influenzae* genetic islands associated with chronic pulmonary infection. *PLoS One*. 2012;7(9):e44730. doi: 10.1371/journal.pone.0044730. Epub 2012 Sep 6. PubMed PMID: 22970300; PubMed Central PMCID: PMC3435294.
26. Ahmed A, **Earl J**, Retchless A, Hillier SL, Rabe LK, Cherpes TL, Powell E, Janto B, Eutsey R, Hiller NL, Boissy R, Dahlgren ME, Hall BG, Costerton JW, Post JC, Hu FZ, Ehrlich GD. Comparative genomic analyses of 17 clinical isolates of *Gardnerella vaginalis* provide evidence of multiple genetically isolated clades consistent with subspeciation into genovars. *J Bacteriol*. 2012 Aug;194(15):3922-37. doi: 10.1128/JB.00056-12. Epub 2012 May 18. PubMed PMID: 22609915; PubMed Central PMCID: PMC3416530.
27. Hiller, N.L., Eutsey, R.A., Powell, E., **Earl, J.**, Janto, B., Martin, D., Dawid, S., Ahmed, A., Longwell, M., Dahlgren, M., Ezzo, S., Tettelin, S., Daugherty, S.C., Mitchel, T.C., Hillman, T., Buchinsky, F.J., Tomasz, A., de Lencastre, H., Post, J.C., Hu, F.Z., and Ehrlich, G.D. Comparative Genomics of Phenotypically Diverse Clinical Pandemic Multidrug-Resistant *Streptococcus pneumoniae* Strains from the PMEN1 lineage. *PLoS ONE* 6(12):e28850, 2011
28. Rath CM, Janto B, **Earl J**, Ahmed A, Hu FZ, Hiller L, Dahlgren M, Kreft R, Yu F, Wolff JJ, Kweon HK, Christiansen MA, Håkansson K, Williams RM, Ehrlich GD, Sherman DH. Meta-omic characterization of the marine invertebrate microbial consortium that produces the chemotherapeutic natural product ET-743. *ACS Chem Biol*. 2011 Nov 18;6(11):1244-56. doi: 10.1021/cb200244t. Epub 2011 Sep 20. PubMed PMID: 21875091; PubMed Central PMCID: PMC3220770.

Curriculum vitae

29. Janto, B., Ahmed, A., Ito, M., Liu, J., Hicks, D.B., Pagni, S., Fackelmayer, O., Smith, T-A., **Earl, J.**, Elbourne, L., Paulsen, I., Kolstø, A-B., Tourasse, N.J., Ehrlich, G.D., Boissy, R., Ivey, D.M., Li, G., Xue, Y., Ma, Y., Hu, H.Z.,* and Krulwich, T.A.* The genome of alkaliphilic *Bacillus pseudofirmus* OF4 reveals adaptations that support the ability to grow in an external pH range from 7.5 to 11.4 *Environmental Microbiology*. 13(12):3289-3309, 2011
30. Boissy R, Ahmed A, Janto B, **Earl J**, Hall BG, Hogg JS, Pusch GD, Hiller LN, Powell E, Hayes J, Yu S, Kathju S, Stoodley P, Post JC, Ehrlich GD, Hu FZ. Comparative supragenomic analyses among the pathogens *Staphylococcus aureus*, *Streptococcus pneumoniae*, and *Haemophilus influenzae* using a modification of the finite supragenome model. *BMC Genomics*. 2011 Apr 13;12:187. doi: 10.1186/1471-2164-12-187. PubMed PMID: 21489287; PubMed Central PMCID: PMC3094309.
31. Davie, J.J., **Earl, J.**, de Vries, S. P.W., Ahmed, A, Hu, F.Z., Bootsma, H.J., Stol, K., Hermans, P.W.M., Wadowsky, R.M., Ehrlich, G.D., Hays, J., Campagnari, A.A. Comparative Analysis and Supragenome Modeling of Twelve *Moraxella catarrhalis* Clinical Isolates. *BMC Genomics* 12(1):70, 2011.
32. Hiller NL, Ahmed A, Powell E, Martin DP, Eutsey R, **Earl J**, Janto B, Boissy RJ, Hogg J, Barbadora K, Sampath R, Lonergan S, Post JC, Hu FZ, Ehrlich GD. Generation of genic diversity among *Streptococcus pneumoniae* strains via horizontal gene transfer during a chronic polyclonal pediatric infection. *PLoS Pathog*. 2010 Sep 16;6(9):e1001108. doi: 10.1371/journal.ppat.1001108. PubMed PMID: 20862314; PubMed Central PMCID: PMC2940740.
33. Ehrlich GD, Ahmed A, **Earl J**, Hiller NL, Costerton JW, Stoodley P, Post JC, DeMeo P, Hu FZ. The distributed genome hypothesis as a rubric for understanding evolution in situ during chronic bacterial biofilm infectious processes. *FEMS Immunol Med Microbiol*. 2010 Aug;59(3):269-79. doi: 10.1111/j.1574-695X.2010.00704.x. Epub 2010 May 28. Review. PubMed PMID: 20618850; PubMed Central PMCID: PMC2910629.
34. Harris, G., and **J. Earl** Perspectives on Pollution and the Basis of Fact: The Case of Environmental Degradation by the Hoosier Magnetics Plant in Ogdensburg, New York. 2006 *AJES* Vol.13 (No.1).

P. RESEARCH PRESENTATIONS

Rust Belt Microbiome October 2022 Poster Near Full Ribosomal Human-Associated Fungal Microbiome Database

Microbiology Virtual Week Labroots September 2020 Talk Applications of Machine Learning to Predict Clinical Provenance of *Haemophilus influenzae*

International Lyme and Associated Diseases Society October 2019 Talk Big Data: A Researcher's Perspective

International Society of Otitis Media June 2019 panel session Microbiota: What do we know? Where do we want to go? What is holding us back?

International Society of Otitis Media June 2019 Poster Machine Learning Approaches to Predict *Haemophilus influenzae* Associated Host Disease State, Host Tissue, and Gene “Dark Matter”

Beyond 16S: Strain level microbiome profiling using long read sequencing March 2019 – Talk Pacifying the Peculiar Problem Profile of Pacbio

Sequencing and Finishing Analysis and the Future May 2018 – Talk Predicting Disease and Ecological Niche of Non-Typeable *Haemophilus influenzae* With Machine Learning

Monell Chemical Senses Center Dec 2017 – Talk Oneliner functions in R for Bioinformatics

Evo-Nei Symposium Temple University Sept 2017 – Talk Comparison of Two Machine Learning Techniques to Predict Virulence, And Habitat Of Non-Typeable *Haemophilus Influenzae* Via Gene Possession

ISCB Conference Prague 2017 – Poster Comparison of Two Machine Learning Techniques to Predict Virulence, and Habitat of Non-Typeable *Haemophilus influenzae* Via Gene Possession

Monell Chemical Senses Center 2016 – Talk Creating Functions in R, using R for statistical analysis

International Symposium on Molecular Medicine and Infectious Disease 2016 - Poster presentation Characterization of the Sinonasal Microbiome Using Pacbio Sequencing and MCSMRT

Microbial Population Biology Gordon Conference 2015 – Poster Niche Partitioning of Sino-Nasal Microbiome

Microbiology and Immunology Lab Meeting 2015 –Talk Sino-nasal Microbiome Analysis

Pacific Biosciences User Group Meeting 2015 – Talk Novel 16s Microbiome Analysis Methods Using Pacbio Sequencing

Drexel Discovery Day 2014 – Talk Comparative Genomics Pipeline: *Moraxella catarrhalis* Serumsensitive and Serumresistant Populations

American Society for Microbiology 2013 – Poster Whole Genome Comparative Analyses of Multiple Species from the Family Pasteurellaceae

Center for Genomic Sciences 2012 – Talk Bioinformatics at the Center for Genomic Sciences

Horizontal Gene Transfer as a Mechanism of Diversity Generation in *S. pneumoniae*. Polymicrobial Infections and Biofilms in Otitis Media. 10th International Symposium on the Recent Advances in Otitis Media, June 7, 2011, New Orleans, LA. (Plenary Session Talk)

Center for Genomic Sciences 2011 – Talk Using the Program Notung to Identify Putative Genomic Transfers, Duplications, and Losses of Genes

International Society for Computational Biology 2010 – Poster Comparative Genomics of *Gardnerella vaginalis* using Notung

EXHIBIT 17C

Curriculum Vitae

Name: Dan E. Krane

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Address: Department of Biological
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Wright State University
Dayton, OH 45435-0001

Phone: (937) 775-2257 (lab)
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(937) 426-9270 (office)

Educational background:

B.S. (1985) in Biology and Chemistry at John Carroll University, University Heights, OH

Ph.D. (1990) Biochemistry program of the Department of Molecular and
Cell Biology, The Pennsylvania State University, University Park, PA

Research interests: Molecular and genome evolution; human population substructuring;
forensic DNA profiling; bioinformatics.

Training and positions held:

Undergraduate researcher (1984-1985) Department of Chemistry, John Carroll
University

Graduate assistant (1985-1990) Department of Molecular and Cell Biology, The
Pennsylvania State University

Participant (1988) UCLA International School on Molecular Evolution

Research Associate (1990-1991) Howard Ochman and Daniel L. Hartl's laboratory,
Department of Genetics, Washington University School of Medicine

Research Associate (1991-1993) Daniel L. Hartl's laboratory, Department of Organismic
and Evolutionary Biology, Harvard University

Assistant Professor (1993-2000) Department of Biological Sciences, Wright State
University.

Affiliate Member of the Biomedical Sciences faculty (1994-1995) Wright State
University.

Associate Member of the Biomedical Sciences faculty (1995-present) Wright State
University.

Associate Professor (2000-2007) Department of Biological Sciences, Wright State
University.

Associate Director, Biomedical Sciences PhD program (2000-2002) Wright State
University.

University Faculty President (2011-2014, 2019), Wright State University.

University Faculty Vice President (2017-2019), Wright State University.

Chair (2012-2019), Ohio Faculty Council.

Special Assistant for Completion Initiatives (2016-2017), Ohio Department of Higher
Education.

Interim Dean and Chief Administrative Officer (2019-2022), Wright State University – Lake
Campus.

Training and positions held (continued):

President, CEO and Senior Analyst, Forensic Bioinformatics, Inc. (2002-present).

Graduate Faculty, Wright State University Microbiology and Immunology Program (2003-present) Environmental Sciences Ph.D. Program (2003-present).

Professor (2007-present) Department of Biological Sciences, Wright State University.

Entrepreneur in Residence (2020-present), Ohio Department of Higher Education.

Awards, honors, and grant support:

American Institute of Chemists Student Research and Recognition Foundation Award (1985).

Pella Fay Braucher Scholarship from The Pennsylvania State University College of Science (1985).

UCLA International School on Molecular Evolution Fellowship (1988).

The R. Adams Dutcher Fund Award from The Pennsylvania State University Biochemistry Program (1990).

The W. R. Keck Fellowship from the Washington University School of Medicine (1990).

Collegium Summer Institute on Faith and Intellectual Life Fellowship (1993).

Wright State University Alumni Grant for "Computer assisted DNA analysis" for \$2,650 (1993).

Research Challenge Grant for \$25,000 from Wright State University (1994) for "The influence of regional GC-content on neutral substitutions".

Finalist, "Teacher of the Year Award," Wright State University, College of Science and Mathematics (1994, 1995, 1997 and 2002).

The Dean of the College of Science and Mathematics "Special Award for Outstanding Teaching," Wright State University, College of Science and Mathematics (1995).

Principal investigator: Ohio biological survey for \$500 for "Molecular characterization of Black and Sugar Maples in Ohio." (1995-1996).

Honorary induction into Alpha Lambda Delta, the National Academic Honor Society for Freshmen (1996).

"Teacher of the Year Award," Wright State University, College of Science and Mathematics (1997 and 2008).

Co-investigator (G. Allen Burton, project director): U.S. EPA grant for \$61,814 for "Assessment of sediment quality in the Black River." (1997).

Co-investigator (G. Allen Burton, project director): U.S. EPA grant for \$449,499 for "Sediment contamination assessment methods: Validation of standardized and novel approaches." (1997).

Principal investigator: U.S. EPA grant for \$420,277 for "Intraspecies genetic diversity measures of environmental impacts." (1998-2002).

Principal investigator: Wright State University Early Start/Augmentation grant for \$17,998 for "DNA quantification center for assessing changes in genetic diversity levels" (1999).

Principal investigator: Ohio biological survey for \$500 for "Survey of the terrestrial isopods of Ohio." (1999-2000).

Awards, honors, and grant support (continued):

Principal investigator: Ohio biological survey for \$500 for “Survey of the Chironomid species of Ohio.” (2001-2002).

Principal investigator: Various sources of compensation for consulting regarding forensic DNA analyses made payable to Wright State University for approximately \$125,000. (1993-2002).

Principal investigator: Wright State University Technology Commercialization Initiative Grant for \$99,985 for “Commercialization of DNA profiling expertise.” (2001-2002).

Co-investigator (Mike Raymer, PI): National Science Foundation (Computer Science Directorate) grant for \$542,056 (\$47,254 under the direct control of D. E. Krane) for “Crossing the interdisciplinary barrier: An integrated undergraduate program in bioinformatics.” (2001-2005).

Co-investigator (Keith Grasman, PI): Wright State University College of Science and Mathematics Research Incentive Fund project for \$30,000 for “Environmental health assessments using toxicogenomic technologies.” (2001-2003).

Co-investigator (Gerald Alter, PI): Wright State University College of Science and Mathematics Research Incentive Fund project for \$30,000 for “Establishing an applied biomedical computing center: Using the nucleotide excision repair complex as a paradigm.” (2001-2003).

Co-investigator (with Keith Grasman): Canadian Wildlife Service (Toronto, ON office) for \$5,000 for “The effects of environmental contaminants on sex ratios in young herring gulls in areas of concern.” (2001-2002).

Participant: State of Ohio Biotechnology Research and Technology
Transfer grant for \$5.5 million (\$1.9 million to Wright State University; \$600,293 for bioinformatics work) (2002-2005).

Principal investigator: Wright State University Technology Commercialization Initiative Grant for \$9,007 for “Developing software that generates forensic DNA profiles and meaningful statistics from mixed evidence samples.” (2006).

Co-investigator (with Joe Bartoszek): Systematics Research Fund for \$1,122 for “Phylogeny of hybrid unisexual Ambystomatid salamanders, a new genome.” (2008-2009).

Principal investigator: Research Initiative Grant from Forensic Bioinformatics, Inc. for \$53,338 for “Persistence and Transfer of STR DNA profiles.” (2010-2012).

Principal investigator: Wright State University Teaching Innovation Grant for \$4,270 for “Engaging students in forensic DNA profiling.” (2012-2013).

Omicron Delta Kappa, Honorious Causa member, Wright State University Circle, National Leadership Honorary Society, 2012.

Fellow, American Council on Education Leadership Development Program, 2014-2015 cohort; University of Notre Dame, host institution.

Principal investigator: Executive on-loan grant from the Ohio Department of Higher Education for \$61,500 for “Bridges to Success: Co-requisite remediation for mathematics gateway courses as part of degree pathways.” (2016-2017).

College of Science and Mathematics Outstanding Service Award, Wright State University, 2017.

Awards, honors, and grant support (continued):

Co-investigator (with Jeanna Matthews, Clarkson University; Nathan Adams, Forensic Bioinformatics; Jessica Goldthwaite, New York City Legal Aid; Surya Mattu, Propublica; and David Madigan, Columbia University): Magic Grant for \$50,000. Decoding differences in forensic DNA software. (2018-2019).

Publications:

- Cheng, J.-F., D. E. Krane and R. C. Hardison. 1988. Nucleotide sequence and expression of rabbit globin genes $\zeta 1$, $\zeta 2$, and $\zeta 3$: Pseudogenes generated by block duplications are transcriptionally competent. *J. Biol. Chem.* **263**:9981-9993.
- Krane, D. E. and R. C. Hardison. 1990. Short interspersed repeats in rabbit DNA can provide functional polyadenylation signals. *Mol. Biol. Evol.* **7**:1-8.
- Krane, D. E. and R. C. Hardison. 1990. Short interspersed repeats in rabbit DNA propagated by successive waves of retrotransposition. Abst. #745, Session 50, ASMBM/AAI 1990 Meeting, FASEB Journal.
- Krane, D. E., A. G. Clark, J.-F. Cheng and R. C. Hardison. 1991. Subfamilies and clustering of C repeats within the rabbit genome. *Mol. Biol. Evol.* **8**:1-30.
- Hardison, R. C., D. E. Krane, D. J. Vandenberg, J.-F. Cheng, J. Mansberger, J. A. Taddie, S. Schwartz, X. Huang, and W. Miller. 1991. Sequence and comparative analysis of the rabbit alpha-like globin gene cluster reveals a rapid mode of evolution in a G+C rich region of mammalian genomes. *J. Mol. Biol.*, **222**:233-249.
- Yost, S., M. James-Pederson, J. Xu, D. E. Krane, R. Miller, T. Zeigler and R. C. Hardison. 1991. Intragenic sequences and proteins regulating the rabbit α -globin gene. Pp. 220-234 in G. Stamatoyannopoulos and A. W. Nienhuis, eds. *The regulation of hemoglobin switching*. Johns Hopkins University Press, Baltimore.
- Krane, D. E., D. L. Hartl and H. Ochman. 1991. Rapid determination of nucleotide content and its application to the study of genome structure. *Nucl. Acids Res.*, **19**:5181-5185.
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Presentations:

- Cheng, J.-F., D. E. Krane, and R. C. Hardison. July, 1987. The expression and evolution of zeta globin genes. Sixth summer symposium in molecular biology – Developmental gene regulation, The Pennsylvania State University, University Park, PA.
- Krane D. E. July, 1988. Subfamily relationships and the structure of rabbit C repeats. UCLA school on molecular evolution, The University of California, Los Angeles.
- Krane D. E., and R. C. Hardison. July, 1989. Rabbit C repeats and their role in the evolution of the rabbit genome. Eighth summer symposium in molecular biology – DNA protein interactions, The Pennsylvania State University.
- Krane D. E. April, 1990. The molecular evolution of a short repetitive element in rabbits. Biology departmental seminar, University of Illinois at Champagne-Urbana.
- Krane, D. E. and R. C. Hardison. May, 1990. Short interspersed repeats in rabbit DNA propagated by successive waves of retrotransposition. ASMBM/AAI 1990 Meeting.
- Hardison, R. C., S. E. Yost, M. James-Pederson, D. E. Krane and J. Xu. May, 1990. Intragenic sequences and protein factors regulating expression of the rabbit alpha-globin gene. ASMBM/AAI 1990 Meeting.
- Krane D. E. September, 1990. The rabbit and human alpha and beta globin gene clusters: An empirical analysis of two different isochores. Department of Genetics, Washington University School of Medicine, St. Louis, MO.
- Hardison, R. C., S. E. Yost, M. James-Pederson, D. E. Krane and J. Xu. September, 1990. Intragenic sequences and protein factors regulating expression of the rabbit alpha-globin gene. Seventh Annual Conference on Hemoglobin Switching, Arlie House, VA.
- Krane, D. E. February, 1991. A new method for the analysis of the compartmentalization of vertebrate genomes. Biology and Chemistry Departments, John Carroll University, University Hts., OH.
- Krane, D. E. July, 1991. Analyses of the isochore structure of eukaryotic genomes. St. Louis Red Cross, St. Louis, MO.

Presentations (continued):

- Krane, D. E. June, 1992. DNA profiling and the implications of population substructuring. Merimac Community College summer seminar series for gifted students, St. Louis, MO.
- Krane, D. E. October, 1992. Population genetics and forensic DNA typing. North Carolina Biotechnology Center/BASF Corporation Lecture Series in Biotechnology, The University of North Carolina at Charlotte.
- Krane, D. E. December, 1992. DNA profiling: A primer. Special seminar for the Missouri State Trial Lawyers Association, St. Louis, MO.
- Krane, D. E. March, 1993. Unresolved issues in the forensic application of DNA profiling. Department of Biology, Morehead State University, Morehead, KY.
- Krane, D. E. February, 1994. The structure and evolution of warm-blooded vertebrate genomes. Department of Biochemistry and Molecular Biology, Wright State University, Dayton, OH.
- Krane, D. E. April, 1994. A homogenating bias in the accumulation of mutations in primate isochores. Museum of Comparative Zoology, Harvard University, Cambridge, MA.
- Krane, D. E. and D. Barr. May, 1994. Evolutionism vs. Creationism on "Current Perspectives: WAZU (102.9 FM), Dayton, OH.
- Krane, D. E. and R. Keyes. May, 1994. Evolution/Creation Discussion, sponsored by the Wright State University Campus Crusade for Christ, Dayton, OH.
- Krane, D. E., M. Malinowski, E. W. Morgan and B. Gorman. January, 1995. Scientific Evidence on Trial. Wright State Policy Forum, Dayton, OH.
- Krane, D. E. February, 1995. Forensic applications of DNA. The Dayton Sertoma Club, Dayton, OH.
- Krane, D. E. April, 1995. DNA forensics. 1995 Bi-state conference of the Indiana and Ohio Societies for Clinical Laboratory Science, Fairborn, OH.
- Krane, D. E. June, 1995. Computer applications in DNA analyses. 1995 Regional meeting of the Academic Computing Society, Dayton, OH.
- Krane, D. E. December, 1995. Forensics in the '90's. The University of Cincinnati and Benjamin/Cummings. Cincinnati, OH.
- Krane, D. E. February, 1996. Polymorphisms at hypervariable loci and human population substructuring. Heidelberg College, Tiffin, OH.
- Krane, D. E., P. Donnelly and M. Kreitman. February, 1996. An afternoon symposium on the statistical interpretation of DNA evidence. DePaul University, Chicago, IL.
- Krane, D. E. April, 1996. Forensics in the '90's. The University of Massachusetts at Worcester and Benjamin/Cummings. Worcester, MA.

Presentations (continued):

- Sternberg, D. V., G. A. Burton, D. E. Krane and K. Grasman. April, 1996. Randomly amplified polymorphic DNA markers in determinations of genetic variation in populations affected by stressors. Abstr. Annu. Meet. Soc. Env. Toxicol. Chem., Washington, D.C., p. 259, no. P0882.
- Krane, D. E. May, 1996. DNA profiling: from start to finish. State of Missouri Public Defenders, St. Louis, MO.
- Krane, D. E. January, 1996. Strong base-composition altering mutational biases operating within primate genomes are dependent upon isochore GC-contents. American Society for Human Genetics Meeting, Minneapolis, MN.
- Hostler, D. P. and D. E. Krane. July, 1996. The dependence of rate and mode of evolution on genomic context within primates. Fifteenth summer symposium in molecular biology – Genome and chromatin structure, The Pennsylvania State University, University Park, PA.
- Skepner, A. P. and D. E. Krane. July, 1996. The application of random amplification of polymorphic DNA to phylogenetic reconstructions. Fifteenth summer symposium in molecular biology – Genome and chromatin structure, The Pennsylvania State University, University Park, PA.
- Steinbrugge, K. and D. E. Krane. July, 1996. A re-analysis of the function and role of SINEs within mammalian genomes. Fifteenth summer symposium in molecular biology – Genome and chromatin structure, The Pennsylvania State University, University Park, PA.
- Krane, D. E. October, 1996. Isochore-dependent mutational biases: A new perspective on random genetic drift. The University of Dayton, Dayton, OH.
- Krane, D. E. January, 1997. Minor shifts in genomic GC-content alter amino acid fixational bias. International Society of Molecular Evolution meeting, Guanacaste, Costa Rica.
- Krane, D. E. February, 1997. The potential and pitfalls of DNA profiling. The Harvard Club of Dayton, Dayton, OH.
- Krane, C. M. and D. E. Krane. April, 1997. The potential of molecular genetics. American Association of University Women, Dayton, OH.
- Krane, D. E. April, 1997. Compositional bias of point substitutions and insertion events in *Alu-J* repetitive sequences. The Jacques Monod Institute of Molecular Genetics, Paris, France.
- Krane, D. E. May, 1997. Isochore-dependent mutational biases and the neutral theory of molecular evolution. International Conference on Molecular Biology and Evolution, Munich (Kongresshaus Garmisch-Partenkirchen), Bavaria, Germany.
- Krane, D. E. September, 1997. The influence of genomic context upon neutral substitutions. Wright State University, Department of Biological Sciences, Dayton, OH.
- Krane, D. E. November, 1997. The influence of large-scale genomic context upon neutral substitutions. The University of Cincinnati, Department of Medical Genetics, Cincinnati, OH.

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- Krane, D. E. February, 1998. From genes to genomes and beyond: Societal implications of genetics and biotechnology. Xenia Rotary Club, Xenia, OH.
- Krane, D. E. March, 1998. The influence of large-scale genomic context upon amino acid replacements. The Pennsylvania State University, Department of Biology, State College, PA.
- Sternberg, D. V., G. A. Burton, D. E. Krane and K. Grasman. April, 1998. Randomly amplified polymorphic DNA markers in determinations of genetic variation in aquatic species affected by stressors. Annu. Meeting Central Great Lakes Regional Chapter Society of Environmental Toxicology and Chemistry. East Lansing, MI.
- York, Allen J. and D. E. Krane. April, 1997. Evolution and function of highly repeated short sequences within the rabbit genome. (OH. J. Sci., 98:7). 107th meeting of the Ohio Academy of Science, Middletown, OH.
- Skepner, Adam P. and D. E. Krane. April, 1997. Molecular analyses reveal genetic similarity of *Acer saccharum* and *Acer nigrum*. (OH. J. Sci., 98:14). 107th meeting of the Ohio Academy of Science, Middletown, OH.
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- Krane, D. E. April, 1999. DNA profiling as a means of assessing environmental impacts. John Carroll University, Department of Chemistry, University Heights, OH.
- Krane, D. E. October, 1999. The potential and pitfalls of forensic DNA profiling. Wilberforce University, Natural Sciences Division, Wilberforce, OH.
- Grunwald, B., S. A. Roush, and D. E. Krane. November, 1999. Genetic diversity measures of terrestrial isopods as ecoindicators. Society of Environmental Toxicology and Chemistry 20th annual meeting, Philadelphia, PA.
- Krane, D. E., D. C. Sternberg, B. Grunwald, S. A. Roush, and G. A. Burton. November, 1999. RAPD DNA profile-based measures of genetic diversity are correlated with environmental impacts. Society of Environmental Toxicology and Chemistry 20th annual meeting, Philadelphia, PA.
- Krane, D. E. March, 2000. Examiner bias in laboratory analyses of forensic DNA evidence. Miscarriages of Justice conference (co-hosted by the University of California at Irvine and the California Public Defenders' Association), Newport Beach, CA.

Presentations (continued):

- Krane, D. E. May, 2000. Genetic diversity measures of environmental impacts. 2000 STAR Ecosystem Indicators Progress Review Workshop, Las Vegas, NV.
- Krane, D. E. May, 2000. Effects of stressors on genetic diversity in naturally occurring populations, Ohio Valley Chapter of SETAC, 17th annual meeting, College Corner, OH.
- Newburn, E. and D. E. Krane. August, 2000. Molecular Identification Markers of Chironomid Species for Use as an Ecoindicator of Aquatic Systems, Poster and abstract, American Chemical Society National Meeting, Washington D.C.
- Ott, L. and D. E. Krane. August, 2000. Genetic diversity in Pacific herring populations, Poster and abstract, American Chemical Society National Meeting, Washington D.C.
- Krane, D. E. October, 2000. Three generations of DNA profiling: What problems still remain? Eastern Kentucky University, Richmond, KY.
- Newburn, E. and D. E. Krane. November, 2000. Molecular Identification Markers of Chironomid Species for Use as an Ecoindicator of Aquatic Systems, Poster and abstract, 20th Annual SETAC National Meeting, Nashville, TN.
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- Krane, D. E. and B. Grunwald, Jr. November, 2000. Genetic diversity as an ecoindicator, Invited presentation, 20th Annual SETAC National Meeting, Nashville, TN.
- Krane, D. E. December, 2000. Correlations between genetic diversity and exposure to stress, Biology Departmental Seminar, Akron University, Akron, OH.
- Krane, D. E. January, 2001. Business opportunities in the area of DNA consulting. Information Technology Research Initiative, Executive Board Meeting, Wright State University, Dayton, OH.
- Newburn, E. and D. E. Krane. March, 2001. Molecular Identification Markers of Chironomid Species for Use as an Ecoindicator of Aquatic Systems, Poster and abstract, MEEC Conference, Oxford, OH.
- Jastremski, K. and D. E. Krane. March, 2001. Genetic diversity in pill bugs at remediated and unremediated strip mines throughout Ohio, Poster and abstract, MEEC Conference, Oxford, OH.
- Walker, S., J. Amon, and D. E. Krane. April, 2001. A genetic comparison of *Lythrum salicaria* and *Lythrum vibratum*. Ohio Academy of Sciences 111th meeting, Tiffin, OH.
- Schmidt, S., D. Cipollini, and D. E. Krane. April, 2001. RAPD-PCR assessment of the genetic diversity within *Alliaria petiolata*. Ohio Academy of Sciences 111th meeting, Tiffin, OH.

Presentations (continued):

- Burton, G. A., M. Morris, D. E. Krane, K. Grasman, W. Carmichael, S. Berberich, D. Organisciak and J. Lucot. April, 2001. Human and environmental risk assessment related research at Wright State University. EPA/DOD special conference on toxicology, Dayton, OH.
- Krane, D. E. May, 2001. Hallmarks of research and forensic science. Third annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. E. August, 2001. Genomes as information storage systems. Summer Institute on Advanced Computation, Wright State University, Dayton, OH.
- Krane, D. E. September 2001. Genetic diversity of naturally occurring populations as an ecoindicator. Biology Departmental Seminar, Northern Kentucky University, Highland Heights, KY.
- Krane, D. E. September, 2001. The potential and pitfalls of forensic DNA profiling. Sigma Xi Distinguished Lecturer Series, Northern Kentucky University, Highland Heights, KY.
- Krane, D. E. September, 2001. The science behind forensic DNA profiling. Engineer's Club of Dayton Sertoma lecture series, Dayton, OH.
- Doom, T, M. Raymer, D. Krane and O. Garcia. February, 2002. A proposed undergraduate bioinformatics curriculum for computer scientists. Proceedings of the 2002 ACM Special Interest Group on Computer Science Education (SIGCSE 2002), Covington, KY.
- Krane, D. E. May, 2002. Genophiler: Advantages of automated review of forensic DNA evidence. Fourth annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. E. June, 2002. Reaching out to computer science and biology majors interested in bioinformatics – at the same time. Introducing Bioinformatics to Undergraduate Curricula Conference, hosted by Wheaton College, Norton, MA.
- Krane, D. E. March, 2003. Commercialization: Why do it? Ohio Valley Affiliates for Life Sciences, Kingsgate Conference Center, Cincinnati, OH.
- Gilder, J. R., D. E. Krane, T. E. Doom and M. L Raymer. April, 2003. Identifying patterns in DNA change. Proceedings of the 2003 Midwest Artificial Intelligence and Cognitive Science Conference (MAICS 2003: **34**, 78-84). Cincinnati, OH.
- Gilder, J., S. Ford, M. Raymer, T. Doom and D. Krane. September, 2003. Differences in electropherogram peak heights reported by different versions of the GeneScan software. Promega Meeting, Phoenix, AZ.
- Raymer, M. L., T. E. Doom and D. E. Krane. September, 2003. Bioinformatics: Crossing the interdisciplinary boundary. NSF grantees meeting, Washington, DC.
- Krane, D. E. October, 2003. Evaluating forensic DNA evidence. Indiana State Investigators Meeting, Indianapolis, IN.
- Krane, D. E. October, 2003. Bioinformatics education: Crossing the interdisciplinary boundary. Keynote address; Bio21: Teaching Biology with Bioinformatics, Chapel Hill, NC.

Presentations (continued):

- Krane, D. E. November, 2003. Evaluating forensic DNA evidence. Virginia State Bar Association Capital Litigation Meeting, Richmond, VA.
- Krane, D. E. December, 2003. Evaluating forensic DNA evidence. Indiana Public Defender's Capital Litigation Meeting, Indianapolis, IN.
- Krane, D., M. Raymer and T. Doom. March, 2004. Bioinformatics at Wright State University. Ohio Valley Affiliates for Life Sciences, University of Louisville, Louisville, KY.
- Converse, K. and D. Krane. March, 2004. Forensic DNA testing and review. "Life in the Balance" conference and annual meeting of the National Association of Criminal Defense Lawyers, Memphis, TN.
- Krane, D. E. March, 2004. Evaluating forensic DNA evidence. Featured address for "Life in the Balance" conference and annual meeting of the National Association of Criminal Defense Lawyers, Memphis, TN.
- Krane, D. E. April, 2004. Evaluating forensic DNA evidence. "Mindful Explorations" seminar series funded by the William H. and Jean R. Reller Endowment, Indiana University East, Richmond, IN.
- Cooper, G., M. Raymer, T. Doom, D. Krane and N. Futamura. May, 2004. Indexing genomic databases. Proceedings of the 2004 IEEE international symposium on Bioinformatics and Bioengineering (BIBE), Taichung (Taiwan), p. 587-591.
- Krane, D. E. October, 2004. Forensic DNA evidence: collection, mixture and degradation. Virginia State Bar Association Capital Litigation Meeting, Richmond, VA.
- Krane, D. E. October, 2004. Evaluating forensic DNA evidence. Mississippi Public Defenders' Capital Litigation Meeting, Biloxi, MS.
- Thompson, W. C. and D. E. Krane. February, 2005. Evaluating forensic DNA evidence. National Association of Criminal Defense Lawyers Annual Meeting, featured presentation, New Orleans, LA.
- Krane, D. E. April, 2005. Evaluating forensic DNA evidence. Cuyahoga County Capital Litigation Seminar, Cleveland, OH.
- Krane, D. E. April, 2005. The strengths and weakness of forensic DNA profiling techniques. Biology departmental seminar, John Carroll University, University Heights, OH.
- Krane, D. E. April, 2005. Deciphering the human genome with bioinformatics techniques. Café Scientifique Seminar Series, Cox Arboretum, Dayton, OH.
- Krane, D. E. May, 2005. Objective interpretation of forensic DNA testing evidence. Seventh annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. E. and W. C. Thompson. July, 2005. Evaluating forensic DNA evidence. North Carolina Academy of Defense Lawyers, Sunset Beach, NC.

Presentations (continued):

- Krane, D. E., T. E. Doom and M. L. Raymer. August, 2005. Assessing the implications for close relatives in the event of similar but non-matching DNA profiles. Fourth annual Expert Forum on the Science of DNA Profiling, University of Dayton School of Law, Dayton, OH.
- Heizer, E. and D. Krane. September, 2005. Correlation between major codon usage and amino acid biosynthetic costs in eight prokaryotic species. Wright State University Biology Department Research Forum, Dayton, OH.
- Sharma, M. and D. Krane. September, 2005. Molecular characterization of Chironomid Species and their use as bioindicators. Wright State University Biology Department Research Forum, Dayton, OH.
- Gilder, J. R. and Krane, D. E. October, 2005. Objective evaluation of DNA evidence. Indiana University East, Richmond, IN.
- Krane, D. E. October, 2005. Evaluating forensic DNA evidence: What software can and cannot do. Illinois Institute for Continuing Legal Education Death Penalty Litigation Seminars, Springfield, IL.
- Rowland, C, R. Van Trees, M. Taylor, and D. Krane. February, 2006. Was the Shawnee war chief Blue Jacket a Caucasian? 58th Annual Meeting of the American Academy of Forensic Sciences, Seattle, WA.
- Krane, D. E. March, 2006. Essential elements of a review of forensic DNA profile evidence. National Legal Aid and Defender Association National Meeting, Philadelphia, PA.
- Krane, D. E. March, 2006. Objective characterization of technical artifacts in forensic DNA profiles. Illinois Institute for Continuing Legal Education Scientific Evidence Seminars, Chicago, IL.
- Rowland, C, R. Van Trees, M. Taylor, and D. Krane. April, 2006. Was the Shawnee war chief Blue Jacket a Caucasian? Annual Meeting of the Ohio Academy of Science, Dayton, OH.
- Gilder, J. R., T. E. Doom, M. L. Raymer, K. Inman, and D. E. Krane. April, 2006. Resolution of forensic DNA mixtures. Annual Meeting of the Ohio Academy of Science, Dayton, OH.
- Krane, D. E. May, 2006. Familial searches and debating the significance of DNA database "cold hits." Illinois Institute for Continuing Legal Education Death Penalty Litigation Seminars, Springfield, IL.
- Krane, D. E. May, 2006. GenoStat®: A user-friendly alternative to PopStats for calculating random match probabilities. Eighth annual DePaul University Law School and Cook County Public Defenders Seminar Series on DNA Analysis, Chicago, IL.
- Raiford, D. W., D. E. Krane, T. E. Doom and M. L. Raymer. July, 2006. An investigation of codon usage bias: Isolation and visualization of translation bias in organisms exhibiting multiple biases. The Ohio Collaborative Conference on Bioinformatics, Athens, OH.

Presentations (continued):

- Krane, D. E., T. E. Doom and M. L. Raymer. August, 2006. Run-specific limits of quantitation and detection (an alternative to minimum peak height thresholds for DNA profile analyses). Fifth annual Expert Forum on the Science of DNA Profiling, Sinclair Center, Dayton, OH.
- Krane, D. E. September, 2006. Evaluating forensic DNA evidence. Wright State University Department of Biological Sciences departmental seminar, Dayton, OH.
- Krane, D. E. and R. Cassanova. September, 2006. Evaluating forensic DNA evidence. Indiana Public Defender's Capital Litigation Meeting, Indianapolis, IN.
- Raiford, D. W., D. E. Krane, T. E. Doom, and M. L. Raymer. October, 2006. Isolation and visualization of codon usage biases. Proceedings of the 6th IEEE Symposium on Bioinformatics and Bioengineering (BIBE 2006), Washington, DC.
- Krane, D. E. October, 2006. Evaluating forensic DNA evidence. Illinois Continuing Legal Education (ICLE) program, Springfield, IL.
- Krane, D. E. December, 2006. Amino acid cost and codon usage biases in six prokaryotic genomes: A whole genome analysis. Oklahoma State University Microbiology Department Seminar, Stillwater, OK.
- Krane, D. E. February, 2007. Run-specific limits of quantitation and detection (an alternative to minimum peak height thresholds). American Academy of Forensic Sciences (AAFS) 59th annual meeting, San Antonio, TX.
- Krane, D. E. and J. R. Gilder. November, 2006. Essential elements of a defense review of DNA testing results. Midwestern Academy of Forensic Sciences (MAFS) annual meeting, Indianapolis, IN.
- Krane, D. E. January, 2007. Evaluating forensic DNA evidence. National Association of Criminal Defense Lawyers Annual Meeting, New Orleans, LA.
- Krane, D. E. February, 2007. Assessing the implications for close relatives in the event of similar but non-matching DNA profiles. American Academy of Forensic Sciences (AAFS) 59th annual meeting, San Antonio, TX.
- Krane, D. E. February, 2007. Empirical analysis of the STR profiles resulting from conceptual mixtures. American Academy of Forensic Sciences (AAFS) 59th annual meeting, San Antonio, TX.
- Krane, D. E. March, 2007. Some of the problems associated with LCN (Low Copy Number) DNA testing. The Forensic Institute 2007 Forensic e-Symposium on Human Identification: Profiling of degraded and low amounts of DNA.
- Krane, D. E. March, 2007. The statistics of DNA profiling – a day long workshop. The Washington, DC Public Defenders' Office, Washington, DC.
- Krane, D. E., J. R. Gilder, E. Ungvarsky, and A. Jamieson. May, 2007. Essential elements of a defense review of DNA testing results. Mid-Atlantic Academy of Forensic Sciences (MAAFS) annual meeting, Washington, DC.

Presentations (continued):

- Krane, D. E., T. E. Doom and M. L. Raymer. August, 2007. Run-specific limits of quantitation and detection: an alternative to minimum peak height thresholds for DNA profile analyses. Sixth annual Expert Forum on the Science of DNA Profiling, Sinclair Center, Dayton, OH.
- Krane, D. E., T. E. Doom and M. L. Raymer. August, 2007. Familial searches and cold hit statistics. Sixth annual Expert Forum on the Science of DNA Profiling, Sinclair Center, Dayton, OH.
- Raiford, D. W., D. E. Krane, T. E. Doom, and M. L. Raymer. October, 2007. A multi-objective genetic algorithm that employs a hybrid approach for isolating codon usage bias indicative of translational efficiency. Proceedings of the 7th IEEE Symposium on Bioinformatics and Bioengineering (BIBE 2007), volume 1, pages 278-285, Cambridge, MA.
- Krane, D. E. and W. C. Thompson. October, 2007. Evaluating forensic DNA evidence – a day-long workshop. Northern Ireland Criminal Bar Association, Belfast, Northern Ireland.
- Krane, D. E. and Angel Carracedo. December, 2007. Forensic DNA profiling – a two day-long workshop. Chilean Department of Forensic Sciences, Santiago, Chile.
- Krane, D. E. April, 2008. Expert witnesses: What are they thinking? Mad Anthony Writers' Convention, Hamilton, OH.
- Krane, D. E. May, 2008. Familial searching in policy and practice. Science in the Courtroom for the 21st Century: Issues in Forensic DNA, DePaul Center for Science and the Cook County Public Defender, Chicago, IL.
- Krane, D. E. May, 2008. Y-STR testing validation and the Virginia example. Science in the Courtroom for the 21st Century: Issues in Forensic DNA, DePaul Center for Science and the Cook County Public Defender, Chicago, IL.
- Krane, D. E. May, 2008. The science and pseudoscience of DNA profiling. Cuyahoga County Bar Association, Cleveland, OH.
- Krane, D. E. September, 2008. Emerging issues in forensic DNA profiling: databases and advisory boards. National Center for State Legislatures Annual Meeting, Columbus, OH.
- Krane, D. January, 2009. Evaluating forensic DNA evidence. Fifth National Seminar on Forensic Evidence and the Criminal Law, Philadelphia, PA.
- Krane, D. E., S. Ford, J. R. Gilder, K. Inman, A. Jamieson, R. Koppl, I. L. Kornfield, D. M. Risinger, N. Rudin, M. S. Taylor, W. C. Thompson. February 2009. Sequential unmasking: Determining what information is crucial and what is extraneous in a forensic analysis. American Academy of Forensic Sciences (AAFS) 61st annual meeting, Denver, CO.
- Krane, D. May, 2009. Evaluating forensic DNA evidence. Virginia Public Defenders' continuing education seminar series, Richmond, VA.

Presentations (continued):

- Krane, D. and J. Gilder. June, 2009. Evaluating forensic DNA evidence. The Netherlands Bar Association and Leiden University Law School, The Netherlands.
- Gilder, J. and D. Krane. May, 2009. Searching for (and finding) relatives in forensic DNA databases. Eleventh annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Gilder, J. and D. Krane. May, 2009. SWGDAM recommendations regarding familial searches. Eleventh annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. and J. Gilder. May, 2009. New developments in DNA technology and litigation. Eleventh annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. July, 2009. Evaluating forensic DNA evidence. National Association of Death Penalty Litigators annual meeting, Airlie, VA.
- Krane, D. November, 2009. Evaluating forensic DNA evidence. Ohio Academy of Criminal Defense Lawyers Death Penalty Seminars, Columbus, OH.
- Krane, D. January, 2010. The science (and pseudoscience) of forensic DNA profiling. Pub-Science series, sponsored by the Boonshoft Museum of Discovery, Dayton, OH.
- Rowland, C. and D. Krane. February, 2010. The National Academy of Sciences report and the Law Commission Consultation paper: Differences and similarities between the United States and England and Wales. The American Academy of Forensic Sciences 63rd Annual Scientific Meeting, Seattle, WA.
- Gilder, J. and D. Krane. February, 2010. Examining of the case of the Deventer murder in the Netherlands. The American Academy of Forensic Sciences 63rd Annual Scientific Meeting, Seattle, WA.
- Gilder, J. and D. Krane. February, 2010. Beer, Wine, and Forensic Science. The American Academy of Forensic Sciences 63rd Annual Scientific Meeting, Seattle, WA.
- Gilder, J. and D. Krane. February, 2010. Discovering relatives in STR DNA databases. The American Academy of Forensic Sciences 63rd Annual Scientific Meeting, Seattle, WA.
- Krane, D. March, 2010. Low copy number (LCN) DNA profiling. The Innocence Project, Cardozo Law School, New York, NY.
- Krane, D. April, 2010. Evaluating forensic DNA evidence. Steelman Visiting Scientist Lecture Series, Lenoir-Rhyne University, Hickory, NC.
- Krane, D. April, 2010. Establishing parameters for objective interpretation of DNA profile evidence. Steelman Visiting Scientist Lecture Series, Lenoir-Rhyne University, Hickory, NC.
- Krane, D. May, 2010. Low Copy Number DNA Testing and New developments in DNA technology. Twelfth annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.

Presentations (continued):

Krane, D. and K. Inman. August, 2010. The science (and pseudoscience) of forensic DNA profiling. A day-long workshop held for an international audience in St. Croix, The United States Virgin Islands.

Krane, D. September, 2010. Forensic DNA profiling at the 2010 Annual Meeting of the Ohio Judicial Conference: The intersection of law, science and ethics. September, 2010, Dublin, OH.

Krane, D. September, 2010. The science (and pseudoscience) of forensic DNA profiling. A day-long workshop sponsored by the Office of the Attorney General, St. Thomas, The United States Virgin Islands.

Krane, D. November, 2010. Low copy number (LCN) DNA profiling. Promega Meeting on Human Identification, San Antonio, TX.

Krane, D. April, 2011. Forensic DNA profiling: interpretation, statistics and challenges (a series of three presentations), New York City DNA College, New York, NY.

Krane, D. May, 2011. Suspect-centric combined probabilities of inclusion. Thirteenth annual Cook County Public Defenders' short course on DNA analysis, Chicago, IL.

Krane, D. October, 2011. Forensic DNA profiling and the use of Y-STRs in casework. Mississippi Public Defender Conference, Choctaw, MS.

Krane, D. November, 2011. Forensic DNA profiling. Federal Bar Council, Mohonk Mountain House, New Paltz, NY.

Krane, D. November, 2012. Attaching weight to DNA profiles. Doughty Street Chambers, London, England.

Krane, D. November, 2012. Evaluating Forensic DNA profiling. Missouri Bar Fall Continuing Legal Education Workshop, Kansas City, MO.

Krane, D. December, 2012. DNA technology in court. Forensic DNA Profiling Video Series, <http://youtu.be/Xz3mQS5WwIM>.

Krane, D. December, 2012. Generating forensic DNA profiles. Forensic DNA Profiling Video Series, <http://youtu.be/iksXzsL2Y2I>.

Krane, D. December, 2012. Statistical weight of single source DNA profiles. Forensic DNA Profiling Video Series, <http://youtu.be/EVf4HqUI0Hk>.

Krane, D. December, 2012. Statistical weight of mixed DNA profiles. Forensic DNA Profiling Video Series, <http://youtu.be/daRBT0pFA1A>.

Krane, D. December, 2012. Implications of database searches for DNA profiling statistics. Forensic DNA Profiling Video Series, <http://youtu.be/eY4s1cEk-BQ>.

Krane, D. December, 2012. Artifacts and noise in DNA profiling. Forensic DNA Profiling Video Series, <http://youtu.be/94NnYCKesQU>.

Krane, D. December, 2012. Observer effects in DNA profiling. Forensic DNA Profiling Video Series, <http://youtu.be/XpXxUrhDUi4>.

Krane, D. December, 2012. What can go wrong with DNA profiling. Forensic DNA Profiling Video Series, <http://youtu.be/q4ZU6wb76pU>.

Presentations (continued):

- Krane, D. March, 2013. Forensic DNA profiling. Take Our Daughters and Sons to Work Day, Wright State University, Dayton, OH.
- Krane, D. May, 2013. Advances in forensic DNA profiling. Fourteenth annual Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. September, 2013. The science (and pseudoscience) of forensic DNA profiling. Special guest presenter, Writer's Police Academy, Jamestown, NC.
- Krane, D. September, 2013. Statistical weights for mixed DNA profiles. Doughty Street Chambers, London, England.
- Krane, D. September, 2013. Bayesian approaches to weighting DNA profile evidence. Northern Ireland Criminal Bar Association, Belfast, Northern Ireland.
- Krane, D. February, 2014. The time has come to analyze DNA profile databases. Annual meeting of the American Academy of Forensic Sciences, Jurisprudence section platform presentation, Seattle, WA.
- Krane, D. February, 2014. Suspect-Centric Combined Probability of Inclusion: A means of attaching objective statistical weights to mixed DNA profiles where drop out may have occurred. Annual meeting of the American Academy of Forensic Sciences, Criminalistics section platform presentation, Seattle, WA.
- Houston, E., and D. Krane. February, 2014. Effect of machine laundering additives on human blood. Annual meeting of the American Academy of Forensic Sciences, Poster presentation, Seattle, WA.
- Krane, D. April, 2014. Forensic DNA profiling. Take Our Daughters to Work Day, Wright State University, Dayton, OH.
- Krane, D. May, 2014. The science (and pseudoscience) of forensic DNA profiling. Biology Departmental Seminar, Youngstown State University, Youngstown, OH.
- Krane, D. May, 2014. Attaching statistical weights to mixed DNA profiles where drop out may have occurred. Fifteenth annual Cook County Public Defenders' forensics forum, hosted by DePaul University, Chicago, IL.
- Krane, D. May, 2014. The implications of database analyses to CODIS searches. Fifteenth annual Cook County Public Defenders' forensics forum, hosted by DePaul University, Chicago, IL.
- Krane, D. June, 2014. Attaching statistical weights to DNA profiles. Kingsley Napley Chambers, London, England.
- Krane, D. June, 2014. Statistical weights for low-level mixed DNA profiles. Doughty Street Chambers, London, England.
- Krane, D. June, 2014. Attaching statistical weights to DNA profiles. University College London Crime and Forensic Science distinguished lecturer seminar program, London, England.
- Krane, D. and W. C. Thompson. June 2014. Complex, mixed DNA profiles. The National Innocence Project's DNA College, hosted by Yeshiva University, New York, NY.

Presentations (continued):

- Krane, D. and W. C. Thompson. June 2014. Low copy number DNA profiling. The National Innocence Project's DNA College, hosted by Yeshiva University, New York, NY.
- Krane, D. June 2014. Software approaches for attaching statistical weights to complex mixed DNA profiles. The National Innocence Project's DNA College, hosted by Yeshiva University, New York, NY.
- Krane, D. January, 2015. The science (and pseudoscience) of forensic DNA profiling. Montgomery County Library seminar series, Kettering, OH.
- Krane, D. September, 2014. Exploring bias in forensic DNA profiling. TEDxDayton, Dayton, OH.
- Krane, D. January, 2015. The science (and pseudoscience) of forensic DNA profiling. Biology Departmental Seminar, University of Notre Dame, Notre Dame, IN.
- S. Al-Awadi, M. Sabbaha, N. Adams, A. Marshall, C. Rowland and D. Krane. February, 2015. Pairwise Comparisons as a Means of Validating Iraqi Muslim and Christian Allele Frequency Databases (poster). 67th Annual Meeting of the American Academy of Forensic Sciences. Orlando, FL.
- Coble, M. D. and D. Krane. April, 2015. Low-level DNA mixtures and interpretation. Science, cell phones and social media – Finding & using evidence in post-conviction cases. National Association of Criminal Defense Lawyers in collaboration with the Innocence Network, Orlando, FL.
- Krane, D. May, 2015. Sequential unmasking: A means of minimizing observer effects in forensic interpretation. Forensic bias and error – Causes and corrections. Sixteenth annual Cook County Public Defenders' forensics forum, hosted by John Marshall Law School, Chicago, IL.
- R. Koppl, D. Krane, N. Adams. July, 2015. Minimizing and leveraging bias in forensic science. National Institute of Standards and Technology International Symposium on Forensic Science Error Management. Washington, DC.
- Krane, D. and K. Inman. October, 2015. Probabilistic genotyping in forensic DNA profiling. DNA Bootcamp, hosted by the Office of the Federal Public Defender, Northern District of California, and Contra Costa County Public Defender, Berkeley School of Law, Oakland, CA.
- Krane, D. October, 2015. Interpretation errors in DNA profiling. Biology Department Seminar Series, Wright State University, Dayton, OH.
- Krane, D. November, 2015. Examiner bias and mixture interpretation in DNA profiling. Legal Aid Society of New York, DNA College, Yeshiva University Law School, New York, NY.
- Krane, D. November, 2015. Probabilistic genotyping (as in TrueAllele®). Virginia Bar Association Capital Defense Workshop, Richmond, VA.
- Krane, D. December, 2015. Analyses of DNA profile databases. Cook County Public Defenders' Forensic DNA Unit, Chicago, IL.

Presentations (continued):

- Adams, N. and D. Krane. February, 2016. Black boxes and due process: Transparency in expert software systems. Annual meeting of the American Academy of Forensic Sciences, Jurisprudence section platform presentation, Las Vegas, NV.
- Krane, D., Rowland, C. and N. Adams. February, 2016. Disputed DNA stats for a low-level sample: A case study. Annual meeting of the American Academy of Forensic Sciences, Jurisprudence section platform presentation, Las Vegas, NV.
- Adams, N., R. Chakraborty, C. Rowland and D. Krane. February, 2016. Complex mixtures and the minimum number of contributors: A case study (poster presentation). 68th Annual meeting of the American Academy of Forensic Sciences, Las Vegas, NV.
- N. Adams and D. Krane. February, 2016. Black Boxes and Due Process: Transparency in Expert Software Systems. 68th Annual Meeting of the American Academy of Forensic Sciences. Las Vegas, NV.
- D. Krane, C. Rowland and N. Adams. February, 2016. Disputed DNA Stats for a Low-level Sample: A Case Study. 68th Annual Meeting of the American Academy of Forensic Sciences. Las Vegas, NV.
- Krane, D. and A. Roth. April, 2016. Emerging legal issues surrounding DNA mixture statistics and probabilistic genotyping software. Northern District of California 2016 Judicial Conference, Napa Valley, CA.
- Krane, D. April, 2016. The Bridges to Success Initiative: Co-requisite remediation in the context of guided pathways and gateway mathematics courses. Ohio Department of Higher Education Convenings, Spitzer Conference Center (Lorain County Community College) and Sharonville Convention Center (Sharonville, OH).
- Krane, D. June, 2016. Attaching statistical weights to mixed samples where allelic dropout may have occurred. 17th annual Cook County Public Defenders' forensics forum, hosted by Loyola University Law School, Chicago, IL.
- Krane, D. June, 2016. Probabilistic genotyping: What is inside the black boxes? 17th annual Cook County Public Defenders' forensics forum, hosted by Loyola University Law School, Chicago, IL.
- Krane, D. July, 2016. The evolution of forensic DNA profiling. Biology Department seminar, University of Cincinnati, Cincinnati, OH.
- Krane, D. August, 2016. Solving the problem of mixed DNA profiles. 2016 Technology Transition Workshop, "Courtroom Knowledge," Duquesne University, Pittsburgh, PA.
- Krane, D. August, 2016. The case of *WI vs. Avery: Making a Murderer*. Wright State University Alumni College, Wright State University, Dayton, OH.
- Krane, D. September, 2016. Statistics and probabilistic genotyping. DNA Bootcamp, Hennepin County Public Defender's Office, Minneapolis, MN.

Presentations (continued):

- Krane, D. October, 2016. The Bridges to Success Initiative: Technical assistance with course syllabi and remediation exercises. Ohio Department of Higher Education Convening at Ohio University, Dublin, OH.
- Krane, D. October, 2016. Problems with mixture interpretations. New York Legal Aid Society's DNA Unit Intensive Continuing Legal Education Training, "Questioning forensics: Inside the black box," Cordozo Law School, New York, NY.
- Krane, D. November, 2016. Probabilistic genotyping software. 2016 DNA Boot Camp, Office of the Federal Public Defender, Northern District of California and Office of the Public Defender, Contra Costa County. Federal Conference Center, Oakland, CA.
- Krane, D. December, 2016. The Bridges to Success Initiative: Technical assistance with student advising. Ohio Department of Higher Education Convening at Ohio University, Dublin, OH.
- Krane, D. February, 2017. Probabilistic genotyping. DNA Boot Camp 2017, Ninth Judicial Circuit with Central Florida Association of Criminal Defense Lawyers. Orlando, FL.
- Krane, D. February, 2017. Past and present DNA challenges. DNA Boot Camp 2017, Ninth Judicial Circuit with Central Florida Association of Criminal Defense Lawyers. Orlando, FL.
- N. Adams, and D. Krane. March, 2017. Quality Assurance for Software Development in DNA Forensics (poster). Second Annual Genetics in Forensics Congress. London, England
- N. Adams, and D. Krane. March, 2017. Maximum Allele Count Analysis on Novel Test Kits (poster). Second Annual Genetics in Forensics Congress. London, England.
- Krane, D. March, 2017. Advanced DNA. Capital Habeas Unit (CHU) National Conference. Omni La Mansion del Rio Hotel, San Antonio, TX.
- Krane, D. March, 2017. Complex DNA mixtures: Combined probability of inclusion, probabilistic genotyping software issues in innocence cases. They Blinded Me with "Science": Examining the Reliability of Forensic Evidence in Innocence Claims. Sheraton San Diego Hotel & Marina, San Diego, CA
- Krane, D. May, 2017. DNA statistics: PCAST's promise of a new era. Assessing Reliability: Forensic Evidence *after* PCAST. Seventeenth annual Cook County Public Defenders' forensics forum, hosted by Loyola University School of Law, Chicago, IL.
- Krane, D. June, 2017. Mixed DNA profiles, probabilistic genotyping and familial searching. Cuyahoga County Public Defender's Office, Cleveland, OH.
- Krane, D. November, 2017. Statistics and probabilistic genotyping. 2017 DNA Boot Camp, Office of the Federal Public Defender, Northern District of California and Office of the Public Defender, Contra Costa County. Federal Conference Center, Oakland, CA.

Presentations (continued):

- Krane, D. November, 2017. Trace DNA and complex mixtures: Deconstructing the DNA findings. National Association of Criminal Defense Lawyer's 8th Annual Defending Sex Crimes Seminar, Las Vegas, NV.
- Krane, D. February, 2018. Testimony before the Ohio House of Representatives standing committee on Higher Education and Workforce Development regarding HB 66, Representative Mike Duffey, chair. Columbus, OH.
- Krane, D. March, 2018. Testimony before the Ohio House of Representatives Finance Committee subcommittee on Higher Education regarding HB 512, Representative Rick Perales, chair. Columbus, OH.
- Krane, D. and R. Blackburn. March, 2018. A major redesign of a gateway course at Wright State University. TxDLA (Texas Distance Learning Association), Dallas, TX.
- Krane, D. May, 2018. Outcomes of a major redesign of a STEM gateway course. Central State University Faculty Retreat, Springfield, OH.
- Krane, D. and R. Blackburn. June, 2018. Impact of course redesign on student achievement and engagement, NUTN webinar (archived at: <https://bned.zoom.us/recording/share/s2JELhNeXSKMMb0YznRJuhZ42lJnT9RbbYF8DQzCRbCwIumekTziMw>).
- Krane, D. and C. Hughes. June, 2018. Probabilistic genotyping: Where are we now?. National Forensic College, Cardozo Law School, New York, NY.
- Krane, D. August, 2018. Forensic DNA profiling: What role should computers play in making judgement calls? Wright State University Alumni College keynote presentation, Dayton, OH.
- Krane, D. August, 2018. Forensic DNA profiling: What role should computers play in making judgement calls? Wright State University Alumni College keynote presentation, Dayton, OH.
- Krane, D. August, 2018. Complex DNA mixtures: Is the proof in the pudding? Louisiana Association of Criminal Defense Lawyers Forensics Seminar, Baton Rouge, LA.
- Krane, D., A Fraley, N. Guerrieri, and J. Gebhart. September, 2018. Reducing costs with improved results: A conversation with Dr. Dan Krane. National Association of College Auxiliary Services Webinar.
- Krane, D, N. Adams, and C. Hughes. September, 2018. Probabilistic genotyping: A two-day workshop. Los Angeles County Public Defenders' Office, Los Angeles, CA.
- Krane, D. November, 2018. Mixtures and probabilistic genotyping. DNA Boot Camp, Office of the Federal Public Defender, Northern District of California, Oakland, CA.
- Krane, D. November, 2018. Developments in DNA profiling. Death Penalty Seminar, Ohio Association of Criminal Defense Lawyers, Columbus, OH.

Presentations (continued):

- Philpott, K., and D. Krane. February, 2019. The dawn of a new era: Probabilistic genotyping. 2019 Capital Case Defense Seminar, California Attorneys for Criminal Justice and the California Public Defenders' Association, Monterey, CA.
- Barlow, B., and D. Krane. February, 2019. The mixture problem. 2019 Capital Case Defense Seminar, California Attorneys for Criminal Justice and the California Public Defenders' Association, Monterey, CA.
- N. Adams, S. Lorenz, M. Babacianjelodar, J. Matthews and D. Krane. February, 2019. Quantifying the impact of post-validation modifications to Forensic Statistical Tool. 71st Annual Meeting of the American Academy of Forensic Sciences. Baltimore, MD.
- Krane, D. March, 2019. History of forensic DNA uses and challenges. DNA Boot Camp 2019, Ninth Judicial Circuit with Central Florida Association of Criminal Defense Lawyers. Orlando, FL.
- Krane, D. March, 2019. Probabilistic genotyping. DNA Boot Camp 2019, Ninth Judicial Circuit with Central Florida Association of Criminal Defense Lawyers. Orlando, FL.
- Krane, D., and K. Wincko. April, 2019. Reducing costs with improved results: A conversation with Dr. Dan Krane. HLC Annual Conference, Chicago, IL.
- Krane, D. May, 2019. DNA comparisons. 2019 Judges' In-Court Seminar, United States District Court, District of Minnesota, Tofte, MN.
- Krane, D., J. Gebhart, N. Klingbeil, I. Mallett, A. Steele-Middleton, and D. Palmer July, 2019. Reducing costs with improved results: Inclusive Access at Wright State. Ohio Affordable Learning Summit, Ohio Dominican University, Columbus, OH.
- Krane, D. October, 2019. Attaching statistical weights to forensic DNA profiling results. 2019 DNA Workshop, Georgia Public Defender Council, Atlanta, GA.
- Krane, D. October, 2019. Probabilistic genotyping: an approach to attaching statistical weights to mixed samples where allelic dropout may have occurred. 2019 DNA Workshop, Georgia Public Defender Council, Atlanta, GA.
- Krane, D. November, 2019. Attaching statistical weights to forensic DNA profiling results. 2019 DNA Boot Camp, Office of the Federal Public Defender, Northern District of CA and Contra Costa County Public Defender, Oakland, CA.
- Krane, D. November, 2019. Mixed DNA profiles and probabilistic genotyping. 2019 DNA Boot Camp, Office of the Federal Public Defender, Northern District of CA and Contra Costa County Public Defender, Oakland, CA.
- Krane, D. November, 2019. Complex DNA analysis: Low-level and mixed-source samples. Selected Problems in Criminal Justice Administration: Law and Forensic Science (hosted by Keith Findley and Jo Handelsman), University of Wisconsin, Madison, WI.

Presentations (continued):

- Krane, D. January, 2020. Probabilistic genotyping software (PGS): Paradigm shift in DNA mixture interpretation. Questioning Forensics, Brooklyn Law School Forchelli Center, Brooklyn, NY.
- Krane, D. January, 2020. Probabilistic genotyping. Forensic Algorithms Working Group (<https://www.gao.gov/products/GAO-20-479SP>), U.S. Government Accountability Office, Washington, DC.
- Krane, D. March, 2020. Evaluating complex, low-level DNA mixtures. Selected Problems in Criminal Justice Administration: Law and Forensic Science (hosted by Keith Findley and Jo Handelsman), University of Wisconsin, Madison, WI.
- Krane, D. November, 2020. Probabilistic genotyping: The dawn of a new era in DNA profiling. 28th Annual Capital Defense Workshop, The Virginia Bar Association, virtual event.
- Krane, D. April, 2021. Using probabilistic genotyping to attach a statistical weight to mixed DNA profiles. Selected Problems in Criminal Justice Administration: Law and Forensic Science (hosted by Keith Findley and Jo Handelsman), University of Wisconsin, Madison, WI.
- Krane, D. November, 2021. Probabilistic genotyping: The dawn of a new era in DNA profiling. Ohio Public Defender Conference, virtual event.
- Krane, D. March, 2022. How a Crime Lab Generates a Forensic DNA Profile. Wisconsin Forensic University -- Handling DNA Evidence, Pewaukee, WI.
- Krane, D. March, 2022. Observer Effects and Confirmation Bias. Wisconsin Forensic University -- Handling DNA Evidence, Pewaukee, WI.
- Krane, D. March, 2022. Statistical Weights of Single Source and Mixed DNA Profiles. Wisconsin Forensic University -- Handling DNA Evidence, Pewaukee, WI.
- Krane, D. March, 2022. An Introduction to Probabilistic Genotyping. Wisconsin Forensic University -- Handling DNA Evidence, Pewaukee, WI.
- Krane, D. June, 2022. Generating Forensic DNA Profiles. Forensic DNA CLE Program, New Mexico Criminal Defense Lawyers Association, Santa Fe, NM.
- Krane, D. June, 2022. Observer Effects and Confirmation Bias in DNA Profiling. Forensic DNA CLE Program, New Mexico Criminal Defense Lawyers Association, Santa Fe, NM.
- Krane, D. June, 2022. Single Source and Mixed DNA Profile Statistics. Forensic DNA CLE Program, New Mexico Criminal Defense Lawyers Association, Santa Fe, NM.
- Krane, D. June, 2022. Probabilistic Genotyping: The Dawn of a New Era in DNA Profiling. Forensic DNA CLE Program, New Mexico Criminal Defense Lawyers Association, Santa Fe, NM.
- Rowland, C., and Krane, D. January, 2023. Challenges associated with interpreting mixed DNA profiles. 2023 DNA Boot Camp, Office of the Federal Public Defender, Northern District of CA and Contra Costa County Public Defender, Sacramento, CA.

Presentations (continued):

- Rigby, K., and Krane, D. February, 2023. Defending against DNA evidence. Litigating Common Forensic Issues, Forensic Training Unit, Office of the Ohio Public Defender, Columbus, OH.
- Krane, D., and S. Ford. March, 2023. A letter from America: A view of DNA evidence from the other side of the pond. Doughty Street Chambers, London, England.
- Krane, D., and S. Ford. March, 2023. A letter from America: A view of DNA evidence from the other side of the pond. Kingsley-Napley Solicitors, London, England.
- Krane, D., and Adams, N. March, 2023. Probabilistic genotyping software (parts 1 and 2). DNA in 2023 and Beyond, Ninth Judicial Circuit with Central Florida Association of Criminal Defense Lawyers. Orlando, FL.
- Krane, D., and S. Ford. April, 2023. A letter from America: A view of DNA evidence from the other side of the pond. London Criminal Courts Solicitors' Association (LCCSA), London, England.
- Rigby, K., and Krane, D. May, 2023. DNA evidence and working with a forensic expert. Death Penalty Training, Ohio State Bar Association, Columbus, OH.
- Krane, D. May, 2023. The science (and pseudoscience) of DNA profiling. Dayton Regional STEM School, Dayton, OH.
- Ford, S., Adams, N, and Krane, D. July, 2023. An introduction to probabilistic genotyping. Indiana Public Defender Probabilistic Genotyping Training Program, Indianapolis, IN.
- Krane, D. July, 2023. An exploration of factor space as part of internal validation of probabilistic genotyping systems. Indiana Public Defender Probabilistic Genotyping Training Program, Indianapolis, IN.
- Krane, D. August, 2023. The basics of DNA mixtures. Wisconsin Forensic University – Probabilistic Genotyping, Pewaukee, WI.
- Krane, D. August, 2023. Complex mixtures and likelihood ratios. Wisconsin Forensic University – Probabilistic Genotyping, Pewaukee, WI.
- Krane, D. August, 2023. Evaluating validation: Exploration of factor space. Wisconsin Forensic University – Probabilistic Genotyping, Pewaukee, WI.
- Krane, D. September, 2023. The science (and pseudoscience) of DNA profiling. Bellbrook High School Bioengineering Program, Bellbrook, OH.
- Krane, D. September, 2023. Forensic DNA profiling. Lawyers Club of Cincinnati, Cincinnati, OH.
- Krane, D. October, 2023. Introductory DNA for the trial attorney. Plenary session, Texas Criminal Defense Lawyers Association, 20th Annual Forensics Seminar, Austin, TX.
- Krane, D. October, 2023. Advanced issues in DNA profiling (including genetic genealogy). Texas Criminal Defense Lawyers Association, 20th Annual Forensics Seminar, Austin, TX.

Presentations (continued):

- Krane, D. October, 2023. The dawn of probabilistic genotyping. Northern Nevada DNA Bootcamp, Washoe County, NV.
- Krane, D. November, 2023. Evaluating complex, low-level DNA mixtures. Selected Problems in Criminal Justice Administration: Law and Forensic Science (hosted by Professors Keith Findley and Jo Handelsman), University of Wisconsin, Madison, WI.

Graduate students and post-doctoral fellows mentored:

- David P. Hostler, III. 1993-1995, M.S.: The dependence of rate and mode of evolution on genomic context within primates.
- Adam P. Skepner. 1994-1996, M.S.: The application of random amplification of polymorphic DNA to phylogenetic reconstructions.
- Keri Steinbrugge. 1994-1997, M. S. candidate: The role of the predominant SINE within lagomorph genomes.
- Krista E. Bloniarz. 1995-1996, M.S., non-thesis option: The application of RAPD-PCR in genome analyses.
- Cynthia Kiefer. 1996-1999, M.S., non-thesis option: The influence of genome compartmentalization on nucleotide substitutions.
- Allen J. York. 1997-2000, M.S. candidate: The subfamily relationships and functional roles of repetitive elements.
- Dalana Barnett. 1997-2000, M. S. recipient: Characterization of a novel, short and highly repeated sequence in carnivores.
- Terry Oroszi. 1998-2000, M.S. candidate: Characterization of a novel, short and highly repeated sequence in pigs.
- Billy Grunwald. 1998-present, M.S. candidate: Utilization of genetic diversity measures a means of assessing terrestrial environmental impacts.
- John F. Sojda, III. 1999, post-doctoral research fellow: Sequence variation in the superoxide dismutase gene in Caribbean *Drosophila* populations.
- Emmanuel Aigbokhan. 1999-2000, post-doctoral research fellow: Utilization of genetic diversity measures a means of assessing aquatic environmental impacts.
- Lee Ott. 1999-2002, M.S. recipient: Genetic population structures of Pacific Coast herring populations exposed to anthropogenic stressors.
- Erin Newburn. 1999-2002. M.S. recipient: Molecular identification of Chironomid species.
- Balasubramanian Abiramikumar. 1999-2003. M.S. recipient: Characterization of a novel, short and highly repeated sequence in African elephants.
- Michael C. Kuneman. 2001-2003. M.S., non-thesis: Progress in understanding genetic diversity: The use of genetic diversity for assessment, conservation and protection purposes.

Graduate students and post-doctoral fellows mentored (continued):

Randall J. Loges. 2000-2003. M.S. candidate: Genetic diversity and characterization of *Hyallolella azteca* from Ohio, Montana and commercial suppliers.

Krista Jastremski. 2000-2004. M.S. recipient: Changes in genetic diversity within pill bug populations at historically impacted terrestrial sites.

Norman Scott Blair. 2000-2004. M.S. candidate: Molecular characterization of the sex of Great Lakes birds.

Joseph Bartozcek. 2001-2010. Biomedical Sciences Ph. D. recipient: Effects of habitat loss/fragmentation on Ambystomatid salamanders.

Esley Heizer. 2003-2005. M.S. recipient: Correlation between major codon usage and amino acid biosynthetic costs in eight prokaryotic species.

Monita Sharma, 2004-2006, M.S. recipient: Molecular characterization of chironomid species.

Peichang Shi, 2006, M.S., non-thesis option: Gene expression patterns as an indicator of exposure to environmental stresses.

Chad Ferguson, 2004-2009, Environmental Sciences Ph. D. recipient: Using chironomids for environmental impact assessment.

Nina Archie, 2004-2006, M.S. recipient: Characterization of n+4 stutter artifacts in forensic DNA profiles.

Esley Heizer. 2005-2010. Biomedical Sciences Ph.D. recipient: Correlation between major codon usage and amino acid biosynthetic costs in prokaryotes and eukaryotes.

Uohna Foster, 2010-2013, Biomedical Sciences Ph.D. candidate: Persistence and transfer of forensic DNA samples.

Taryn Hunt, 2011-2014, M.S. recipient (non-thesis option): Laundry transfer of DNA from epithelial cells.

Erin Berdanier, 2011-2016, M.S. recipient: Laundry transfer of DNA from blood stains.

Graduate thesis committees served upon:

Keri Pedly. 1993-1994. M.S. recipient.

Liang Shi. 1993-1996. Ph.D. recipient.

Melissa Goldman. 1994-1996. M.S. recipient.

Lou Li. 1994-1997. Ph.D. recipient.

Adrienne Moran. 1994-1996. M.S. recipient.

Steve Hendrix. 1994-1996. M.S. recipient.

David Brown. 1994-1996. M.S. recipient.

Michelle Malotte. 1994-1999. Ph.D. recipient.

David Ellis. 1995-2000. M.S. student.

Scott Rousch. 1995-1997. M.S. recipient.

Graduate thesis committees served upon (continued):

Elizabeth Smucker. 1996-1999. M.S. recipient.
David Sternberg. 1995-2002. M.S. recipient.
Deborah Vallance. 1995-1996. M.S. student.
Andrea Alexander. 1999-2002. M.S. recipient.
Patricia Morgan. 1997-present. Ph.D. candidate.
Billy Grunwald. 1998-2001. M.S. student.
Terry Oroszi. 1998-2001. M.S. student.
Kelly Jo Peterson. 1998-2003. Ph.D. recipient.
Lee Ott. 1999-2002. M.S. recipient.
Erin Newburn. 1999-2002. M.S. recipient.
Balasubramanian Abiramikumar. 1999-2003. M.S. recipient.
Norman Scott Blair. 2000-2005. M.S. candidate.
Randall Loges. 2000-2004. M.S. candidate.
Marc Greenberg. 2001-2002. Ph.D. recipient.
Michael C. Kuneman. 2001-2003. M.S. recipient.
Joseph Bartozcek. 2001-present. Ph.D. candidate.
David Paoletti. 2001-2006. Ph.D. recipient.
Gina Cooper. 2001-2009. Ph.D. recipient.
Jason Gilder. 2001-2003. M.S. recipient.
Sundeep “Sunny” Anand. 2001-2003. M.S. recipient.
Sharon Reilly. 2002-2004. M.S. candidate (non-thesis option).
Prashanth Athri. 2002-2004. M.S. recipient.
Balasubramanian Abiramikumar. 2002-2004. M.S. recipient.
Jeanette Frey. 2003-2005. M.S. recipient.
Esley Heizer. 2003-2005. M.S. recipient.
Doug Raiford. 2003-2005. M.S. recipient.
Ryan Flynn. 2003-2009. M.S. recipient (non-thesis option).
Sridhar Ramachandran. 2003-2007. Ph.D. recipient.
Jason Gilder. 2004-2007. Ph.D. recipient.
Monita Sharma. 2004-2007. M.S. recipient.
Doug Raiford. 2005-2008. Ph.D. recipient.
Chad Ferguson. 2004-2010. Ph.D. recipient.
Esley Heizer. 2005-2010. Ph.D. recipient.
Peichang Shi. 2006. M.S. recipient (non-thesis option).

Graduate thesis committees served upon (continued):

Adam Guess. 2007-2008. M.S. recipient.
Amanda Hanes. 2007-2009. M.S. recipient.
Sushant Taksande. 2008-present. M.S. candidate.
Uohna Foster. 2010-2013. Ph.D. candidate.
Taryn Hunt. 2011-2014. M.S. recipient.
Erin Berdanier. 2011-2016. M.S. recipient.

Undergraduate honors thesis advisees:

Carri Eagler: 1993-1996.	Libby Provci: 1994-1996.
Michelle Gnam: 1994-1996.	Jeanne Uy: 1994-1996
Michelle Lawhun: 1995-1998.	Lora Dodson: 1996-1998.
Jason Soderquist: 1997-1999.	Elizabeth Zimmer: 1998-1999.
Sarah Schmidt: 2000-2001.	Melissa Strain: 2000-2001.
Denada Sharra: 2001-2004.	Roger Fecher: 2005-2006.
Leah Kershner: 2007-2009.	Krista Dona: 2013-2015.

Courses taught/developed:

Molecular Genetics (BIO 211 and 2110). An introduction to molecular biology and genetics for majors in Biological Sciences at Wright State University. Winter, 1994 through 2012; Summer 1998 through 2012; Spring 2020 and 2021.

Cells and Genetics (BIO 112). An introduction to biology for majors in Biological Sciences at Wright State University. (Extensively redeveloped in Summer, 1993) Fall, 1994 through 2000; 2002; 2008 through 2010.

Molecular and Cell Biology Laboratory (BIO 410). An introduction to molecular and cell biology laboratory techniques for majors in Biological Sciences at Wright State University. (Developed course in Winter, 1994) Spring, 1994; (redeveloped in Spring, 2003) Spring, 2003.

Molecular Evolution (BIO 461/661). A senior/graduate level course describing the basis of evolutionary inferences using molecular data including phylogenetic reconstruction and mutational tendencies. Biological Sciences at Wright State University. (Developed course in Winter, 1995) Spring, 1996, 1997, 1999, 2001, 2004 and 2007.

Population Genetics (BIO 460/660). A senior/graduate level course focusing on the statistical basis of changes in allele frequencies within populations of organisms. Biological Sciences at Wright State University. (Developed course in Winter, 1998) Spring, 1998, 2000, and 2003.

Human Genetics (BIO 426/626). A senior/graduate level course on the special considerations and approaches used to study the patterns of inheritance in humans. Biological Sciences at Wright State University. (Developed course in Winter, 2002) Spring, 2002.

Courses taught/developed (continued):

- Advanced Cell Biology (BMS 991/BIO 701). An advanced literature based course survey on the principles of cell structure and function for incoming biomedical sciences PhD students and graduate students in Biology. (Co-developing course in Summer, 1998) Fall, 1998 and 1999.
- Introduction to Research Biology (BIO 702). A graduate level course on current research in biological sciences at Wright State University. Fall, 1993 and 1996.
- Independent Studies in Biology (BIO 499). A senior level course of guided independent, laboratory research for majors in Biology. Winter, 1994 to present.
- Introduction to Bioinformatics (BIO 371/CS 271). A sophomore level course that introduces computer science and biology majors to the most important algorithms and current problems in bioinformatics. Spring, 2002 through 2012.
- Bioinformatics algorithms (BIO 471/CS 471). A senior level, capstone course focusing on algorithm development for biology and computer science students in the Wright State bioinformatics program. Fall, 2002 through 2011.
- Honors Genetics (BIO 119). A course featuring selected readings on genetics and evolution for Honor's students. Biological Sciences at Wright State University. (Developed course in Summer, 1994) Fall, 1994 through 2000; 2002, 2004 through 2010.
- Bioinformatics algorithms (BIO 4710/CS 4710). A senior level, capstone course focusing on algorithm development for biology and computer science students in the Wright State bioinformatics program. Fall, 2012.
- Cells and Genetics (BIO 1120). An introduction to biology for majors in Biological Sciences at Wright State University. (Co-taught with Dr. Emily Kramer) Fall, 2012.
- Cells and Genetics (BIO 1120). An introduction to biology for majors in Biological Sciences at Wright State University. Fall, 2013, Fall 2015, Fall 2016, Fall 2017 (as a major revision including transition to a new textbook and implementation of co-remediation sections), Summer 2018, Fall 2018, Summer 2020, Fall 2022, Summer 2023, and Fall 2023.
- Honors Genetics (BIO 1190). A course featuring selected readings on genetics and evolution for Honor's students. Biological Sciences at Wright State University. Fall, 2012, 2013, 2015, 2016, 2017, 2018, and 2023.
- First Year Seminar (UVC 1010). A course introducing incoming students to college life. University College, Wright State University. Fall, 2012 and 2013.
- Senior Seminar (BIO 4920). A capstone course on presenting scientific information. Biological Sciences at Wright State University. Summer, 2013 through 2018.
- Introduction to Bioinformatics (BIO 3710/CS 2710). A sophomore level course that introduces computer science and biology majors to the most important algorithms and current problems in bioinformatics. Spring, 2013 and 2014.

Courses taught/developed (continued):

Forensic DNA Profiling (BIO 3710/ATH 3800). Application of critical thinking skills to forensic DNA profiling in a scale-up setting. Cross-listed in Biology and Anthropology at Wright State University. Spring, 2013, 2014, 2016 (developed as a 100% on-line course in 2016), Springs 2017 to 2024.

Health and Disease (BIO 1070). An introductory Biology course for non-majors about how the human body functions and the social, political, and cultural aspects of public health. Developed and taught, Spring 2023 and 2024.

Academic service at Wright State University:

Biological Sciences Molecular and Cell Biology Curriculum Development Committee, 1993 to present.

Science Apprenticeship Program for Women and Minority Students (mentor and co-investigator, Prem Batra – founding program director), 1994 to 2005.

Short Term Research Experience/Access for Minority Students (STREAMS) (faculty advisor and co-investigator, Robert Putnam – program director), 1994 to 2003.

Computer-assisted Learning Center Committee (elected chair), 1993 to 1996.

Ohio Science Fair Judge and Awards Presenter, 1994 to 1997.

Biological Sciences Seminar Program Committee, 1994 to 2019, and 202 to 2024 (Chair in 2005 to 2011).

College of Science and Mathematics Computer Network Facilitation Committee, 1994 to 1996.

Biomedical Sciences PhD Program Nomination Committee, elected to terms running from 1994 to 1996, from 2005 to 2007 and from 2009 to 2011.

Developmental Biology Search Committee, 1994.

Biology Departmental Honors and Scholarships Committee, 1995 to 2001.

Cell Biology Search Committee, 1995.

Research and Sponsored Programs Associate Director Search Committee, 1995.

University Resident Life Committee, 1995 to 1996.

Computer-assisted Learning Center Committee, 1996 to 1999.

Space and Equipment Allocation Committee, 1997 to 2000.

Faculty liaison for Wright State University's varsity baseball team, 1997 to present.

University Commencement Committee, 1998 to 2000.

University Honors' Committee, 1998 to 2001.

Biological Sciences Undergraduate Curriculum Committee, 1998 to 2001; 2003 to 2005; 2007 to 2009.

Plant Physiologist Search Committee, 1998.

Academic service at Wright State University (continued):

College of Science and Mathematics Faculty Development Committee, elected 1999 to 2001; Appointed Biology Department Representative for 2007-2008 and for 2008-2009 and for 2012-2013.

Cell/Molecular Biologist Search Committees, 2000; 2008 (co-chair).

Information Technology Research Initiative, Research Committee, 2000 to 2004.

College of Science and Mathematics Scholarships Committee, 2000 to 2001.

College of Science and Mathematics Dean Search Committee, 2001 to 2002.

Assistant to the Director (Technology Transfer) of the Office of Research and Sponsored Programs Search Committee, 2002.

Aquatic Biologist Search Committee, 2002-2003.

University Athletics Council, elected to terms running from 2002 to 2004 and 2005 to 2006; Faculty Senate Appointee 2006 to 2007 (elected Vice-Chair in 2006 to 2007; elected Chair 2009-2011; past-chair 2011-2013); Senate representative (2013-2015).

Athletics Council Pre-game Lecture Committee (chair), 2007-2014.

Athletics Council Blackboard to Backboard Challenge Committee (2010-2013).

Athletics Council Gender Equity Sub-committee, 2003 to 2006, and 2008-2011.

Athletics Council Team Liaison Sub-committee, 2002 to 2008.

Athletics Council Athletic Director Review Sub-committee, 2002-2007 (Chair in 2005-2006).

Athletics Council Constitution and By-laws Sub-committee, 2006-2008 and 2018-2020 (Chair).

Athletics Council Student Welfare Committee, 2009-2014.

Research and Sponsored Programs Technology Transfer Director Search Committee, 2007.

Cell/Molecular Biologist Search Committee, 2007-2008 (Chair in 2008).

Steering Committee, College of Science and Mathematics, elected 2006 to 2007 and 2008 to 2009 (elected Chair for 2007-2008, 2008-2009, 2009-2010, 2010-2011 and 2011-2012 academic years).

Vice President for Advancement Search Committee, 2008.

College of Science and Mathematics Academic Mediation Committee, 2007-present.

College of Science and Mathematics representative (elected) to the Wright State University Faculty Senate, 2009-2010.

Director of the Wright State University Ervin J. Nutter Center Search Committee, 2010.

Wright State University representative to the Ohio Faculty Council (secretary), 2010-2012.

Academic service at Wright State University (continued):

Wright State University representative to the Ohio Faculty Council (vice chair), 2012-2013.

Wright State University representative to the Ohio Faculty Council (chair), 2013-2019.

Faculty Senate ad hoc Committee on the Master Planning Process (chair), 2010-2011.

Semester Conversion Director Search Committee, 2010.

University Commencement Committee, 2011-2014.

Graduate Council, 2011-2014.

Vice President for Business and Fiscal Affairs Search Committee, 2011.

University Faculty Budget Priority Committee (chair), 2010-2014, 2016-2019.

Faculty Senate Executive Committee (chair), 2010-2014, 2015-2019.

Faculty Senate ad hoc committee on First Year Seminars, 2012-2014.

University President's Cabinet, 2012-2014.

University Mission Driven Allocation Budget Model Executive Committee, 2012-2014.

University Diversity Advisory Council, 2012-2014.

Permanent Provost Search Committee, 2012-2013.

Academic Integrity Conduct Review Panelist, 2012-2013.

President-elect of the Wright State University Faculty, 2010-2011.

President of the Wright State University Faculty, 2011-2014 and 2019-2021.

Wright State University Task Force on Affordability and Efficiency, chair, 2015-2019.

Wright State University Foundation Archives Mini-campaign, Executive leadership team member, 2016-2018.

Wright State University Foundation 360-review, 2016-2017.

State of Ohio Representative to Complete College America, 2016-2018.

Ohio's Complete College America Co-requisite Work Plan Committee, 2016-2017.

Vice President of the Wright State University Faculty, 2017-2019.

Faculty Senate Textbook Affordability ad hoc committee, chair, 2017.

University Undergraduate Academic Policies Committee, chair, 2017-2019.

University Undergraduate Student Success Committee, chair, 2017-2019.

University Program Effectiveness Review Committee, co-lead, 2017-2019.

Ohio's Complete College America Co-requisite Work Plan Committee, 2016-2017.

Faculty Senate Textbook Affordability ad hoc committee, chair, 2017, 2018.

University Undergraduate Student Success Committee, chair, 2017-2019.

University Program Efficiency Review Committee, co-lead, 2017-2019.

Academic service at Wright State University (continued):

University Assurance of Learning Committee, Faculty representative, 2018-2019.
University Seat Management Committee, co-chair, 2018-2019.
University Strategic Enrollment Steering Committee, Senate representative, 2017-2019.
Ohio Department of Higher Education Transfer Assurance Guarantee Steering Committee, Faculty representative, 2018-2019.
Wright State Summer Forensic Science Camp coordinator, 2014-2019.
University Promotion and Tenure Committee, 2019-2020.
Clinical Lab Sciences Director Search, co-chair, 2022-2023.
Clinical Lab Sciences Instructor Search, co-chair, 2022-2024.
Wright State College of Graduate Programs and Honors Studies RISE Tour Criminology and Forensic Science, co-chair, 2023.
Biological Sciences Department Faculty Development Committee, chair, 2023-2024.

Court recognized expert in DNA profiling:

Missouri vs. Nethery (St. Charles, MO, 1991).
Iowa vs. Ripperger (Burlington, IA, 1992).
North Carolina vs. Fisher (Charlotte, NC, 1992).
Illinois vs. Tynes (Kankakee, IL, 1992).
Nebraska vs. Bundy (Columbus, NE, 1992).
North Carolina vs. White (Edenton, NC, 1993).
North Carolina vs. Jones (Winnsboro, NC, 1993).
Ohio vs. Honzu (Columbus, OH, 1994).
Ohio vs. Saylors (Urbana, OH, 1994).
Ohio vs. McGuire (Dayton, OH, 1994).
Ohio vs. Brewer (Hillsboro, OH, 1995).
South Carolina vs. Eubanks (Columbia, SC., 1995).
Ohio vs. Parks (Columbus, OH, 1995).
Ohio vs. Oldham (Hamilton, OH, 1995).
California vs. Strange (Nevada City, CA, 1996).
California vs. Wenger (Long Beach, CA, 1996).
United States vs. Lowe (First Circuit, Boston, MA, 1996).
Washington vs. Gore (Seattle, WA, 1996).
Virginia vs. Gray (Martinsville, VA, 1996).
Kentucky vs. Tipton (Stanton, KY, 1997).
California vs. Allen (Compton, CA, 1997).

Court recognized expert in DNA profiling (continued):

Virginia *vs.* Brogan (Roanoke, VA, 1998).
Missouri *vs.* Taylor (St. Louis, MO, 1998).
Ohio *vs.* Sapp (Springfield, OH, 1998).
Missouri *vs.* White (St. Louis, MO, 1998).
Indiana *vs.* Smith (Middletown, IN, 1999).
Indiana *vs.* Jones (Vincennes, IN, 2000).
Florida *vs.* Esty (Pensacola, FL, 2000).
Indiana *vs.* Williams (Terre Haute, IN, 2001).
Minnesota *vs.* Roman Nose (St. Clair, MN, 2001).
Massachusetts *vs.* Greineder (Welsley, MA, 2001).
Indiana *vs.* Wilburn (Covington, IN, 2001).
South Dakota *vs.* Luce (Aberdeen, SD, 2002).
Minnesota *vs.* Bailey (Minneapolis, MN, 2002).
California *vs.* Howard (Los Angeles, CA, 2002).
California *vs.* Quinones (San Francisco, CA, 2002).
Minnesota *vs.* Traylor (Minneapolis, MN, 2002).
Ohio *vs.* Knott (Athens, OH, 2002).
Indiana *vs.* Guffey (Tipton, IN, 2002).
Indiana *vs.* Ward (Rockport, IN, 2002).
California *vs.* Robinson (Sacramento, CA, 2003).
New Mexico *vs.* Arviso (Farmington, NM, 2003).
California *vs.* Cheung (Orange County, CA, 2003).
Ohio *vs.* Henderson (Athens, OH, 2003).
Ohio *vs.* Fears (Lebanon, OH, 2003).
Maryland *vs.* Daniels (Frederick and Rockville, MD, 2003).
United States *vs.* Zephier (Sioux Falls, SD, 2003).
Montana *vs.* Jones (Lewistown, MT, 2004).
Indiana *vs.* Cooper (Goshen, IN, 2004).
New Mexico *vs.* Garcia (Albuquerque, NM, 2004).
New York *vs.* Alvarez (Schenectady, NY, 2004).
Ohio *vs.* Hines (Cleveland, OH, 2004).
Victoria State Coroner's Inquest into the Death of Jaidyn Leskie (Melbourne, Victoria, Australia, 2004 and 2005)
Montana *vs.* Misner (Great Falls, MT, 2005).

Court recognized expert in DNA profiling (continued):

California *vs.* Avila (Orange County, CA, 2005).
Minnesota *vs.* Bailey (Minneapolis, MN, 2005).
United States *vs.* Jenkins (Washington DC District Court, 2005).
Iowa *vs.* LaMasters (Waterloo, IA, 2005).
Minnesota *vs.* Temple (Minneapolis, MN, 2005).
Michigan *vs.* Leiterman (Ann Arbor, MI, 2005).
Michigan *vs.* Spagnola (2nd Circuit Court of Appeals, Benton Harbor, MI, 2005).
Ohio *vs.* McClure (Batavia, OH, 2005).
Virginia *vs.* Davis (Norfolk, VA, 2005).
Maryland *vs.* Derr (La Plata, MD, 2006).
Colorado *vs.* Brownlow (Adams County, CO, 2006).
Maryland *vs.* Odom (Prince George's County, MD, 2006).
Virginia *vs.* Riddick (Hampton Circuit Court, Hampton, VA, 2006).
Illinois *vs.* Rivera (Chicago, IL, 2006).
California *vs.* Robinson (Los Angeles, CA, 2006).
Regina *vs.* Sean Hoey (Northern Ireland High Court, Belfast, NI, 2006).
Arizona *vs.* Bigger (Tucson, AZ, 2007).
Ohio *vs.* Matthews (Xenia, OH, 2008).
United States *vs.* Davis (US District Court of MD, 2008).
United States *vs.* Garner (Fort Eustis, VA, 2008).
United States *vs.* Hennis (Fort Bragg, NC, 2008).
Colorado *vs.* Tunis (Golden, CO, 2008).
Regina *vs.* Broughton (Oxford Crown Court, Oxford, England, 2009).
California *vs.* Smith (Sacramento, CA, 2009).
New York *vs.* Megnath (Queens, NY, 2009).
Virgin Islands *vs.* Xavier (St. Croix, Virgin Islands District Court, 2010).
Regina *vs.* Canning (Belfast Crown Court, Belfast, Northern Ireland, 2010).
Regina *vs.* Broughton (Oxford Crown Court, Oxford, England, 2010).
Regina *vs.* Walsh (Belfast Crown Court, Belfast, Northern Ireland, 2011).
Colorado *vs.* Rodriquez (Golden, CO, 2011).
Illinois *vs.* Gonzalez (Chicago, IL, 2011).
Regina *vs.* Duffy and Shivers (Belfast Crown Court, Belfast, Northern Ireland, 2011).
Regina *vs.* Dos Santos (Central Criminal Court, London, England, 2012).
Oregon *vs.* Garrett (Portland, OR, 2012).

Court recognized expert in DNA profiling (continued):

Regina vs. Deacon (Central Criminal Court, London, England, 2013).
United States vs. McCluskey (US District Court of AZ, 2013).
Regina vs. Dos Santos (Central Criminal Court, London, England, 2013).
Regina vs. Colhoun (Newry Crown Court, Newry, Northern Ireland, 2013).
Ohio vs. McKenna (Dayton, OH, 2014).
Regina vs. Colhoun (Newry Crown Court, Newry, Northern Ireland, 2014).
Missouri vs. McBenge (St. Charles, MO, 2014).
United States vs. Henning (Fort Leavenworth, KS, 2015).
United States vs. Smalls (Brooklyn, NY, 2015).
New York vs. James (Staten Island, NY, 2015).
New York vs. Hillary (Canton, NY, 2016).
Regina vs. Simms (Oxford Crown Court, England, 2016).
Washington vs. Fair (Seattle, WA, 2017).
Illinois vs. Flores-Mora (Chicago, IL, 2017).
United States vs. Fell (US District Court of VT, 2017).
New York vs. Rochard (New York, NY, 2017).
Regina vs. Hussain (Central Criminal Court, London, England, 2017).
Florida vs. Clark (Palm Beach, FL, 2017).
Regina vs. Abbas Uddin (Norwich Crown Court, England, 2018).
United States vs. Oldman (Casper, WY, 2018).
United States vs. Elmore (San Francisco, CA, 2019).
United States vs. Gissantaner (Grand Rapids, MI, 2019).
United States vs. Lewis (Minneapolis, MN, 2019).
Colorado vs. Root (Denver, CO, 2019).
Andersen vs. City of Chicago (Chicago, IL, 2020).
Texas vs. Colone (Beaumont, TX, 2020).
Texas vs. Escobar (Austin, TX, 2020).
Regina vs. Trotter (Croydon Crown Court, England, 2020).
United States vs. Cooke (Wilmington, DE, 2022).
New York vs. Burrus (New York, NY, 2022).
United States vs. Cortorreal (New York, NY, 2022-2023).
United States vs. Cutbank (Minneapolis, MN, 2023).
Washington vs. Nicholas (Seattle, WA, 2023).
Georgia vs. Deeds (Eastman, GA, 2023).

Court recognized expert in DNA profiling (continued):

Hawaii vs. Thompson (Honolulu, HI, 2023).

Texas vs. Colone (Beaumont, TX, 2023).

United States vs. Ortiz (San Diego, CA, 2024).

Professional service:

Featured appearances on “20/20,” “Court TV,” “CBS Nightly News,” “Unsolved Mysteries,” “BBC Newsnight,” “BBC Panorama,” “CBS’s 48 Hours,” “True Crime” podcast, and numerous appearances on all Dayton-area local TV broadcasts.

Technical consultant for “Court TV,” “CBS Nightly News,” NBC’s “Unsolved Mysteries,” CBS’s “Sixty Minutes,” CBS’s “Eye to Eye with Connie Chung,” the Gannette News Service, “Weekly Reader Magazine,” “The Washington Post,” “The Los Angeles Times,” and “The Dayton Daily News.”

Reviewer for the journals: “Appraisals,” “Molecular Biology and Evolution,” “Genetics,” “Genomics,” “Journal of Molecular Evolution” “The American Biology Teacher,” “IEEE Bioinformatics,” and “Accountability in Research.”

Presiding officer, Animal Molecular Biology Section, Ohio Academy of Science 107th Annual Meeting at Miami University-Middletown, April 1998.

Review panel member, U. S. Environmental Protection Agency “Ecological Indicators Panel,” 1999, 2000, 2001, 2002, 2004 and 2006.

Review panel member, U. S. Environmental Protection Agency “Nanotechnology Panel,” 2006.

Ad hoc reviewer for the Hudson River Foundation, 2002 and 2004.

Fairness in Forensics,” with Roger Koppl, op ed published in several newspapers, 12-17 August 2008, including Newark Star-Ledger, The Olympian (Olympia, Washington), Hartford Courant (Sunday edition), Herald-Leader (Lexington, Kentucky; Sunday edition), Lake Wylie Pilot (Lake Wylie, South Carolina), Daily Herald (Provo, Utah), The Modesto Bee (Modesto, California), Tri-city Herald (south-central Washington), The News & Observer (Raleigh, Durham, and Chapel Hill, North Carolina), Belleville News-Democrat (Belleville, Illinois), The Bellingham Herald (Bellingham, Washington), The Fresno Bee (Fresno, California) and the Anchorage Daily News.

“Science Rules the FBI Should Obey,” with Roger Koppl, op ed published in several newspapers, 13-16 January 2010, including the Cleveland Plain Dealer, Fort Worth Star-Telegram Press Democrat (Santa Rosa, California), Bradenton Herald (Florida), Wake Forest News & Observer, The News Tribune (Tacoma, Washington), and The Fresno Bee (Fresno, California).

David R. Hopkins and Dan E. Krane, “Higher education: An investment guaranteed to pay off.” An op-ed piece published in major newspapers in Ohio during the month of September, 2013.

David R. Hopkins and Dan E. Krane, “Education – An equal opportunity path to the American dream.” An op-ed piece published in major newspapers in Ohio during the month of November, 2013.

Professional service (continued):

National Event Supervisor (Forensic Science), Science Olympiad, Wright State University, Dayton, OH 2013.

Gubernatorial appointee, Forensic Chemistry Representative to the Scientific Advisory Committee for the Virginia Department of Forensic Science. (appointed by Governor Mark Warner for a term of 2005-2006; reappointed by Governor Tim Kaine for a term of 2006 to 2010).

Familial Search Subcommittee of the Virginia Scientific Advisory Committee, Chair (2006 to 2007).

Y-STR Validation Subcommittee of the Virginia Scientific Advisory Committee, Chair (2008).

Ohio Board of Regents Faculty Credentials Committee (co-chair), (2012).

Participant, Expert meeting for the US General Accountability Office's study of forensic algorithms, facilitated by the US National Academy of Science's Computer Science and Telecommunications Board (2020).

Member, US National Institute of Standards and Technology's Organization of Scientific Area Committee (OSAC) for Forensic Science Scientific and Technical Review Panel for the OSAC Proposed Standard "Standards for Setting Analytical and Stochastic Thresholds for Application to Forensic DNA Casework Using Electrophoresis Platforms." (2020-2021).

NASA iTech Pitch Competition Judge (2019-2023).

Penn State University Eberly College of Science Pitch Competition Mentor and Judge (2021-present).

Ohio Department of Higher Education PITCHX Competition Selection Panel Member (2021-2023).

Ohio Area 8 Workforce Development Board, Member (2019-2022).

Intra-University Council Regional Dean Council, Member (2019-2022).

Mercer County (OH) Chamber of Commerce, Member (2019-2022).

Greene County (OH) CATS Transit Board, Member (2022-present).

Precinct Judge/Voting Location Manager, Greene County, Ohio, Board of Elections (2022-present).

Administrative responsibilities:

Faculty advisor, Wright State University Biological Sciences Association. (1994 to 2002; 2023 to present).

Organizer and co-founder, Wright State University Molecular Biology Retreat. (1995 to 2003).

Chapter president, Sigma Xi (National Scientific Honor Society). (1997 to 2001).

Associate director's board member, The Engineers' Club of Dayton. (1997 to 2001).

Board of Directors, Chairman, Forensic Bioinformatic Services, Inc. (2002 to present).

Special Assistant for Completion Initiatives, Executive on-loan to administer the \$470,000 Bridges to Success Initiative. Ohio Department of Higher Education, (2016 to 2017).

Administrative responsibilities (continued):

Entrepreneur-in-Residence, Ohio Department of Higher Education, (2019 to present).

Interim Dean and Chief Administrative Officer, Wright State University, Lake Campus (2019-2022).

EXHIBIT 18A

Dr. Istvan Albert
Research Professor of Bioinformatics
Pennsylvania State University

Life Sciences Building, MSC 206C,
University Park 16801, PA
Email: iaa1@psu.edu
Web: <https://www.ialbert.me>

Professional Training

Stanford University, CA, USA	Bioinformatics Certificate	2004
University of Notre Dame, IN, USA	Ph.D. Physics	2001
Babes-Bolyai University, CL, RO	M.Sc. Physics	1996
Babes-Bolyai University, CL, RO	B.Sc. Physics	1995

Industry Certifications

IBM Corporation, USA	Certified XML Developer	2002
SUN Microsystems, USA	Certified Java Programmer	2003

Positions and Employment

2015 – present	Research Professor of Bioinformatics, Biochemistry and Molecular Biology, Pennsylvania State University
2009 – present	Director of the Bioinformatics Consulting Center, Pennsylvania State University,
2015 – 2020	Director of the Online Graduate Certificate in Applied Bioinformatics, Pennsylvania State University,
2010 – 2015	Research Associate Professor of Bioinformatics, Biochemistry and Molecular Biology, Pennsylvania State University
2006 – 2010	Research Assistant Professor of Bioinformatics, Biochemistry and Molecular Biology, Pennsylvania State University
2003 – 2006	Research Associate, Huck Institutes for the Life Sciences, Pennsylvania State University
2001 - 2003	Staff Scientist, Department of Computer Science, University of Minnesota
1996 - 2001	Research Assistant, Department of Physics, University of Notre Dame

Notable accomplishments

- Author of the Biostar Handbook, a comprehensive and practical introduction into Bioinformatics. <https://www.biostarhandbook.com/> The book has been adopted into bioinformatics curricula across the world.
- Program director of the online graduate certificate program **Applied Bioinformatics**, offered by the Penn State World Campus between 2015 and 2020. Since launching the program, we have enrolled over 150 full-tuition students.
- Lead developer of **BioStar: An Online Question & Answer Resource for the Bioinformatics Community**: <http://www.biostars.org>. Since 2010, it has become the world's most widely accessed bioinformatics resource. As of today, the site is visited by over 2 million unique users per year, generating over a million page views per month.
- Director of the **Bioinformatics Consulting Center** at Penn State. This organization, proposed and deployed under my supervision, aims to create bioinformatics support services targeted at scientists affiliated with Penn State. We have helped faculty secure research funding from individual grants to large-scale efforts of over \$30 million.

Skills:

- Over ten years of experience with high dimensionality data analysis, genomic data, and visualization.
- Over ten years of experience training students, scientists, and non-technical participants.
- Successful in securing funding from governmental and private agencies.
- Well-versed in applications of genomics in science.
- Published more than 70 peer-reviewed scientific works.
- Served as a scientific expert in high-profile legal cases.

Teaching Experience

- Course instructor for **BMBB 852, Applied Bioinformatics**. I have developed a new course that covers scientific computing and bioinformatics education for life scientists. The course started as a special topics course, and within two years, it has been adopted as a required course for the Bioinformatics and Genomics Ph.D. program. In **2014**, I was awarded the **Paul M. Althouse Outstanding Teaching Award**.
- Under my initiative and leadership, Penn State launched the **Applied Bioinformatics Online Graduate Certificate** offered via the Penn State World Campus. I was the program director for this effort, coordinating the work necessary to launch a certificate requiring the completion of 4 different courses.

Supervisory roles

- Currently supervising a full-time staff member in the position of Bioinformatics Research Associate.
- Served on the Ph.D. and M.Sc. committees of over twenty students.
- Advising and meeting regularly with dozens of PIs, postdoctoral researchers, and graduate students from various departments. In the past year alone, we have assisted over twenty research groups with their data analysis needs.

Advisory roles

I have advised many students in both official and unofficial capacities. A subset of these individuals includes:

- Aswathy Sebastian, Thesis Advisor (2018-2024)
- Siddarth Wekhande, Master's Thesis Committee Member (2018 - 2019).
- Natay Abera, Staff Researcher, (2017-2020).
- Ed Provencher, Ph.D. Dissertation Committee Member (2020 - present).
- Taejun Chun, Ph.D. Dissertation Committee Member (2019 - present).
- Mitchel Goodwin, Ph.D. Dissertation Committee Member (2020 - present).
- Stephanie Collins, Ph.D. Dissertation Committee Member (2018 - 2023).
- Emily Van Syock, Ph.D. Dissertation Committee Member (2018 - 2023).
- Emma Rose, Ph.D. Dissertation Committee Member (2018 - 2023).
- Laura Jimenez, Master. Dissertation Committee Member (2018 - 2022).
- Nabeel Ahmed, Penn State, Ph.D. Dissertation Committee Member (2015 - 2019).
- Ana Maria Gonzales, Penn State, Ph.D. Dissertation Committee Member (2015 - 2019).
- Balaji Kumar, Penn State, Ph.D. Dissertation Committee Member (2019 - 2021).
- Zachary Mandell, Penn State, Ph.D. Dissertation Committee Member (2019 - 2022).
- Robert Nichols, Penn State, Ph.D. Dissertation Committee Member (2015 - October 2, 2019).
- Ben Niu, PSU, Ph.D. Dissertation Committee Member (January 1, 2013 - December 31, 2018).
- Utsav Pandey, PUS, Ph.D. Dissertation Committee Member (January 1, 2013 - December 31, 2018).
- Sartok Rahman, Penn State, Ph.D. Dissertation Committee Member (2019 - Present).
- Eric Wafula, Penn State, Ph.D. Dissertation Committee Member (2016 - 2019).
- Yinan Wan, Master's Thesis Advisor (2010-2014)

I serve on about 4-5 Ph.D student committees each academic year.

Academic Service

- Served as a referee on over 70 scientific papers in Physics, Computer Science, and Bioinformatics.
- Served as a grant reviewer for various scientific organizations both in the US and internationally.
- Actively involved in the admission process of Penn State Bioinformatics and Genomics Ph.D. programs. I interview and evaluate a large number of students each year.
- Active participant on the Biostar website, created over 3000 posts imparting advice to newcomers to this field.

List of Publications

I have published in three distinct scientific fields: **Physics**, **Computer Science**, and **Life Sciences**. In each of these fields, I have co-authored works published in the *most highly rated and selective journals* or conferences of that scientific domain: *Physical Review Letters*, *Conference on Human Factors in Computing Systems*, *Bioinformatics*, *Genome Research*, and *Nature*.

1. Albert, I. (2024). GeneScape: A Python package for gene ontology visualization. *Journal of Open Source Software* 9(98), 6624. DOI: 10.21105/joss.06624 <https://doi.org/10.21105/joss.06624>
2. Zeng, H., Ali, S., Sebastian, A., Ramos-Medero, A. S., Albert, I. (Author), Dean, C., & Liu, A. (2024). CPLANE protein INTU regulates growth and patterning of the mouse lungs through cilia-dependent Hh signaling. *Developmental biology* 515, 92--101.
3. Laurel R Seemiller, Lisa R Goldberg, Aswathy Sebastian, Sue Rutherford Siegel, Craig Praul, Dana Zeid, Istvan Albert, Jacob Beierle, Camron D Bryant, Thomas J Gould, Alcohol and fear conditioning

produce strain-specific changes in the dorsal hippocampal transcriptome of adolescent C57BL/6J and DBA/2J mice, *Alcohol: Clinical and Experimental Research*, (2024)

4. Lauren N McKinley, McCauley O Meyer, Aswathy Sebastian, Benjamin K Chang, Kyle J Messina, Istvan Albert, Philip C Bevilacqua; Direct testing of natural twister ribozymes from over a thousand organisms reveals a broad tolerance for structural imperfections, *Nucleic Acids Research*, (2024)
5. Kulkarni, S., Morrissey, A., Sebastian, A., Keller, C. A., Giardine, B., Smith, C., Akinniyi, O. T., Arnaoutov, A., Albert, I. (Author), Mahony, S., & others (2024). Human CCR4-NOT is a global regulator of gene expression and is a novel silencer of retrotransposon activation. *bioRxiv*, 2024--09
6. Godin, Mitchell J; Sebastian, Aswathy; Albert, Istvan; Lindner, Scott E; Long-Read Genome Assembly and Gene Model Annotations for the Rodent Malaria Parasite *Plasmodium yoelii* 17XNL *Journal of Biological Chemistry* 299 (7) (2023)
7. Misra, Sougat; Lee, Tai-Jung; Sebastian, Aswathy; McGuigan, John; Liao, Chang; Koo, Imhoi; Patterson, Andrew D; Rossi, Randall M; Hall, Molly A; Albert, Istvan; Loss of selenoprotein W in murine macrophages alters the hierarchy of selenoprotein expression, redox tone, and mitochondrial functions during inflammation *Redox Biology* (2023)
8. Bellfy, Lauren; Smies, Chad W; Bernhardt, Alicia R; Bodinayake, Kasuni K; Sebastian, Aswathy; Stuart, Emily M; Wright, Destiny S; Lo, Chen-Yu; Murakami, Shoko; Boyd, Hannah M; The clock gene *Per1* may exert diurnal control over hippocampal memory consolidation *Neuropsychopharmacology* (2023)
9. Piperaquine-resistant PfCRT mutations differentially impact drug transport, hemoglobin catabolism and parasite physiology in *Plasmodium falciparum* asexual blood stages John Okombo, Sachel Mok, Tarrick Qahash, Tomas Yeo, Jade Bath, Lindsey M Orchard, Edward Owens, Imhoi Koo, Istvan Albert, Manuel Llinás, David A Fidock *PLoS pathogens* 18 (10), (2022)
10. Chai, Zhi; Lyu, Yafei; Chen, Qiuyan; Wei, Cheng-Hsin; Snyder, Lindsay M; Weaver, Veronika; Sebastian, Aswathy; Albert, István; Li, Qunhua; Cantorna, Margherita T; RNAseq studies reveal distinct transcriptional response to vitamin A deficiency in small intestine versus colon, uncovering novel vitamin A-regulated genes *The Journal of nutritional biochemistry* (2022)
11. Kamens, Helen M; Miller, Carley N; Caulfield, Jasmine I; Zeid, Dana; Horton, William J; Silva, Constanza P; Sebastian, Aswathy; Albert, Istvan; Gould, Thomas J; Fishbein, Diana; Adolescent stress reduces adult morphine-induced behavioral sensitization in C57BL/6J mice *Frontiers in Behavioral Neuroscience* 15 (2022)
12. Saini, Mohit Kumar; Sebastian, Aswathy; Shirotori, Yoshiki; Soulier, Nathan T; Garcia Costas, Amaya M; Drautz-Moses, Daniela I; Schuster, Stephan C; Albert, Istvan; Haruta, Shin; Hanada, Satoshi; Genomic and Phenotypic Characterization of Chloracidobacterium Isolates Provides Evidence for Multiple Species *Frontiers in Microbiology* (2022)
13. Lin, Yishan; Grembi, Jessica A; Goots, Sara S; Sebastian, Aswathy; Albert, István; Brennan, Rachel A; Advantageous microbial community development and improved performance of pilot-scale field systems treating high-risk acid mine drainage with crab shell *Journal of Hazardous Materials* (2022)
14. Saini, Mohit Kumar; Yoshida, Shohei; Sebastian, Aswathy; Hara, Eri; Tamaki, Hideyuki; Soulier, Nathan T; Albert, Istvan; Hanada, Satoshi; Tank, Marcus; Bryant, Donald A; *Eliaoreaea tepida*, sp. nov., a Moderately Thermophilic Aerobic Anoxygenic Phototrophic Bacterium Isolated from the Mat Community of an Alkaline Siliceous Hot Spring in Yellowstone National Park, WY, USA *Microorganisms* (2022)

15. Lindner, Scott E; Swearingen, Kristian E; Shears, Melanie J; Sebastian, Aswathy; Walker, Michael P; Vrana, Erin N; Hart, Kevin J; Minns, Allen M; Albert, Istvan; Sinnis, Photini; Addendum: Transcriptomics and proteomics reveal two waves of translational repression during the maturation of malaria parasite sporozoites *Nature communications* 13 (2022)
16. Chai, Zhi; Lyu, Yafei; Chen, Qiuyan; Wei, Cheng-Hsin; Snyder, Lindsay M; Weaver, Veronika; Sebastian, Aswathy; Albert, István; Li, Qunhua; Cantorna, Margherita T; Transcriptional Profiling of the Small Intestine and the Colon Reveals Modulation of Gut Infection with *Citrobacter rodentium* According to the Vitamin A Status *Nutrients* (2022)
17. Rufai, S. B., McIntosh, F., Poojary, I., Chothe, S., Sebastian, A., Albert, I. (Author), Praul, C. A., Venkatesan, M., Mahata, G., Maity, H., Dandapat, P., Michael, J. S., Katani, R., Kapur, V., & Behr, M. A. (2021). Complete Genome Sequence of *Mycobacterium orygis* Strain 51145. *Microbiology resource announcements*, 10(1).
18. Goldberg, L., Zeid, D., Kutlu, M. G., Cole, R. D., Lallai, V., Sebastian, A., Albert, I. (Author), Fowler, C., Parikh, V., & Gould, T. (2021). Paternal nicotine enhances fear memory, reduces nicotine administration, and alters hippocampal genetic and neural function in offspring. *Addiction biology*, 26(1), e12859. ISBN/ISSN #/Case #/DOI #: 1355-6215
19. Ford, S. A., Albert, I. (Author), Allen, S. L., Chenoweth, S. F., Jones, M. J., Koh, C., Sebastian, A., Sigle, L. T., & Mcgraw, E. (2020). Artificial selection finds new hypotheses for the mechanism of *Wolbachia*-mediated dengue blocking in mosquitoes. *Frontiers in microbiology*, 11, 1456.
20. Saini, M. K., ChihChe, W., Soulier, N., Sebastian, A., Albert, I. (Author), Thiel, V., Bryant, D. A., Hanada, S., & Tank, M. (2020). *Caldichromatium japonicum* gen. nov., sp. nov., a novel thermophilic phototrophic purple sulfur bacterium of the Chromatiaceae isolated from Nakabusa hot springs, Japan. *International journal of systematic and evolutionary microbiology*, 70(11), 5701--5710.
21. Rosenthal, E. R., Sebastian, A., Potnis, N., Albert, I. (Author), & Bull, C. (2020). Comparative genomic analysis of the lettuce bacterial leaf spot pathogen. *Plant Health 2020 Online*.
22. Aberra, N., Sebastian, A., Maloy, A. P., Rees, C. B., Bartron, M. L., & Albert, I. (Author) (2020). Bioinformatics recipes: creating, executing and distributing reproducible data analysis workflows. *BMC Bioinformatics*, 21(1), 292.
23. Yeh, Y.-T., Gulino, K., Zhang, Y., Sabestien, A., Chou, T. W., Zhou, B., Lin, Z., Albert, I. (Author), Lu, H., Swaminathan, V., Ghedin, E., & Terrones Maldonado, M. (2020). A rapid and label-free platform for virus capture and identification from clinical samples. *Proceedings of the National Academy of Sciences of the United States of America*, 117(2), 895-901.
24. Ford, S., Allen, S. D., Sebastian, A., Albert, I. (Author), Chenoweth, S., & Mcgraw, E. (2019). Using Evolutionary Approaches to Dissect the Genetic Basis of *Wolbachia*-Mediated Blocking of Dengue Virus in *Aedes Aegypti*. *American Journal of Tropical Medicine and Hygiene*, 101, 386--386.
25. Goldberg, L., Zeid, D., Kutlu, M. G., Cole, R. D., Lallai, V., Sebastian, A., Albert, I. (Author), Fowler, C. D., Parikh, V., & Gould, T. (2019). Paternal nicotine enhances fear memory, reduces nicotine administration, and alters hippocampal genetic and neural function in offspring. *Addiction biology*, e12859
26. Ford, S. A., Allen, S., Ohm, J. R., Sigle, L. T., Sebastian, A., Albert, I. (Author), Chenoweth, S. F., & Mcgraw, E. (2019). Selection on *Aedes aegypti* alters *Wolbachia*-mediated dengue virus blocking and fitness. *Nature Microbiology*, 4(11), 1832-1839.

27. Horton, W. J., Jensen, M., Sebastian, A., Praul, C. A., Albert, I. (Author), & Bartell, P. A. (2019). Transcriptome Analyses of Heart and Liver Reveal Novel Pathways for Regulating Songbird Migration. *Scientific reports*, 9(1), 6058.
28. Chothe, S. K., Sebastian, A., Thomas, A., Nissly, R., Byukusenge, M., Wolfgang, D. R., Mor, S. K., Goyal, S., Albert, I. (Author), Jayarao, B. M., & others (2018). Whole-Genome Sequences of 18 Bovine Alphaherpesvirus 1 Field Isolates from Pennsylvania and Minnesota. *Genome Announcements*, 6(17), e00294--18.
29. Liang, X., Hart, K. J., Dong, G., Siddiqui, F. A., Sebastian, A., Li, X., Albert, I. (Author), Miao, J., Lindner, S., & Cui, L. (2018). Puf3 participates in ribosomal biogenesis in malaria parasites. *J Cell Sci*, jcs--212597.
30. Niu, B., Coslo, D. M., Bataille, A., Albert, I. (Author), Pugh, B. F., & Omiecinski, C. J. (2018). In vivo genome-wide binding interactions of mouse and human constitutive androstane receptors reveal novel gene targets. *Nucleic acids research*, 46(16), 8385--8403.
31. Painter, H. J., Chung, N. C., Sebastian, A., Albert, I. (Author), Storey, J. D., & Llin'as, Manuel (2018). Genome-wide real-time in vivo transcriptional dynamics during Plasmodium falciparum blood-stage development. *Nature communications*, 9(1), 2656.
32. Palchak, K., Chothe, S. K., Sebastian, A., Nissly, R. H., Barry, R., Albert, I. (Author), Jayarao, B. M., & Kuchipudi, S. V. (2018). Whole-Genome Sequence of Infectious Pancreatic Necrosis Virus Isolated from Farmed Brook Trout (*Salvelinus fontinalis*) in Pennsylvania. *Genome Announcements*, 6(17), e00360--18.
33. Shabbir, M. Z., Nissly, R. H., Ahad, A., Rabbani, M., Chothe, S. K., Sebastian, A., Albert, I. (Author), Jayarao, B. M., & Kuchipudi, S. V. (2018). Complete Genome Sequences of Three Related Avian Avulavirus 1 Isolates from Poultry Farmers in Pakistan. *Genome announcements*, 6(18), e00361--18.
34. Silva, C. P., Horton, W. J., Caruso, M. J., Sebastian, A., Klein, L., Albert, I. (Author), & Kamens, H. M. (2018). The influence of adolescent nicotine exposure on ethanol intake and brain gene expression. *PloS one*, 13(6), e0198935.
35. Huang, K.-H., Nichols, R. G., Sebastian, A., Albert, I. (Author), Patterson, A. D., & Ross, A Catharine (2017). Gut microbiota increased by omega-3 fatty acids is negatively correlated with hepatic lipid metabolism-associated genes in mice with high carbohydrate diet-induced steatosis. *The FASEB Journal*, 31(1 Supplement), 654--3.
36. Wan, Y., Cheng, G., Liu, X., Hao, S. J., Nisic, M., Zhu, C. D., Xia, Y. Q., Li, W. Q., Wang, Z., Zhang, W., Rice, S. J., Sebastian, A., Albert, I. (Author), Belani, C. P., & Zheng, S. (2017). Rapid magnetic isolation of extracellular vesicles via lipid-based nanoprobes. *Nature biomedical engineering*, 1
37. Chothe, S. K., Sebastian, A., Thomas, A. E., Nissly, R. H., Wolfgang, D. R., Byukusenge, M., Mor, S. K., Goyal, S. M., Albert, I. (Author), Tewari, D., Jayarao, B. M., & Kuchipudi, S. V. (2018). Whole-genome sequence analysis reveals unique SNP profiles to distinguish vaccine and wild-type strains of bovine herpesvirus-1 (BoHV-1). *Virology*, 522, 27-36. ISBN/ISSN #/Case #/DOI #: 0042-6822
38. Bishop, E., Pecchia, J., Wilkinson, V., Albert, I. (Author), & Royse, D. (2016). Effects of spent mushroom compost (SMC) as an ingredient in phase I compost on production of *Agaricus bisporus*. *Compost Science & Utilization*, 24(4), 246--258.
39. Yeh, Y. T., Tang, Y., Sebastian, A., Dasgupta, A., Perea-Lopez, N., Albert, I. (Author), Lu, H.-J., Terrones, M., & Zheng, S. (2016). Tunable and label-free virus enrichment for ultrasensitive virus detection using carbon nanotube arrays. *Science advances*, 2(10), e1601026.

40. Hao, R., Su, S., Wan, Y., Shen, F., Niu, B., Coslo, D. M., Albert, I. (Author), Han, X., & Omiecinski, C. J. (2016). Bioinformatic analysis of microRNA networks following the activation of the constitutive androstane receptor (CAR) in mouse liver. *Biochimica et biophysica acta*, 1859(9), 1228-37. ISBN/ISSN #/Case #/DOI #: 0006-3002
41. Cattadori, I., Sebastian, A., Hao, H., Katani, R., Albert, I. (Author), Eilertson, K. E., Kapur, V., Pathak, A. K., & Mitchell, S. (2016). Impact of Helminth Infections and Nutritional Constraints on the Small Intestine Microbiota. *PloS one*, 11(7), e0159770.
42. Jung, H., Pena-Francesch, A., Saadat, A., Sebastian, A., Kim, D. H., Hamilton, R. F., Albert, I. (Author), Allen, B. D., & Demirel, M. C. (2016). Molecular tandem repeat strategy for elucidating mechanical properties of high-strength proteins. *Proceedings of the National Academy of Sciences of the United States of America*, 113(23), 6478-83. ISBN/ISSN #/Case #/DOI #: 0027-8424
43. Galbraith, D. A., Kocher, S. D., Glenn, T., Albert, I. (Author), Hunt, G. J., Strassmann, J. E., Queller, D. C., & Grozinger, C. M. (2016). Testing the kinship theory of intragenomic conflict in honeybees (*Apis mellifera*). *Proceedings of the National Academy of Sciences of the United States of America*, 113(4), 1020-5. ISBN/ISSN #/Case #/DOI #: 0027-8424
44. Mondal, S., Yakhnin, A. V., Sebastian, A., Albert, I. (Author), & Babitzke, P. L. (2016). NusA-dependent transcription termination prevents misregulation of global gene expression. *Nature microbiology*, 1, 15007.
45. Liermann, L. J., Albert, I. (Author), Buss, H. L., Minyard, M., & Brantley, S. L. (2015). Relating microbial community structure and geochemistry in deep regolith developed on volcanoclastic rock in the Luquillo Mountains, Puerto Rico. *Geomicrobiology Journal*, 32(6), 494--510.
46. Pujol, L., Albert, I. (Author), Magras, C., Johnson, N. B., & Membré, J. M. (2015). Estimation and evaluation of management options to control and/or reduce the risk of not complying with commercial sterility. *International journal of food microbiology*, 213, 124-9. ISBN/ISSN #/Case #/DOI #: 0168-1605
47. Pujol, L., Johnson, N. B., Magras, C., Albert, I. (Author), & Membré, J. M. (2015). Added value of experts' knowledge to improve a quantitative microbial exposure assessment model--Application to aseptic-UHT food products. *International journal of food microbiology*, 211, 6-17. ISBN/ISSN #/Case #/DOI #: 0168-1605
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49. Zhang, L., Nichols, R., Correll, J., Murray, I. A., Tanaka, N., Smith, P., Hubbard, T. D., Sebastian, A., Albert, I. (Author), Hatzakis, E., Gonzalez, F. J., Perdew, G. H., & Patterson, A. D. (2015). Persistent Organic Pollutants Modify Gut Microbiota-Host Metabolic Homeostasis in Mice Through Aryl Hydrocarbon Receptor Activation. *Environmental health perspectives*, 123(7), 679-88. ISBN/ISSN #/Case #/DOI #: 0091-6765
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Funded Research Projects

1. Lipid nanoprobe integrated microdevice for extracellular vesicle isolation and duplex sequencing-based mutation detection for non-invasive lung cancer diagnosis, funded by National Cancer Institute, \$488,116
2. Computation, Bioinformatics, and Statistics (CBIOS) Training Program Renewal, funded by National Institute of General Medical Sciences, \$316,906.
3. Development of automated tools and databases useful for genetic data reduction and analysis, funded by U.S. Fish and Wildlife Service, \$65,000.
4. Environmental Ah Receptor Ligand Impact on the Host-Microbiome Metabolic Axis, funded by National Institute of Environmental Health Sciences, \$344,694; 157, 200.
5. Development of a bioinformatic pipeline and other analysis tools for DNA metabarcode data, funded by U.S. Fish and Wildlife Services, \$45,0000.
6. Vitamin D Fluctuations and the Mucosal Immune Response - Year 8, funded by National Center for Complementary and Integrative Health, \$300,000.
7. Temporal Genomics Mechanisms Underlying Disease and Aging, funded by National Institute on Aging, \$237,900.
8. Development of a bioinformatic pipeline and other analysis tools for DNA metabarcode data, funded by U.S. Fish and Wildlife Service, \$98,909.
9. Global Health, Emerging Infectious Diseases, and Food Safety Implications of Bushmeat Consumption, funded by Defense Threat Reduction Agency, \$776,902.
10. Environmental Ah Receptor Ligand Impact on the Host-Microbiome Metabolic Axis, National Institute of Health \$256,634
11. Transcriptomes and Proteomes of Plasmodium Vivax, funded by National Institute of Allergy and Infectious Diseases, \$169,726.
12. Targeting Dynamics of CAR and PXR in the Mouse and Human Genomes, funded by National Institute of General Medical Sciences, \$37, 375.
13. FXR and the Gut Microbiota as Modulators of Obesity (TSF 14/15), funded by PA Tobacco Settlement Fund, \$167,410.
14. Damage mitigation in signal transduction networks, funded by National Science Foundation, \$164,065.
15. Transcriptones and Preteomes of Plasmodium Vivax, funded by National Institute of Allergy and Infectious Diseases, \$216, 632.
16. Broccoli-mediates functional changes in the gut microbiome, funded by USDA National Institute of Food and Agriculture, \$447,790.
17. Vitamin A mediated protection from gastrointestinal infection, funded by National Institute of Allergy and Infectious Diseases, \$476,920.
18. Southeast Asia Malaria Research Center Supplement, funded by National Institute of Allergy and Infectious Diseases, \$189,143.
19. MRI: Acquisition of an Illumina HiSeq2000 as a core sequencing instrument for genomics and gene expression research, National Science Foundation, \$569,419.

20. Sex-specific gene expression in malaria parasite *Plasmodium falciparum*, funded by Institute of Allergy and Infectious Diseases, \$223,500.
21. High resolution mapping of function elements in the yeast genome (Principal Investigator: Pugh, Benjamin F.), funded by National Human Genome Research Institute, \$350,000.
22. Penn State Clinical and Translational Science Institute (Co-Principal Investigators: McHale, Susan M., Kris-Etherton, Penny M., Vanden Heuvel, John P., Aronson, Keith R., Miller, Webb C., Slavkovic, Aleksandra B., Marks, Jonathan H., Chow, Mosuk, West, Sheila G., Nembhard, Harriet B., Pawelczyk, James A., funded by National Center for Research Resources, \$4,457,207.
23. Tailoring genomic data to the needs of experimental biologists and educators (Principal Investigator: Nekrutenko, Anton), funded by National Science Foundation, \$234,556.
24. A computational platform for merging genomics and molecular evolution (Principal Investigator: Nekrutenko, Anton), funded by National Science Foundation, \$261,385
25. Bioinformatics Consulting Center at University Park and Hershey Medical Center, Phase II (TSF) (Principal Investigator: Rosenberger, James, L.), funded by PA Tobacco Settlement Fund, \$82,554.

EXHIBIT 18B

Michael L. Metzker
(last updated April 24, 2025)

I. General Biographical Information

a. Personal:

Home address: 12015 Surrey Lane, Houston, TX 77024
Date of birth: September 20, 1962
Citizenship: United States

b. Education:

1984 University of California — Davis, Davis, CA
B.S. — Biochemistry & Biophysics
1996 Baylor College of Medicine, Houston, TX
Ph.D. — Molecular & Human Genetics

c. Academic Appointments:

2014-to-2019 Adjunct Associate Professor, Department of Molecular & Human
Genetics & Human Genome Sequencing Center,
Baylor College of Medicine, Houston, TX
2009-to-2019 Adjunct Associate Professor, Department of Chemistry,
Rice University, Houston, TX
2009-to-2014 Associate Professor, Department of Molecular & Human Genetics &
Human Genome Sequencing Center,
Baylor College of Medicine, Houston, TX
2009-to-2014 Adjunct Associate Professor, Cell & Molecular Biology,
Baylor College of Medicine, Houston, TX
2001-to-2008 Adjunct Assistant Professor, Department of Chemistry,
Rice University, Houston, TX
2000-to-2008 Adjunct Assistant Professor, Cell & Molecular Biology,
Baylor College of Medicine, Houston, TX
1999-to-2008 Assistant Professor, Department of Molecular & Human Genetics &
Human Genome Sequencing Center,
Baylor College of Medicine, Houston, TX

d. Corporate positions and other professional experiences:

2013-to-Present Founder, President & CEO, RedVault Biosciences, Houston TX
2022-to-2023 Co-founder & CTO, 454 Bio, Inc.
2012 Founder, CTO, LaserGen, Inc.
2010 Consulted with Law & Order SVU on the episode, *The Quickie*
2009 Appeared on ABC's *20/20* profiling Collin Co. HIV criminal case
2009 Collin Co. work appeared on *Oprah*
2007-to-2009 Expert witness for HIV criminal case, Collins Co., TX
2004 Expert witness for HIV criminal case, Thurston Co., WA

2003	Appeared on <i>truTV's</i> series <i>Forensics Files</i> in episode #152, "Shot of Vengeance"
2002-to-2012	Founder, President & CEO, LaserGen, Inc., Houston TX
1997-to-1999	Expert witness for HIV criminal case, Lafayette, LA
1996-to-1999	Senior Research Biologist, Merck Research Laboratories, West Point, PA
1987-to-1991	Associate Scientist, Applied Biosystems, Inc. (ABI), Foster City, CA
1984-to-1987	Research Chemist, Bio-Rad Laboratories; Richmond, CA
1983-to-1984	Laboratory Technician, Aerojet-General Corporation; Sacramento, CA

e. Prior Expert Experience

In the past five years, I have provided expert testimony at a Markman hearing, trial or deposition in the following cases:

- Plexxikon, Inc. v. Novartis Pharmaceuticals Corp., 4:17-cv-04405-HSG (EDL; on behalf of Plexxikon, Inc.)
- Guardant Health, Inc. v. Foundation Medicine, Inc. CA No. 17-1616 (LPS) (CJB, on behalf of Foundation Medicine, Inc.)
- ArcherDx, Inc. v. Qiagen Inc. CA 18-cv-01019-MN-CJB (on behalf of Qiagen)
- Illumina, Inc. v. Natera, Inc. CA 3:18-cv-1662-SI (on behalf of Natera)
- Illumina, Inc v. Complete Genomics, Inc. Case No. 20-cv-1465 (on behalf of Complete Genomics)
- Complete Genomics, Inc. v. Illumina, Inc & Illumina Cambridge, LTD. Case No. 19-970-MN (on behalf of Complete Genomics)
- Pillar Biosciences, Inc. v. Swift Biosciences, Inc. Case No. IPR2021-00401 (on behalf of Swift Biosciences)
- Ravgen, Inc. v. Ariosa Diagnostics, Inc.; Roche Sequencing Solutions, Inc.; Roche Molecular Systems, Inc. (collectively "Roche") Case No. 20-cv-1646 (on behalf of Roche)
- Illumina Cambridge Limited and Illumina Singapore Pte Limited ("Illumina") v. Comercial Rafer, S.L. and MGI Latvia Tech, SIA ("MGI"), Commercial Court of Barcelona, Spain, matter 249.1.4 1249/2020-3 (on behalf of MGI)
- Guardant Health, Inc. v. Natera, Inc., Case No. 3:21-cv-04062 (on behalf of Natera)
- DNA Genotek, Inc. v. Spectrum Solutions, Case No. 21-cv-0516 (on behalf of DNA Genotek)
- Twinstrand Biosciences, Inc v. Guardant Health, Inc., Case No. 1:21-cv-01126 (on behalf of Twinstrand Biosciences)
- The Trustees of the University of Pennsylvania and Regenxbio, Inc. v. Sarepta Therapeutics and Sarepta Therapeutics Three, Inc, Case No. 20-1226 (on behalf of The Trustees of the University of Pennsylvania and Regenxbio, Inc)
- Spectrum Solutions v. DNA Genotek, Inc., *Inter Partes* Review IPR2022-01347 (on behalf of DNA Genotek)

- Invitae Corp. v. Natera, Inc.; Case No. 1:21-cv-006699-LPS and 1:21-cv-01635-LPS, (on behalf of Natera); US District Court, District of Delaware
- Natera, Inc., v. Neogenomics Laboratories, Inc., Case No. 1:23-cv-629 (on behalf of Natera)
- 10x Genomics, Inc. & Harvard College v. Vizgen, Inc., Case No. 22-595-MFK (on behalf of Vizgen)

II. Research Information

a. Research Support

1 — Pending research support:

Technical description: RedVault proposes development of a low cost, rapid, and accurate POC assay for the detection of syphilis, chlamydia, and/or gonorrhea that could facilitate early detection, thus potentially reducing transmission and sequelae as well as improve therapeutic outcomes in the clinic.

Funding agency: NIH

Investigator relationship: PI: Michael Metzker

Proposed date of funding: 09/30/2025– 09/29/2026

Annual costs: \$308,803

Grant: Not assigned yet, titled, “Detection of small RNAs from urine samples of patients infected with syphilis, chlamydia, and/or gonorrhea using a single POC, multiplex target reporter construct (TRC) assay by lateral flow.”

2 — Completed research support:

Technical description: RedVault proposes development of a low cost, rapid, and accurate POC assay for the detection of chlamydia and gonorrhea that could facilitate early detection, thus potentially reducing transmission and sequelae as well as improve therapeutic outcomes in the clinic.

Funding agency: CDC

Investigator relationship: PI: Michael Metzker

Date of funding: 09/30/2023– 03/31/2025

Annual costs: \$299,928

Grant: 1R43PS005272-01-00, titled, “POC detection of chlamydia and gonorrhea small RNAs using a target reporter construct assay by lateral flow in urine surrogates.”

Technical description: RedVault proposed the study and sequencing of genomes that has led to amazing discoveries in forensics, history, and medicine. Previous methods associated with preparing a DNA sample for sequencing depend on computationally reconstructing small pieces of data to understand genomic structure and variations, which is time intensive, error prone, and not accurate enough for large scale genomic information. The research proposed here is oriented toward significantly improving the methods of sample preparation, which will lead to improved efficiency, accuracy, and reduced costs to sequence DNA, thereby making the technology more accessible to more people.

Funding agency: NIH/NCI

Investigator relationship: PI: Michael Metzker

Date of funding: 02/01/2019 – 04/31/2023

Annual costs: \$224,998

Grant: R43 CA232896-01A1, titled “Solid-phase replication of long template libraries for next-generation sequencing”

Technical description: RedVault Biosciences’ proposes an innovative approach to reliably interrogate plasma specimens for clinically relevant miRNAs. Successful development of this technology may deliver a fundamental advancement in the cancer screening, tumor surveillance, and miRNA research fields.

Funding agency: NIH/NCI

Investigator relationship: PI: Michael Metzker

Date of funding: 06/07/2016 – 03/06/2018

Annual costs: \$199,859

Grant: R43 CA200398-01A1, titled, “Digital Analysis of Plasma miRNA populations in Pancreatic Cancer.”

Technical description: RedVault Biosciences’ proposal here is oriented toward significantly improving the methods of sample preparation, which will lead to improved efficiency, accuracy, and reduced costs to sequence DNA.

Funding agency: NIH/NCI

Investigator relationship: PI: Michael Metzker

Date of funding: 01/14/2016 – 02/13/2017

Annual costs: \$146,801

Grant: R43 CA196134-01A1, titled, “Efficient Creation of Long-Template Libraries for Next-Generation Sequencing”

Technical description: The major goals of this project are to support sequencing and technology development in the areas of human genetics, cancer, the microbiome and comparative genomics.

Funding agency: NIH/NHGRI

Investigator relationship: Richard A. Gibbs; Co-Director Boerwinkle; co-PIs Muzny, Wheeler, Metzker, Worley

Date of funding: 11/01/2011 – 02/08/2015; effective end 02/08/14

Annual costs: \$20,119,270

Grant: U54 HG003273-09, titled, “The Human Genome Sequencing Center”

Technical description: This proposal represents a request for continued funding of the Mayo Clinic Pharmacogenomics Research Network (PGRN) grant, “Pharmacogenetics of Phase II Drug Metabolizing Enzymes.” The Mayo PGRN is an integrated, multidisciplinary, pharmacogenomic research effort that is based on a decades-long focus at Mayo on the pharmacogenetics of phase II (conjugating) drug metabolizing enzymes.

Funding agencies: NIGMS, NHLBI, NCI, NIDA, NICHD, NHGRI, NIMH, NIAMS, ORWH *Investigator*

relationship: Richard Weinshilboum; Co-PIs Gibbs, Metzker, Scherer

Date of funding: 7/01/10 to 06/30/15; effective end 02/08/14

Annual costs: \$425,709

Grant: 2U19GM061388-12, titled “Pharmacogenetics of Phase II Drug Metabolizing Enzymes”

Technical description: This proposal seeks to expand our existing scientific work on HIV forensic studies by developing a robust ‘pathogen toolkit’ for source identification across a range of biological agents

Funding agencies: National Institute of Justice

Investigator: Michael L. Metzker

Date of funding: 01/01/12 to 12/31/13

Annual costs: \$341,017

Grant: 2011-DN-BX-K534 titled, "Extending the Microbial Forensic Toolkit Through Whole Genome Sequencing and Statistical Phylogenomics"

Technical description: This Phase I SBIR grant application proposes three aims: (i) identify the most efficient NGS platform by sequencing *E. coli* MG1655 using six platforms, (ii), conduct mixing experiments using purified gram negative and gram positive bacteria using the platform selected in aim (i), and (iii) conduct mixing experiments described in aim (ii) in the presence of human blood to simulate animal wound models.

Funding agency: Office of the Secretary of Defense, Defense Health Program

Investigator relationship: David Hertzog; co-PI Metzker

Date of funding: 02/01/11 to 08/31/12

Annual costs: \$150,000

Total costs: \$150,000

Contract: W81XWH-12-C-0061, titled "Feasibility Study to Explore NGS Technologies in Pathogen Identification"

Technical description: The goal is to evaluate the feasibility of our next-generation, cyclic reversible termination (CRT) sequencing approach by targeting 1,000 candidate genes on highdensity oligonucleotide chips. *Funding agency:* NIH: NHGRI

Investigator: Michael L. Metzker

Date of funding: 08/01/08 to 05/31/11

Annual costs: \$230,250

Total costs: \$422,125

Grant: 1R21 HG004757, titled "Targeted CRT Sequencing of 1000 Genes in KPD Patients"

Technical description: The goal is to develop ultrafast sequencing-by-synthesis (SBS) technology that is practical on a genomic scale. *Funding agency:* NIH: NHGRI

Investigator: Michael L. Metzker

Date of funding: 10/01/04 to 09/30/08

Annual costs: \$468,575

Total costs: \$2,933,762

Grant: 1 R01 HG003573-01 titled, "Ultrafast SBS Method for large-Scale Human Resequencing"

Technical description: Development of a novel portable DNA sequencer for rapid identification of single nucleotide polymorphisms (SNPs) in common disease.

Funding agency: NIH: NHGRI

Investigator: Michael L. Metzker

Date of funding: 06/07/04 to 02/28/06

Annual costs: \$421,914

Total costs: \$532,761

Grant: 1 R41 HG003265-01 titled, "Development of a Portable PME DNA Sequencer"

Technical description: Development of novel FluoroBase dyes and associated nucleotide triphosphates, which have the potential to create sets of spectrally resolvable dye-terminators.

Special note: Originally awarded to Michael L. Metzker as STTR application: Grant converted in SBIR

Funding agency: NIH:NHGRI

Investigator relationship: Vladislav A. Litosh; co-PI Metzker
Date of funding: 07/11/03 to 12/31/05
Annual costs: \$213,064 *Total direct costs:* \$289,689
Grant: 1 R43 HG002632-01A1 titled, "Synthesis of FluoroBase Nucleotides for DNA Sequencing"

Technical description: The major goal of this project is to produce a draft sequence of the rhesus macaque and bovine genomes and extract maximal biological information from these data.

Funding agency: NIH: NHGRI

Investigator relationship: Richard A. Gibbs; co-Director Weinstock, co-PIs Muzny, Wheeler, Metzker, Worley

Date of funding: 11/10/03 to 10/31/06

Annual direct costs: \$21,028,110 *Total direct costs:* \$89,072,698

Grant: 1 U01 HG02051 titled, "Large Scale Sequencing at BCM-HGSC"

Technical description: The goal of this project is to generate a draft sequence of the genome of *Bos Taurus*.

Funding agency: USDA

Investigator relationship: Richard A. Gibbs; co-Director Weinstock, co-PIs Muzny, Wheeler, Metzker, Worley

Date of funding: 12/01/03 to 11/31/05

Annual direct costs: \$3,879,953 *Total direct costs:* \$7,853,612

Grant: TEXR-2003-05478 titled, "Bovine Genome Sequencing Project (BGSP)"

Technical description: Development of a novel multi-color fluorescent detection apparatus with potential application for direct detection of targeted regions from genomic DNA materials.

Funding agency: NIH: NHGRI

Investigator: Michael L. Metzker

Date of funding: 04/01/03 to 03/31/05

Annual costs: \$150,000 *Total costs:* \$250,000

Grant: 1 R21 HG002443-01A2, titled "Development of Fluorescent Detector for DNA Sequencing"

Technical description: Development of a novel DNA sequencing strategy by synthesis for application in high-throughput single nucleotide polymorphism (SNP) analysis.

Funding agency: NIH: NHGRI

Investigator: Michael L. Metzker

Date of funding: 09/30/03 to 03/31/05

Annual costs: \$310,504 *Total costs:* \$436,400

Grant: 1 R41 HG003072-01 titled, "Screening *Taq* Pol I Variants using 3'-O-Modified-dNTPs"

Technical description: Pilot project to synthesize and characterize modified nucleoside for potential activity against HIV-1.

Funding agency: Robert A. Welch Foundation

Investigator: Michael L. Metzker

Date of funding: 06/01/01 to 07/31/04

Annual costs: \$50,000 *Total costs:* \$158,000

Grant: Q-1518 titled, "Characterization of HIV-1 drug resistance using 3'-saturated nucleotides"

Technical description: Development of sixteen spectrally-resolved dyes for high-throughput nucleic acid detection such as DNA sequencing.

Funding agency: NIH: NHGRI

Investigator relationship: Mathew Mahindaratne; co-PI Metzker – special note: Originally awarded to Michael L. Metzker as STTR application and then was converted in SBIR. *Date of funding:* 07/21/03 to 06/30/05

Annual direct costs: \$214,000 *Total direct costs:* \$214,000

Grant: 1 R43 HG002567-01A2 titled, “Development of Novel Fluorescent Dyes for DNA Sequencing”

Technical description: The major goal of this project is to determine the genome sequence of the rat.

Funding agency: NIH: NHGRI/NHLBI

Investigator relationship: Richard A. Gibbs; co-Director Weinstock, co-PIs Muzny, Wheeler, Metzker, Worley

Date of funding: 02/27/01 to 02/26/04

Annual direct costs: \$10,976,914 *Total direct costs:* \$25,950,547

Grant: 1 U54 HG02345-02 titled, “Draft sequence of the rat genome”

Technical description: The major goal of this project is to prepare two types of extremely sensitive fluorescent label “cassettes” for DNA sequencing that may be used with both dye primer and dye terminator strategies. *Funding agency:* NIH: NHGRI

Investigator relationship: Kevin Burgess; co-PI Metzker

Date of funding: 09/06/01 to 07/31/05

Annual direct costs: \$38,296 *Total direct costs:* \$114,923

Grant: Competing Renewal FDN-S80093 titled, “Unnatural nucleotides for DNA sequencing”

Technical description: To develop and validate novel pooling-based methods for the rapid physical mapping of BAC libraries. *Funding agency:* NIH: NCRR

Investigator relationship: Aleksandar Milosavljevic; co-PI Metzker *Date of funding:* 09/30/02 to 08/31/05

Annual direct costs: \$206,693 *Total direct costs:* \$612,721

Grant: 1 U01 RR18464-01 titled, “Clone pooling methods for physical mapping”

Technical description: The major goals of this project are extensive mapping and sequencing of the mouse genome. *Funding agency:* NIH: NHGRI

Investigator relationship: Richard A. Gibbs; co-Director Weinstock, co-PIs Muzny, Wheeler, Metzker, Worley

Date of funding: 09/30/99 to 09/30/03

Annual direct costs: \$5,316,551 *Total direct costs:* \$20,851,198

Grant: 1 U54 HG02139 titled, “Network for large-scale sequencing of the mouse genome”

Technical description: To produce a draft sequence of *D. pseudoobscura* with annotation and finishing of selected full-length cDNA and gene-rich regions.

Funding agency: NIH: NHGRI

Investigator relationship: Richard A. Gibbs; co-Director Weinstock, co-PIs Richards, Muzny, Wheeler, Metzker, Worley

Date of funding: 05/10/02 to 04/30/03

Annual direct costs: \$3,336,210 *Total direct costs:* \$3,336,210
Grant: 1 U01HG02570 titled, "Sequencing, annotation and assembly of a second *Drosophila*"

b. National Scientific Participation

1 — Editorial/Advisory Boards:

2003-to-2006	<i>Genome Research</i> , Cold Spring Harbor Laboratory Press
2006-to-2012	<i>Advances in Genome Biology & Technology Meeting</i> , Scientific advisor
2011-to-2013	Genome Canada: Advancing Technology Innovation through Discovery (ATID) Advisory Committee

2 — Review panels:

Jul 2025	NIH: (DCAI-13): Small Business: Microbial Diagnostics, Detection and Decontamination
Feb 2024	Panel Chair: (SBIR) contract – Topic 108: Development of Rapid POC Diagnostics for <i>Treponema pallidum</i> (Phase II)
Jan 2022	Panel Chair: (SBIR) contract – Topic 108: Development of Rapid POC Diagnostics for <i>Treponema pallidum</i> (Phase I)
Nov 2019	NIH: ZRG1 SBIR/STTR/R21/R03: Infectious disease diagnostics, methods in sterilization & disinfection Study Section panels: IDM-V (12 & 19) NIH: ZRG1 SBIR: Biomaterials, Delivery, and Nanotechnology Study Section panel, ZRG1 BST-R (10)
Jul 2019	Chair, CIHR: Operating Grant CEEHRC (Epigenetics)
May 2019	Chair, CIHR: Operating Grant: Epigenetics Clinical Translation
Feb 2019	Invited expert on forensics, Arizona State University
Jan 2018	Chair, CEEHRC Phase II competition, Impact grants
Nov 2017	NASA Translational Research Institute Omics Panel
Jul 2017	CEEHRC Phase II: Platform Centres Renewal; Canadian Institutes of Health Research (CIHR)
Mar 2017	CIHR: Project Grant: Spring 2017 competition
Jun 2016	NIH: Sequencing Technology Special Emphasis Panel, ZHG1 HGR-N (M1)
Mar 2016	Disruptive Innovation in Genomics (DIG) Competition, Genome Canada
Jan 2016	Chair: CIHR's Team Grant: CEEHRC (Epigenetics)
Jun 2015	Genome Canada Genomics Innovation Network Technology Development International Review Committee
May 2015	National Center for Advancing Translational Sciences (NCATS), Special Emphasis Panel
Mar 2015	Genome Canada's Membership to the Genomics Innovation Network and Core Operations Support Funds competition
Nov 2014	Genomics, Computational Biology and Technology (GCAT) study section
Oct 2014	Interdisciplinary Molecular Science and Training – Cell, Molecular, and Computational Biology study section
Jun 2014	Genomics, Computational Biology and Technology (GCAT) study section; Transformative research award review
Mar 2014	ISD study section, Bioengineering Sciences and Technologies
Feb 2014	

Jan 2014	NASA study section: "Differential Effects on Homozygous Twin Astronauts Associated with Differences in Exposure to Spaceflight Factors"
Dec 2013	ISD study section, Bioengineering Sciences and Technologies
May 2013	Partnerships for Enhanced Engagement in Research (PEER) Health, NICHD
Apr 2013	Terry Fox New Frontiers Program in Cancer Research
Apr 2013	Science & Technology Innovation Centers' Renewal, Genome Canada
Jan 2013	Canada-Japan CEEHRC Teams in Epigenetics of Stem Cells, CIHR, Co-chair
Aug 2012	Chair: Team Grant: CEEHRC - LOI committee.
Feb 2012	Chair: Epigenomics platform peer review committee, Canadian Institutes of Health research (CIHR)
Feb 2012	Chair: Epigenetics catalyst peer review committee, CIHR
Sep 2011	Ad hoc member of NIH Instrumentation and Systems Development (ISD) study section
Feb 2011	Science & Technology Innovation Center Competition Review: Genome Canada
Nov 2010	ATID Review: Genome Canada
Mar 2010	IDRC P30 REVIEW, ZHD1-MRG-C (ID)
Oct 2009	Genomics, Computational Biology and technology study section, NIH
Jul 2009	DP3 Review, ZDK1 GRB-N(01), NIDDK
Jan 2009	Applied Genomics Research in Bioproducts or Crops (ABC), Genome Canada
Sep 2008	NCI Structural Biophysics Laboratory Site Visit, NCI
Nov 2007	Technology Development Competition, Genome Canada
2005-2007	Permanent member of NIH ISD study section
Apr 2007	Applied Emerging Technologies for Cancer Research, ZCA1 SRRB-4 (M1), NCI
Oct 2006	Applied Emerging Technologies for Cancer Research, ZCA1 SRRB-K (J1), NCI
Jun 2006	Innovative Technologies for the Molecular Analysis of Cancer, ZCA1 SRRBK (O1), NCI
Mar 2006	Applied Emerging Technologies for Cancer Research, ZCA1 SRRB-9 (M1), NCI
Oct 2005	ISD study section [ZRG1 ISD (01)], NIBIB
Oct 2005	Emerging Technologies for Cancer Research, ZCA1 SRRB-4 (J1), NCI
Jul 2005	ISD study section [ZRG1 ISD (01)], NIBIB
Jun 2005	Innovative Technologies for Cancer Research, ZCA1 SRRB-3 (O1), NCI
Mar 2005	ISD study section [ZRG1 ISD (01)], NIBIB
Mar 2005	Innovative Molecular Analysis Technology, ZCA1 SRRB-C (M2), NCI
Nov 2004	ISD study section, ZRG1 ISD (01), NIBIB
Jul 2004	Innovative Molecular Analysis Technology, ZCA1 SRRB-C (O1), NCI
Jul 2004	ISD study section, ZRG1 ISD (01), NIBIB
Jun 2004	Subcommittee E – Cancer Epidemiology, Prevention & Control study section, NCI-E RPRB (X1), NCI

Mar 2004	ISD study section, ZRG1 ISD (01), NIBIB
Dec 2003	Genome Technology & Cytogenetics (GT&C) study section, ZRG1 GNM (90), NHGRI
Oct 2003	Atopic Dermatitis & Vaccinia Network; Clinical Studies Consortium study section [ZAI1 CL-1 (C1), NIAID
Jul 2003	GT&C study section, ZRG1 GNM (90), NHGRI
Nov 2001	Genome study section, CSR-GNM, NHGRI
Jul 2001	Center for Scientific Review – Special Emphasis Panel (CSR-SEP) study section [ZRG1 SSS-Y], NHGRI
Jul 2001	Bioengineering Research Partnership study section [ZRG1 SSS-Y (02)], NHGRI
Apr 2001	CSR-SEP study section [ZRG1 SSS-Y (11) B], NHGRI
Mar 2001	Microbial Genome Project – study section, DOE
Nov 2000	CSR-SEP SBIR/STTR study section [ZRG1 SSS-Y (10)], NHGRI
Mar 2000	CSR-SEP SBIR/STTR study section [ZRG1 SSS-Y (01)], NHGRI
Nov 1999	CSR-SEP SBIR/STTR study section [ZRG1 SSS-Y (01)], NHGRI
Jul 1999	Technologies for Generation of Full-Length Mammalian cDNA study section [CA99-005], NCI
Jul 1999	CSR-SEP SBIR/STTR study section [ZRG1 SSS-Y (01)], NHGRI
Mar 1999	CSR-SEP SBIR/STTR study section [ZRG1 SSS-Y (01)], NHGRI
Mar 1998	SBIR/STTR Molecular Genetics study section [ZRG2 GNM O2B], NHGRI
Mar 1997	Biological & Physiological SEP study section [ZRG2 SSS-Y (15)], NHGRI

3 — Professional societies:

1996-to-present	American Association for the Advancement of Science
2000-to-present	American Chemical Society
2014-to-present	Texas Genetics Society

4 — Invited lectures, presentations, research seminars:

Apr 2016	Critical Path to TB Drug Regimens (CPRT) Workshop, Washington DC, Invited Speaker
May 2015	Advances in Next Generation Sequencing, Online, Keynote speaker
Mar 2013	ABRF- Satellite workshop, Palm Springs, CA; Invited Speaker
Jun 2012	American Society of Microbiology, San Francisco, CA; Invited Speaker
Jun 2012	Copenhagénomics, Copenhagen, Denmark, Invited Speaker
Feb 2012	Advances in Genome Biology & Technology, Marco Island, FL; Speaker
Apr 2011	Next-Gen Sequencing Conference, Boston, MA; Keynote Speaker
Apr 2011	Texas Association for Clinical Laboratory Science (TACLS), Austin, TX; Invited Speaker
Oct 2010	Centre de Regulació Genòmica (CRG) Symposium, Barcelona Spain, Invited Speaker
Jun 2010	ACS Meeting, San Diego, CA; Invited Speaker

May 2010	Next Generation Sequencing Workshop, Lübeck University, Germany; Invited Speaker
May 2010	Genomics Automation Conference, Boston, MA; Invited Speaker
Feb 2009	Advances in Genome Biology & Technology, Marco Island, FL Invited Speaker
Jun 2008	Workshop on Genotyping-Tissue Expression (GTEx) Resource, NIH Invited Participant
Oct 2007	International Conference on Genomics, Shenzhen, China; Invited Speaker
Sep 2007	IBC's Discovery-2-Diagnostics Conference, Philadelphia, PA Invited Chair & Speaker
Feb 2007	Advances in Genome Biology & Technology, Marco Island, FL Invited Speaker
Oct 2006	International Conference on Genomics, Hangzhou, China Invited Speaker
Sep 2006	Genomics of Hyperglycaemia, Elsinore, Denmark Invited Speaker
Feb 2006	Advances in Genome Biology & Technology, Marco Island, FL Invited Speaker
May 2005	5 th Annual RECOMB Satellite meeting on DNA Sequencing Technologies and Computation, Stanford University; Invited Speaker
Feb 2005	Advances in Genome Biology & Technology, Marco Island, FL Invited Speaker
Feb 2004	Advances in Genome Biology & Technology, Marco Island, FL Invited Speaker
Jun 2003	BECON 2003 Symposium on Catalyzing Team Science, NIH Invited Speaker
Jan 2002	Agriculture Program Research General Session, Texas A&M University Invited Speaker
Oct 2001	Genome sequencing and Analysis Conference XIII, San Diego, CA Invited Speaker
Feb 2001	Advances in Genome Biology & Technology, Marco Island, FL Invited Speaker
May 2000	Second Follow-Up Workshop on Priority Setting for Mouse Genomics and Genetics Resources, NIH; Invited Participant
Mar 1998	Full-Length cDNA Cloning: A Workshop on Problems and Solutions, The Banbury Center, Cold Spring Harbor; Invited Participant
May 1997	Workshop on Complete cDNA Sequencing, NIH; Invited Participant

c. Publications

1 — Peer-reviewed articles and reviews:

1. Burgess K, Gibbs RA, **Metzker ML**, and Raghavachari R (1994) Synthesis of an Oxyamide Linked Nucleotide Dimer and Incorporation into Antisense Oligonucleotide Sequences, *J. Chem. Soc., Chem Commun.*, 915-916.

2. **Metzker ML**, Raghavachari R, Richards S, Civitello A, Burgess K, and Gibbs RA (1994) Termination of DNA synthesis by novel 3'-modified-deoxyribonucleoside 5'-triphosphates, *Nucleic Acids Res.* 22, 4259-4267.
3. **Metzker ML**, Allain KM, and Gibbs RA (1995) Accurate determination of DNA in agarose gels using the novel algorithm *GelScann(1.0)*, *Comput. Applic. Biosci.* 11, 187-194.
4. **Metzker ML**, Lu J and Gibbs RA (1996) Electrophoretically Uniform Fluorescent Dyes for Automated DNA Sequencing, *Science* 271: 1420-1422.
5. Ansari-Lari MA, Liu XM, **Metzker ML**, Rut AR and Gibbs RA (1997) The extent of genetic variation in the CCR5 gene. *Nature Genet.* 16: 221-222.
6. Petrukhin K, Koisti MJ, Bakall B, Li W, Xie G, Marknell T, Sandgren O, Forsman K, Holmgren G, Andreasson, S Vujic, M Bergen AAB, McGarty-Dugan V, Figueroa D, Austin CP, **Metzker ML**, Caskey CT, and Wadelius C (1998) Identification of the gene responsible for Best macular dystrophy. *Nature Genet.* 19:241-247.
7. **Metzker ML**, Ansari-Lari MA Liu XL, Holder DJ, and Gibbs RA (1998) Quantitation of MixedBase Populations of HIV-1 Variants by Automated DNA Sequencing with BODIPY DyeLabeled Primers. *BioTechniques* 25:446-462.
8. Hey PJ, Twells RCJ, Phillips MS, Nakagawa Y, Brown SD, Kawaguchi Y, Cox R, Xie G, Dugan V, Hammond H, **Metzker ML**, Todd JA, and Hess JF (1998) Cloning of a novel member of the low-density lipoprotein receptor family. *Gene* 216:103-111.
9. Brown SD, Twells RCJ, Hey PJ, Cox RD, Levy ER, Soderman AR, **Metzker ML**, Caskey CT, Todd JA, and Hess JF (1998) Isolation and characterization of *LRP6*, a novel member of the low density lipoprotein receptor gene family. *Biochem. Biophys. Res. Commun.* 248:879-888.
10. **Metzker ML**, Raghavachari R, Burgess K, and Gibbs RA (1998) Elimination of residual natural nucleotides from 3'-O-modified-dNTP syntheses by enzymatic Mop-Up. *BioTechniques* 25:814-817.
11. Muzny DM, **Metzker ML**, Bouck J, Gorrell JH, Ding Y, Maxim E, and Gibbs RA (1998) Using BODIPY Dye-Primer Chemistry in Large-Scale Sequencing. *IEEE Engineering in Medicine and Biology* 88-93.
12. Allikmets R, Seddon JM, Bernstein PS, Hutchinson A, Sharma S, Gerrard B, Li W, **Metzker ML**, Wadelius C, Caskey CT, Dean M, and Petrukhin K (1999) Rare variants of the best disease gene in patients with age-related macular degeneration and other maculopathies. *Hum. Genet.* 104: 449-453.
13. Bai C, Connolly B, Liu X, Hilliard CA, Galloway SM, Sandig V, Liu Q, **Metzker ML**, Austin CP, and Caskey CT (2000). Overexpression of a new secreted member of tumor necrosis factor receptor family in gastrointestinal tract tumors. *Proc. Natl. Acad. Sci. USA* 97:1230-1235.
14. Sandig V, Youil R, Bett AJ, Franlin LL, Oshima M, Maione D, Wang F, **Metzker ML**, Savino R, Caskey CT (2000) Optimization of the helper-dependent adenovirus system for production and potency *in vivo*. *Proc. Natl. Acad. Sci. USA.* 97:1002-1007.
15. Bouck JB, **Metzker ML**, and Gibbs RA (2000) Shotgun sample sequence comparisons between mouse and human genomes. *Nature Genet.* 25:31-3.
16. Zhang K, Kniazeva M, Han M, Li W, Yu Z, Yang Z, Li Y, **Metzker ML**, Allikmets R, Zack DJ, Kakuk LE, Lagali PS, Wong PW, MacDonald IM, Sieving PA, Figueroa DJ, Austin CP, Gould RJ, Ayyagari R, and Petrukhin K (2001) A 5-bp deletion in *ELOVL4* is associated with two related forms of autosomal dominant macular dystrophy. *Nature Genet.* 27:89-93.
17. International Human Genome Sequencing Consortium: Baylor College of Medicine Human Genome Sequencing Center: Gibbs RA, Muzny DM Scherer SE, Bouck JB, Sodergren EJ,

- Worley KC, Rives CM, Gorrell JH, **Metzker ML**, Naylor SL, Kucherlapati RS, Nelson DL, and Weinstock GM (2001) Initial sequencing and analysis of the human genome. *Nature* 409:860-921.
18. Twells RC, **Metzker ML**, Brown SD, Cox R, Garey C, Hammond H, Hey PJ, Levy E, Nakagawa Y, Philips MS, Todd JA, and Hess JF. (2001) The sequence and gene characterization of a 400kb candidate region for *IDDM4* on chromosome 11q13. *Genomics* 72:231-242.
 19. Dederich DA, Okwuonu G, Garner T, Denn A, Sutton A, Escotto M, Martindale A, Delgado O, Muzny DM, Gibbs RA and **Metzker ML** (2002) Glass Bead Purification of Plasmid Template DNA for High-Throughput Sequencing of Mammalian Genomes. *Nucleic Acids Res.* 30:e32
 20. **Metzker ML**, Mindell DP, Ptak RG, Gibbs RA, and Hillis DM (2002) Molecular Evidence of HIV-1 Transmission in a Louisiana Criminal Case. *Proc. Natl. Acad. Sci. USA* 99:14292-14297.
 21. Twells RCJ, Mein CA, Payne F, Veijola R, Gilbey M, Bright M, Timms A, Nakagawa Y, Snook H, Nutland S, Rance HE, Carr P, Dudbridge F, Cordell HJ, Cooper J, Tuomilehto-Wolf E, Tuomilehto J, Phillips M, **Metzker M**, Hess JF, Todd JA (2003) Linkage and association mapping of the LRP5 locus on chromosome 11q13 in type 1 diabetes. *Human Genet.* 113:99-105.
 22. Ueda H *et al.* (2003) Association of the T-cell regulatory gene CTLA4 with susceptibility to autoimmune disease. *Nature* 423:506-511.
 23. Thoresen LH, Jiao GS, Haaland WC, **Metzker ML**, and Burgess K (2003) Rigid, Conjugated, Fluoresceinated Thymidine Triphosphates: Syntheses and Polymerase Mediated Incorporation Into DNA. *Chem. Eur. J.* 9:4603-4610.
 24. Twells RCJ, Mein CA, Phillips MS, Hess JF, Veijola R, Gilbey M, Bright M, **Metzker ML**, Lie BA, Kingsnorth A, Gregory E, Nakagawa Y, Snook H, Wang WYS, Masters J, Johnson G, Eaves I, Howson JMM, Clayton D, Cordell HJ, Nutland S, Rance H, Carr P and Todd JA (2003) Haplotype Structure, LD Blocks, and Uneven Recombination Within the *LRP5* Gene. *Genome Res.* 13:845-855.
 25. International Human Genome Sequencing Consortium: Baylor College of Medicine Human Genome Sequencing Center (2004) Finishing the euchromatic sequence of the human genome. *Nature* 431:931-945.
 26. Gibbs RA, Weinstock GM, **Metzker ML et al.** (2004) Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature* 428:493-521.
 27. Richards S *et al.* (2005) Comparative genome sequencing of *Drosophila pseudoobscura*: chromosomal, gene, and cis-element evolution. *Genome Res.* 15:1-18.
 28. Ross MT *et al.* (2005) The DNA sequence of the human X chromosome. *Nature* 434:325-337.
 29. Lewis EK, Haaland WC, Nguyen F, Heller DA, Allen MJ, Macgregor RR, Berger CS, Willingham B, Burns LA, Scott GB, Kittrell C, Johnson BR, Curl RF, **Metzker ML** (2005) Color-blind fluorescence detection for four-color DNA sequencing *Proc. Natl. Acad. Sci. USA* 102:5346-5351.
 30. Fernandez R, Zhang Y, Pai S, **Metzker ML**, Schumacher A (2005) *I7Rn6* encodes a novel protein required for Clara cell function in mouse lung development. *Genetics* 172:389-399.
 31. **Metzker ML** (2005) Emerging Technologies in DNA Sequencing. *Genome Res.* 15:1767-1776.
 32. Scherer S *et al.* (2006) The Finished DNA Sequence of Human Chromosome 12. *Nature* 440 346-351.
 33. Muzny D *et al.* (2006) The DNA sequence, annotation and analysis of human chromosome 3. *Nature* 440:1194-1198

34. Jiao G-S, Thoresen LH, KimTG, Haaland WC, Topp MR, Hochstrasser RM, **Metzker ML**, Burgess K (2006) Syntheses, photophysical properties, and applications of through-bond energy transfer cassettes for multiplexing in biotechnology. *Eur. J. Chem.* 12:7816-7826.
35. Wu W, Stupi BP, Litosh VA, Mansouri D, Farley D, Morris S, Metzker S, **Metzker ML** (2007) Termination of DNA synthesis by *N*⁶-alkylated, not 3'-*O*-alkylated, photocleavable 2'-deoxyadenosine triphosphates. *Nucleic Acids Res.* 35:6339-49.
36. **Metzker, ML** (2009) Sequencing in real time. *Nature Biotechnol.* 27:150-151.
37. Haaland WC, Scaduto DI, Maldonado, MR, Mansouri DL, Nalini R, Iyer D, Patel S, Guthikonda A, Hampe CS, Balasubramanyam A, **Metzker ML**. (2009) The "A-β-" subtype of Ketosis-Prone Diabetes (KPD) is not predominantly a monogenic diabetic syndrome. *Diabetes Care* 32:873877.
38. Church DM *et al.* (2009) Lineage-specific biology revealed by a finished genome assembly of the mouse. *PLoS Biol.* 5:e1000112
39. **Metzker ML**. (2010) Sequencing technologies — the next genera on. *Nature Rev. Genet.* 11:31-46
40. The 1000 Genomes Project Consortium. (2010) A map of human genome variation from population-scale sequencing. *Nature* 467:1061-73.
41. Sudmant *et al.* Diversity of human copy number variation and multicopy genes. (2010) *Science* 330:641-646.
42. Scaduto DI, Brown JM, Haaland WC, Zwickl DJ, Hillis DM, **Metzker ML**. (2010) Source identification in two criminal cases using phylogenetic analysis of HIV-1 DNA sequences. *Proc Natl Acad Sci USA* 107:21242-21247.
43. Litosh VA, Wu W, Stupi BP, Wang J, Morris, SE, Hersh MN, **Metzker ML**. (2011) Improved nucleotide selectivity and termination of 3'-OH unblocked reversible terminators by molecular tuning of 2-nitrobenzyl alkylated HOMedU triphosphates. *Nucleic Acids Res.* 39:e39.
44. Leitner, T. **Metzker ML**, et al., (2011) Guideline for HIV in court. *Nature* 473:284
45. Hertzog D, Hersh MN, **Metzker ML**. (2011) A high-performance, low-cost approach to nextgeneration sequencing. *BioOptics World*, Nov-Dec Issue.
46. Mills *et al.* Mapping copy number variation by population-scale genome sequencing. (2011) *Nature*, 470:59-65.
47. Danecek *et al.* (2011) The variant call format and VCFtools. *Bioinformatics*, 27:2156-2158.
48. Conrad *et al.*, (2011) Variation in genome-wide mutation rates within and between human families. *Nature Genet.* 43:712-714.
49. Gravel *et al.* (2011) Demographic history and rare allele sharing among human populations. *Proc. Natl. Acad. Sci. USA.* 108: 11983-11988.
50. Marth *et al.* (2011) The functional spectrum of low-frequency coding variation. *Genome Biol.* 12:R84.
51. Stupi BP, Li H, Wang J, Wu W, Morris SE, Litosh VA, Muniz J, Hersh MN, **Metzker ML**. (2012) Stereochemistry of benzylic carbon substitution coupled with ring modification of 2-nitrobenzyl groups as key determinants for fast-cleaving reversible terminators. *Angew. Chem. Int. Ed.*, 51: 1724-1727.
52. Clarke *et al.* (2012) The 1000 genomes project: data management and community access. *Nature Methods*, 9:459-462

53. Gardner AF, Wang J, Wu W, Karouby J, Li H, Stupi BS, Jack WE, Hersh MN, **Metzker ML** (2012) Improved fidelity and rapid incorporation kinetics of 3'-OH unblocked reversible terminators by Terminator DNA polymerase. *Nucleic Acids Res.*, 40:7404-7415.
54. Doyle VP, Andersen JJ, Nelson BJ, **Metzker ML**, Brown JM (2014) Untangling the influences of unmodeled evolutionary processes on phylogenetic signal in a forensically important HIV-1 transmission cluster. *Mol Phylogenet Evol.*, 75:126-137.
55. Redondo MJ, Muniz J, Rodriguez LM, Iyer D, Vaziri-Sani F, Haymond MW, Hampe CS, **Metzker ML**, Grant SFA, Balasubramanyam A. (2014) Association of *TCF7L2* Variation with Single Islet Autoantibody Expression in Children with Type 1 Diabetes. *BMJ Open Diabetes Res. Care*, 2:e000008.
56. Couturier J, Suliburk JW, Brown JM, Luke DJ, Agarwal N, Yu X, Nguyen C, Iyer D, Kozinetz CA Overbeek PA, **Metzker ML**, Balasubramanyam A, Lewis DE (2015) Human adipose tissue as a reservoir for memory CD4+ T cells and HIV. *AIDS* 29:667-674.
57. Fujimoto K, Coghill LM, Weier CA, Hwang LY, Kim JY, Schneider JA, **Metzker ML**, Brown JM (2017) Lack of Support for Socially Connected HIV-1 Transmission Among Young Adult Black Men Who Have Sex with Men. *AIDS Res Hum Retroviruses*, 33(9):935-940.
58. Yang D, Patel S, Szlachcic WJ, Chmielowiec J, Scaduto D, Putluri N, Sreekumar A, Suliburk J, **Metzker M**, Balasubramanyam A, Borowiak M. (2021) Pancreatic differentiation of stem cells reveals pathogenesis of a syndrome of Ketosis-Prone Diabetes. *Diabetes*, 2021 Aug 3;db201293. doi: 10.2337/db20-1293. Online ahead of print.

2 — Book Chapters:

1. Caskey CT, Liu O, **Metzker ML**, Gerhold D, and Austin CP (1998) Functional Analysis of Human Genes. GENOMICS, Commercial Opportunities from a Scientific Revolution, p. 55-68. In GK Dixon, LG Copping, and D Livingstone (Eds.). Bios Scientific Publishers Ltd., Oxford.
2. **Metzker ML** and Caskey CT (2001) Polymerase chain reaction. In *Encyclopedia of Life Sciences*. Macmillan References Ltd., London.
3. **Metzker ML** and Caskey CT (2006) Polymerase chain reaction. In *Encyclopedia of Medical Devices and Instrumentation* by JG Webster (Ed.), Second edition, Volume 5, John Wiley & Sons, Inc., Hoboken, New Jersey.
4. **Metzker ML** (2006) Emerging Technologies in DNA Sequencing. In *Genomes, Cold Spring Harbor Monograph Series* by HE Sussman and MA Smit (Eds.), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.
5. **Metzker ML** (2007) Advances in next-generation DNA sequencing technologies. In *Comparative Genomics: Basic and Applied Research* by JR Brown (Ed.), Taylor & Francis, Boca Raton, FL.
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7. **Metzker ML** (2014) Polymerase chain reaction. In *Discoveries in Modern Science: Exploration, Invention, Technology*. Macmillan References Ltd., London.

3— Posters:

1. **Metzker ML** (2008) Sequencing technologies — the next generation. *Nature Reviews Genetics* and *Nature Genetics*, Invited Project — <http://www.nature.com/nrg/posters/sequencing/index.html>

d. US issued patents, US patent applications, EP Patents, PCT applications

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2. Gibbs RA, Richards S, Civitello A, Burgess K, Raghavachari R, **Metzker ML** (1993) PCT Application No. WO 93/05183. Method and device for rapid DNA or RNA sequencing determination by a base addition sequencing scheme; filed Sep 9, 1991.
3. Cathcart GR, Breenan-Marquez T, Bridgham JA, Golda G, Guiremand HA, Hane M, Hoff LB, Lachenmeier E, Kronick MN, Keith DH, Mayrand PE, **Metzker ML**, Mordan WJ, McBride LJ, Shigeura J, Ting CH, and Whiteley NM (1995) US Patent 5,443,791. Automated molecular biology laboratory.
4. **Metzker ML** and Gibbs RA (1997) US Patent 5,614,386. Alternative dye-labeled primers for automated DNA sequencing.
5. **Metzker ML** and Gibbs RA (1997) PCT Application No. WO 97/00967 Alternative dye-labeled primers, ribonucleotides, deoxyribonucleotides and dideoxyribonucleotides dideoxyribonucleotides for automated DNA analysis and homogeneous amplification/ detection assays; filed June 21, 1996.
6. **Metzker ML** and Gibbs RA (1998) US Patent 5,728,529. Alternative dye-labeled ribonucleotides, deoxyribonucleotides and dideoxyribonucleotides for automated DNA analysis.
7. Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H, Hey P, Kawaguchi Y, Merriman TR, **Metzker ML**, Nakagawa Y, Phillips MS, Twells RCJ (1998) PCT Application No. WO 98/46743. Novel LDL-receptor; filed. Apr 15, 1998.
8. **Metzker ML** and Gibbs RA (1999) US Patent 5,861,287. Alternative dye-labeled primers for automated DNA sequencing.
9. **Metzker ML** and Gibbs RA (1999) US Patent 5,994,063. Substituted 4,4 difluoro-4-bora-3A,4A-diaza-s-indacene compounds for homogeneous amplification/ detection assays.
10. Petrukhin K, Caskey CT, **Metzker ML**, Wadelius, C (1999) PCT Application No. WO 99/43695. Best's Macular Dystrophy gene; filed Feb 22, 1999.
11. Petrukhin K, Caskey CT, Li W, **Metzker ML** (2000) PCT Application No. WO 00/61606. Novel human voltage-gated potassium channel; filed Apr 14, 1999.
12. Liu XL, Bai C and **Metzker ML** (2001) PCT Application No. WO 01/42434. DNA molecules encoding human NHL a DNA helicase; filed Dec 9, 1999.
13. Todd JA, Twells RCJ, Hess JW, Hey P, Caskey CT, Hammond H, **Metzker ML** (2001) PCT Application No. WO 01/29213. Human Sit4 associated proteins like (SAPL) proteins and encoding genes; uses therefo.
14. Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H, Hey P, Kawaguchi Y, Merriman TR, **Metzker ML**, Nakagawa Y, Phillips MS, Twells, RCJ (2003) US Patent 6,545,137. Receptor.
15. Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H, Hey P, Kawaguchi Y, Merriman TR, **Metzker ML**, Nakagawa Y, Phillips MS, Twells RCJ (2003) US Patent 6,555,654. LDL-receptor.

16. **Metzker ML** (2003) US Patent Application Publication No. US2003/0180769. Substituted 4,4-difluoro-4-bora-3A,4A-diaza-s-indacene compounds for 8-color DNA sequencing; filed Feb 5, 2003.
17. Scott GBI, Kittrell C, Curl RF, and **Metzker ML** (2003) PCT Application No. WO 03/021212. Pulsed-multiline excitation for color-blind fluorescence detection; filed Aug 28, 2002.
18. Liu XL, Bai C and **Metzker ML** (2004) US Patent 6,762,042. DNA molecules encoding human NHL a DNA helicase.
19. Scott GBI, Kittrell C, Curl RF, and **Metzker ML** (2006) US Patent 6,995,841. Pulsed-multiline excitation for color-blind fluorescence detection.
20. Petrukhin K, Caskey CT, **Metzker ML**, Wadelius C (2006) US Patent 7,005,290. Best's Macular Dystrophy gene.
21. Petrukhin K, Caskey CT, **Metzker ML**, Wadelius C (2006) US Patent Application Publication No. 2006/0105364. Best's Macular Dystrophy gene, filed Sep 27, 2006.
22. Petrukhin K, Caskey CT, Li W, **Metzker ML** (2006) European Patent EP 1 173 465 B1. Novel human voltage-gated potassium channel.
23. Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H, Hey P, Kawaguchi Y, Merriman TR, **Metzker ML**, Nakagawa Y, Phillips MS, Twells RCJ (2007) US Patent 7,244,577. Method of screening for modulator of LRP5 activity.
24. Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H, Hey P, Kawaguchi Y, Merriman TR, **Metzker ML**, Nakagawa Y, Phillips MS, Twells RCJ (2007) European Patent EP 0 988 379 B1. LDL-receptor.
25. Wu W, Litosh V, Stupi B, **Metzker ML**. (2008) PCT Application No. US2008/070749. Photocleavable labeled nucleotides and nucleosides and methods for their use in DNA sequencing; filed: Dec 5, 2007.
26. Liu XL, Bai C and **Metzker ML** (2008) US Patent 7,361,491. DNA molecules encoding human NHL a DNA helicase.
27. Scott GBI, Kittrell C, Curl RF, and **Metzker ML** (2009) US Patent 7,511,811. Pulsed-multiline excitation for color-blind fluorescence detection.
28. Litosh V, Hersh M, Stupi B, Wu W, **Metzker ML**. PCT Application No. US2009/152353. Nucleotides and nucleosides and methods for their use in DNA sequencing. *Filed*: Jun 11, 2009.
29. Wu W, Litosh V, Stupi B, **Metzker ML**. (2011) US Patent 7,893,227. 3'OH unblocked nucleotides and nucleosides, base modified with non-cleavable, terminating groups and methods for their use in DNA sequencing.
30. Wu W, Litosh V, Stupi B, **Metzker ML**. (2011) US Patent 7,897,737. 3'OH unblocked nucleotides and nucleosides, base modified with photocleavable, terminating groups and methods for their use in DNA sequencing.
31. Wu W, Litosh V, Stupi B, **Metzker ML**. (2011) US Patent 7,964,352. 3'OH unblocked nucleotides and nucleosides, base modified with photocleavable, terminating groups and methods for their use in DNA sequencing.
32. Lafferty WM, Beechem J, Hongye S, **Metzker ML** (2011) US Patent Application Publication No. 2011/0311963. Method and Apparatus for Addressable Flow Cells in Single Molecule Sequencing; filed March 16, 2011.
33. Lafferty WM, Beechem J, Hongye S, **Metzker ML** (2011) PCT Application No. WO/2011/116120. Method and Apparatus for Addressable Flow Cells in Single Molecule Sequencing; filed March 16, 2011.

34. Scott GBI, Kittrell C, Curl RF, and **Metzker ML** (2012) US Patent 8,089,628. Pulsed-multiline excitation for color-blind fluorescence detection.
35. Litosh V, Stupi B, Hersh M, Wu W, **Metzker ML**. (2012) US Patent 8,148,503. Labeled nucleotides and nucleosides and methods for their use in DNA sequencing.
36. Wu W, Litosh V, Stupi B, **Metzker ML**. (2012) US Patent 8,198,029. 3'OH unblocked nucleotides and nucleosides, base modified with non-cleavable, terminating groups and methods for their use in DNA sequencing.
37. Wu W, Litosh V, Stupi B, **Metzker ML**. (2013) US Patent 8,361,727. 3'OH unblocked nucleotides and nucleosides, base modified with photocleavable, terminating groups and methods for their use in DNA sequencing.
38. Litosh V, Stupi B, Hersh M, Wu W, **Metzker ML**. (2013) US Patent 8,497,360. Nucleotides and nucleosides and methods for their use in DNA sequencing.
39. Litosh V, Stupi B, Hersh M, Wu W, **Metzker ML**. (2014) US Patent 8,887,905. Nucleotides and nucleosides and methods for their use in DNA sequencing.
40. Stupi B, Li H, Wu W, Hersh MN, Hertzog D, Morris SE, **Metzker ML**. (2014) US Patent 8,889,860. 3'-OH unblocked, fast photocleavable terminating nucleotides and methods for nucleic acid sequencing.
41. Wu W, Litosh V, Stupi B, **Metzker ML**. (2013) US Patent 8,969,535. Photocleavable labeled nucleotides and nucleosides and methods for their use in DNA sequencing.
42. Stupi B, Li H, Wu W, Hersh MN, Hertzog D, Morris SE, **Metzker ML**. (2013) PCT Application No. 2013/040257. 5-methoxy 3'-OH Unblocked, fast photocleavable terminating nucleotides and methods for nucleic acid sequencing; filed September 13, 2012.
43. Litosh V, Stupi B, Hersh M, Wu W, **Metzker ML**. (2015) US Patent 9,200,319. Nucleotides and nucleosides and methods for their use in DNA sequencing.
44. **Metzker ML**, Weier CA (2015) PCT WO2015/157747. Systems and methods for clonal replication and amplification of nucleic acid molecules for genomic and therapeutic applications.
45. Stupi B, Li H, Wu W, Hersh MN, Hertzog D, Morris SE, **Metzker ML**. (2016) US Patent 9,399,798. 3'-OH unblocked, fast photocleavable terminating nucleotides and methods for nucleic acid sequencing; to be issued Jul 26, 2016.
46. **Metzker ML**, Weier CA (2016) US Patent Application Publication No. 15/122,543. Systems and methods for clonal replication and amplification of nucleic acid molecules for genomic and therapeutic applications; filed Aug 30, 2016.
47. Litosh V, Stupi B, Hersh M, Wu W, **Metzker ML**. (2016) European Patent 2 125 856 B1. Photocleavable labeled nucleotides and nucleosides and labeled nucleotides and nucleosides for their use in DNA sequencing.
48. Stupi B, Li H, Wu W, Hersh MN, Hertzog D, Morris SE, **Metzker ML**. (2017) US Patent 9,689,035. 3'-OH unblocked, fast photocleavable terminating nucleotides and methods for nucleic acid sequencing.
49. **Metzker ML**, Weier CA (2017) PCT Application No. PCT/US2017/036129. Target reporter constructs and uses thereof; filed Jun 6, 2017.
50. Stupi B, Li H, Wu W, Hersh MN, Hertzog D, Morris SE, **Metzker ML**. (2017) US Patent 9,689,035. 3'-OH unblocked, fast photocleavable terminating nucleotides and methods for nucleic acid sequencing.
51. Litosh V, Stupi B, Hersh M, Wu W, **Metzker ML**. (2017) European Patent 2 307 565 B1. Reversible nucleosides and nucleotides terminators and their use in DNA sequencing.

52. Stupi B, Li H, Wu W, Hersch MN, Hertzog D, Morris SE, **Metzker ML**. (2018) US Patent 10,041,115. 3'-OH unblocked, fast photocleavable terminating nucleotides and methods for nucleic acid sequencing.
53. Stupi B, Li H, Wu W, Hersch MN, Hertzog D, Morris SE, **Metzker ML**. (2020) European Patent EP 2 755 984 B1. 5-Methoxy. 3'-OH unblocked, fast photocleavable terminating nucleotides and methods for nucleic acid sequencing.
54. Stupi B, Li H, Wu W, Hersch MN, Hertzog D, Morris SE, **Metzker ML**. (2021) US Patent 11,001,886. 3'-OH unblocked, fast photocleavable terminating nucleotides and methods for nucleic acid sequencing.
55. **Metzker ML**, Weier CA (2021) European Patent EP 3 129 505 B1. Methods for clonal replication and amplification of nucleic acid molecules for genomic and therapeutic applications.
56. Stupi B, Li H, Wu W, Hersch MN, Hertzog D, Morris SE, **Metzker ML**. (2021) European Patent EP 3 670 523 B1. 5-Methoxy. 3'-OH unblocked, fast photocleavable terminating nucleotides and their use in methods for nucleic acid sequencing.
57. **Metzker ML**, Weier CA (2022) U.S. Patent No. 11,299,769. Target reporter constructs and uses thereof.
58. **Metzker ML**, Weier CA (2022) U.S. Patent Application No. 17/702,152. Target reporter constructs and uses thereof, filed Mar 23, 2022.
59. **Metzker ML**, Weier CA (2024) European Patent Application EP 4 372 102. Target reporter constructs and uses thereof.

III. Teaching Information:

a. Courses taught at BCM:

- | | |
|--------------|--|
| 2000-to-2018 | <i>Molecular Methods</i> : All first-year graduate students are required to take this course. Three lectures taught: <i>cDNA and Genomic Libraries</i> , <i>First-generation Sequencing and Genotyping</i> , and <i>Next-generation Sequencing</i> . |
| 2001-to-2003 | <i>Mammalian Genetics</i> : All first-year genetics student are required to take this class. One lecture taught: <i>Mammalian Genome Analysis</i> . |

b. Graduate student training:

- | | |
|--------------|---|
| 2008-to-2011 | Major advisor for Diane Scaduto, graduated with PhD from CMB program |
| 2007-to-2010 | Thesis committee member for Rocio Benabentos, CMB program |
| 2004-to-2006 | Major advisor for Michele Sexton, graduated with MS degree from CMB program |
| 2001-to-2007 | Major advisor for Wade C. Haaland, graduated with PhD from CMB program |
| 2001-to-2005 | Thesis committee member for Teresa Venezia, graduated with PhD from CMB program |
| 2001-to-2013 | Qualifying examination reviewer for 1-2 Genetics & CMB students 2000-to-2013
First year student rotations (1-2 per year) |

c. Post-doctoral training:

2001-to-2003	Mathew Mahindaratne, Ph.D., now at UT San Antonio
2003-to-2004	Ernest Lewis, Ph.D., now at Rice University
2003-to-2006	Ming Fa, Ph.D.

d. Minority undergraduate student internships:

Summer 2004	Lamin Bangura, now at Ross University Medical School in Dominica(Caribbean)
Summer 2005	Rosalie Bangura, now at BCM
2006-to-2007	Demetra Farley, now in graduate school at Southwestern Medical Center, Division of Basic Science Program- Cancer Biology training track (began 2007)
Summer 2006	Mindy Smith, now at Chicago Medical School of Rosalind Franklin University of Medicine and Science
Summer 2006	Quincy Johnson, now at Texas A&M University Graduate School of Engineering (began 2007)
Summer 2007	Dionne Watson, student at Prairie View A&M University
Summer 2008	Nicholas Chambers, student at Prairie View A&M University
Summer 2009	Ogechi Nwaobia, student at University of Texas, Austin
Summer 2010	Brian Tenner, Southern Methodist University and Crist Cuffee, Virginia Polytechnic Institute and State University
2010-to-2013	Jesse Muniz, University of Texas at Brownsville graduate, B.S. Biology

e. Innovation Norway in Houston internships

Spring 2011	Liv Arnica Forberg Hovland, now Editorial Assistant/Senior Adviser for the Tax Directorate
Spring 2015	Stian A. Weiseth, Norwegian University of Life Sciences, Master of Science student in Innovation and Entrepreneurship
Spring 2015	Hanne Hansen, Bergen University College, Master of Science student in Innovation and Entrepreneurship
Spring 2016	Espen Svendsen, Bergen University College, Master of Science student in Innovation and Entrepreneurship
Spring 2016	Ingrid-Helen Liabø,, Norwegian University of Life Sciences, Master of Science student in Innovation and Entrepreneurship
Spring 2017	Axel William Nilsen, Norwegian University of Life Sciences, Master of Science student in Innovation and Entrepreneurship

f. Local lectures

Jun 2008	Repeat of DNA Day Celebration Lecture for high school students, organized by the Office of Diversity and Community Outreach's Office of Diversity and Community Outreach at BCM
Apr 2008	DNA Day Celebration Lecture for high school students, organized by the Office of Diversity and Community Outreach at BCM

IV. Service information:

Administrative assignment:

2002-to-2013	Member: BCM Patent and Copyright Committee
2007-to-2013	Member: HGSC New Faculty Search Committee

EXHIBIT 18C



Nisha Mody, Ph.D.

Managing Director

Nisha Mody, Ph.D., is a Managing Director with Secretariat and specializes in financial and economic consulting on intellectual property cases, business valuation cases, antitrust cases and unfair business practices cases, among others. She is an expert in the application of economic methods to complex business disputes and is retained in cases requiring economic analyses, financial analyses, valuations and/or damages-related analyses. Dr. Mody has constructed damages models in litigation involving reasonable royalties, lost profits, market share assessments, and but-for scenarios. She has also performed valuations of intellectual property (patents and trademarks) as well as valuations of tangible assets, including evaluating damages by applying econometric analyses to large databases.

With more than 20 years of experience in consulting and economic research, Dr. Mody is well regarded among the most prestigious law firms for her expert testimony. Her economic analyses have been affirmed by the Federal Circuit in three matters. She has given deposition/trial testimony in over 80 matters.

In addition to her work with Intensity, Dr. Mody was a Co-Founder/Partner, at Eurekanomics LLC. Prior to that, she served for almost a decade as a Partner for a top tier economic consulting firm. There she worked on many high-stakes litigation projects. Before that, Dr. Mody spent over a decade at leading consulting firms.

Dr. Mody was previously a lecturer at the Santa Clara University School of Law and has authored articles in *Les Nouvelles*.

Dr. Mody received a Ph.D. in Political Economy and Public Policy from the University of Southern California, and a B.A. from Pomona College.

Education

Ph.D. Political Economy and Public Policy, University of Southern California, Los Angeles, 1999. Concentrations: International Economics, Industrial Organization, Antitrust Economics.

B.A. International Relations, Pomona College, Claremont, 1993. Concentrations: Development Economics, Latin American Studies.

Professional Experience

Secretariat (formerly Intensity, LLC). Managing Director, 2021 to present.

Eurekanomics LLC. Co-Founder/Partner, 2020 to 2021.

OSKR, LLC. Partner, 2010 to 2019.

Santa Clara University School of Law, Intellectual Property LL.M. Program. Adjunct Professor/Lecturer, 2010-2012. Course: The Economics and Finance of Intellectual Property.

The CapAnalysis Group, LLC. Managing Principal, 2007 to 2010. Senior Vice-President, 2005 to 2006. Vice-President, 2004. Senior Economist, 2003.

Maxiam, LLC. Senior Advisor, 2003 to 2010.

LECG, LLC (Formerly, LECG, Inc. and Navigant Consulting), Senior Managing Economist, 1999 to 2003.

Econ One Research, Inc. Economist, 1998 to 1999.

Publications and Papers

Mody, Nisha and Evan Schulz: "Anchors Away! An Appeal for Reference Rates When Calculating Prejudgment Interest." (2018) *Les Nouvelles*, 236-241.

Expert Testimony

Aortic Innovations v. Edwards Lifesciences et al. Case No. 1:23-CV-158-JPM. District of Delaware. Retained by Goldman Ismail Tomaselli Brennan & Baum LLP. Report, Deposition. Case filed 2/13/2023.

LiTL v. Dell Technologies Inc. and Dell Inc. Case No. 1:23-cv-00121-RGA. District of Delaware. Retained by Farella Braun + Martel. Report. Case filed 10/16/2023.

Gilead Sciences, Inc. v. Cipla Limited, Lupin Ltd., Laurus Labs Limited, Case No. 1:22-cv-00615-MN. District of Delaware. Retained by Bartlit Beck LLP. Report, Deposition. Case filed 5/9/2022.

Marvin Pietruszka et al. v. Koruon Daldalyan et al., Case No: 23STCV05448. Superior Court of California, County of Los Angeles. Retained by Daar & Newmann, Deposition. Case filed 3/10/2023.

Lexos Media IP, LLC v. Overstock.com, Inc., Case No: 2:22-cv-02324. US District Court for Kansas. Retained by Fish & Richardson P.C. Report, Deposition, Sur-rebuttal. Case filed 8/16/2022.

Cranial Technologies, Inc. v. Ottobock SE & Co. KGAA, Active Life LLC, and Ottobock Healthcare LP. C.A. No. 2:23-cv-02320-CBM-E. US District Court for the Central District of California. Retain by Haug Partners LLP. Report, Deposition. Case filed 4/9/2024.

DIVX, LLC v. Renesas Electronics Corporation. JAMS Reference No. 5240001028, JAMS Arbitration. Retained by Dechert. Report, Deposition, Arbitration Testimony. Case filed 10/11/2023.

Takeda Pharmaceuticals U.S.A., Inc. v. Mylan Pharmaceuticals, Inc. Case No: 1:19-cv-2216-RGA. US District of Delaware. Retained by Haug Partners LLP. Report, Deposition. Case filed 12/20/2019.

Resonant v. Sony Games Corporation and Sony Inc. Case No. 2:22cv00424-JRG. US District Court for the Eastern District of Texas. Retained by Erise IP. Reports, Deposition. Case filed 10/26/2022.

In the Matter of Certain Video Capable Electronic Devices, Including Computers, Streaming Devices, Televisions, and Components and Modules Thereof. Investigation No. 337-TA-1380. US International Trade Commission. Retained by Morgan, Lewis & Bockius LLP and Perkins Coie (representing Respondents HP, Inc. and Amazon). Report, Trial. Case filed 10/31/2023.

Dynapass Holdings LLC v. JPMorgan Chase et al. Case No. 2:22-cv-00212-JRG-RSP. US District Court for the Eastern District of Texas. Retained by Jones Day. Reports. Case filed 6/17/2022.

In the Matter of Certain Video Capable Electronic Devices, Including Computers, Streaming Devices, Televisions, Cameras, and Components and Modules Thereof. Investigation No. 337-TA-1379. US International Trade Commission. Retained by Morgan, Lewis & Bockius LLP and Perkins Coie (representing Respondents HP, Inc. and Amazon). Reports. Deposition. Trial. Case filed 10/31/2023.

FOX Factory, Inc. v. SRAM LLC. Case No: 1:23-cv-00313-RM-KLM. US District Court for the District of Colorado. Retained by Finnegan. Reports, Deposition. Case filed 7/13/2022.

DIVX, LLC v. Mitsubishi Electric Co. Ltd. JAMS Reference No. 5240000886, JAMS Arbitration. Retained by Dechert LLP. Report. Case filed 8/17/2023.

Lionra Technologies Ltd. v. Palo Alto Networks, Inc. Case No: 2:22-cv-00334-JRG-RSP US District Court for the Eastern District of Texas, Marshall Division. Retained by Erise IP. Reports, Deposition. Case filed 8/29/2022.

Blue Yonder Group, Inc. v. Kinaxis Inc. and Kinaxis Corp., Case No: 3:20-cv-03636. US District Court for the Northern District of Texas, Dallas Division. Retained by Fish and Richardson P.C. Report, Deposition. Case filed 12/14/2020.

Zunum Aero, Inc. v. The Boeing Company; Boeing HorizonX Ventures, LLC. Case No: 2:21-cv-00896. US District Court for the Western District of Washington. Retained by Hueston Hennigan LLP. Reports, Deposition, Trial. Case filed 7/2/2021.

Rayos del Sol Solar Project, LLC v. Trina Solar (U.S.), Inc., Case No: 22CV006392. Superior Court of the State of California. Retained by Susman Godfrey. Disclosure, Deposition. Case Filed 2/2/2022.

Viasat, Inc. v Kioxia Corporation and Kioxia America, Inc. Case No. 6:21-cv-01231. US District Court for the Western District of Texas. Retained by Bartlit Beck LLP. Reports, Depositions. Case filed 11/29/2021.

Wavetronix, LLC v. Iteris, Inc. Case No. 6:21-vc-00899. US District of the Western District of Texas. Retained by Fish and Richardson P.C. Report, Deposition. Case filed 8/27/2021.

Lexos Media IP, LLC v. Office Depot, Inc. Case No: 2:22-CV-00273. US District Court for the Eastern District of Texas. Retained by Perkins Coie. Report. Case filed 7/21/2022.

Lexos Media IP, LLC v. Amazon.com, Inc. Case No: 2:22-CV-00169-JRG. US District Court for the Eastern District of Texas. Retained by Perkins Coie. Report. Case filed 5/24/2022.

Walter Kidde Portable Equipment, Inc. v. First Alert, Inc. and BRK Brands, Inc. Case No. 6:22-cv-00566-ADA-DTG. US District Court for the Western District of Texas. Retained by Fish & Richardson P.C. Report, Deposition. Case filed 6/2/2022.

Lauri Valjakka v. Netflix, Inc. Case No. 4:22-cv-01490-JST. US District Court for the Northern District of California. Retained by Perkins Coie. Report. Deposition. Case filed 3/9/2022.

Invitae Corporation v. Natera, Inc. Case Nos. 1:21-cv-00669 and 1:21-cv-01635. US District Court for the District of Delaware. Retained by Groombridge, Wu, Baughman & Stone. Report. Deposition. Cases filed 5/7/2021 and 11/21/2021.

Metacluster, UAB v. Bright Data, LTD. Case No. 2:22-CV-011-JRG-RSP. US District Court for the Eastern District of Texas. Retained by Cherian LLP. Report. Deposition. Case Filed 5/10/2022.

LoganTree, LP v. Fossil Group, Inc. Case No. 1:21-CV-385. US District Court for the District of Delaware. Retained by Fish & Richardson P.C. Report. Deposition. Case Filed 3/16/2021.

DivX, LLC, v. Alps Alpine Co., LTD. JAM Case No: 5240000289 Retained by Tyz Law Firm, LLP. Report. Deposition. Case filed/amended 3/15/2023.

Marco A. Fernandez, individually and as a representative of the class v. CoreLogic Credco, LLC. Case No. 3:20-cv-1262-JM-AGS. US District Court for the Southern District of California. Retained by Hueston Hennigan LLP. Report. Deposition. Case Filed 9/28/2020.

Global eTicket Exchange LTD. v. Ticketmaster LLC and LiveNation Worldwide, Inc. Case No. 6:21-cv-00399. US District Court for the Western District of Texas. Retained by Fish & Richardson, P.C. Report. Deposition. Case Filed 4/23/2021.

ViaTech Technologies, Inc. v. Adobe Inc. Case No. 20-358-RGA. US District Court for Delaware. Retained by Perkins Coie. Report. Deposition. Trial. Case Filed 5/24/2019.

Bluebonnet Internet Media Services, LLC v. Pandora Media Services LLC Case No. 3:21-cv-08294-VC. US District Court for the Northern District of California. Retained by Fenwick & West. Report. Case Filed 8/12/2020.

Takeda Pharmaceutical Co. Ltd., et al. v. Norwich Pharmaceutical, Inc. Case No. 20-cv-8966. US District Court for the District of New Jersey. Retained by Haug Partners. Report. Deposition. Trial. Case Filed 7/15/2020.

In the Matter of Certain Refrigerator Water Filtration Devices and Components Thereof. Inv. No. 337-TA-1290, United States International Trade Commission. Retained by Dentons (representing Complainant, LG). Report. Deposition. Trial. Case filed 12/14/2021.

Hoffmann-La Roche, Inc. Chugai Pharmaceutical Co. Ltd. And Genentech, Inc. v. Fresenius Kabi USA, LLC. Case No. 1:20-cv-00394-RGA US District Court for the District of Delaware. Retained by Paul, Weiss Rifkind, Wharton & Garrison LLP. Report. Deposition. Case Filed 3/19/2020.

Sensormatic Electronics, LLC v. Genetec (USA) Inc. and Genetec Inc. Case No. 1:20-CV-00760-MN. US District Court for the District of Delaware. Retained by Fish & Richardson, P.C. Report. Deposition. Case filed 6/5/2020.

Palantir Technologies, Inc. v. Marc L. Abramowitz. Case No. 5:19-cv-06879. US District Court for the Northern District of California. Retained by Hueston Hennigan LLP. Report. Deposition. Case filed 9/1/2016 (state matter).

Her Majesty the Queen in Right of Canada as Represented by the Minister of Agriculture and Agri-Food v. Van Well Nursery, Inc. Monson Fruit Company, Inc. Gordon Goodwin and Sally

Goodwin. Case No. 2:20-CV-00181-SAB. US District Court for the Eastern District of Washington. Retained by Dentons. Report. Deposition. Case filed 5/18/2020.

Longhorn HD LLC v. NetScout Systems, Inc. Case No. 2:20-cv-00349-JRG. US District Court for the Eastern District of Texas, Marshall Division. Retained by Erise IP. Report, Deposition, Trial. Case filed 11/5/2020.

Synkloud Technologies, LLC v. Nuance Communications, Inc. Case No. 1:20-cv-10564. US District Court for the District of Massachusetts. Retained by Lamkin IP Defense. Report, Supplemental Report, Deposition. Case filed 3/20/2020.

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Sentient Sensors, LLC v. Cypress Semiconductor Corporation. Case No: 1:19-cv-01868-MN. US District of Delaware. Retained by Fish & Richardson, P.C. Report. Case filed 10/4/2019.

The Coleman Company, Inc. v. Team Worldwide Corporation and Cheng-Chung Wang. Case No: 2:20-CV-00351-RGD. US District Court for the Eastern District of Virginia. Retained by Ruyak Cherian. Report, Supplemental Report; Rebuttal Report, Deposition. Case filed 6/29/2020.

Alexsam, Inc. v. Cigna Corporation, et al. Case No: 2:20-cv-00081-JRG-RSP. US District Court for the Eastern District of Texas. Retained by Fish & Richardson, P.C. Report, Deposition. Case filed 3/18/2020.

Philips North America, LLC v. Garmin International, Inc. and Garmin LTD. Case No. 2:19-cv-06301-AB-KS. US District Court for the Central District of California. Retained by Erise IP and Lamkin IP Defense. Report, Deposition. Case filed 7/22/2019.

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In the Matter of Certain Percussive Massage Devices, Inv. No. 337-TA-1206, United States International Trade Commission. Retained by Dentons (representing Respondents, multiple companies). Report. Deposition. Declaration. Case filed 6/16/20.

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CliniComp International, Inc. v. athenahealth, Inc. Case No. 18-CV-00425-LY. US District Court for Western District of Texas. Retained by Manatt, Phelps & Phillips, LLP. Report, Deposition. Case filed 5/21/18.

M2M Solutions LLC and Blackbird Technology LLC v. Sierra Wireless America, Inc. and Sierra Wireless, Inc. Civil Action No. 1:14-cv-01102-RGA. US District Court for Delaware. Retained by Nixon Peabody. Report. Case filed 8/26/14.

FlatFrog Laboratories AB v. Promethean Ltd. and Promethean, Inc. Civil Action No. 1:19-cv-02246-MN, US District Court for Delaware, Retained by Finnegan. Declaration. Case filed 12/11/19.

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Intervision Systems, LLC v. Ben Escobar, et al. Case No. CGC-18-565117, Superior Court of the State of California, County of San Francisco. Retained by Dentons. Deposition. Case filed 3/20/18.

In re PersonalWeb Technologies, LLC et al. Case No. 5:18-md-02834-BLF, US District Court for the Northern District of California. Retained by Fenwick & West (representing Twitch Interactive). Report. Case filed 9/13/18.

In re Koninklijke Philips Patent Litigation, Case No. 4:18-cv-01885-HSG, US District Court for the Northern District of California. Retained by Perkins Coie (representing Microsoft). Reports, Deposition. Initial related case filed 12/18/15

RMail Limited, et al., v. RightSignature, LLC, Farmers Group, Inc. Farmers Insurance Company, Inc., Case No. 2:11-cv-300-JRG, US District Court for the Eastern District of Texas, Retained by Fish & Richardson, Report, Deposition. Case filed 6/24/11.

Synchronoss Technologies, Inc. v. Egnite, Inc. Case No. 4:16-cv-00120-HSG-KAW. Transferred to US District Court for the Northern District of California, Retained by Dentons. Report, Deposition. Case filed 1/26/15.

Infinity Computer Products, Inc. v. Epson America, Inc. Case: 2:18-cv-02532-RGK-RAO. US District Court for the Central District of California, Retained by Kilpatrick Townsend. Reports. Case filed 6/30/10.

Synchronoss Technologies, Inc. v Dropbox, Inc. Case No. 4:16-cv-00119-HSG. Transferred to US District Court for the Northern District of California, Retained by Dentons. Report, Deposition. Case filed 3/27/15.

MSignia, Inc. v InAuth, Inc. Case: 8:17-cv-1289. US District Court for the Central District of California. Retained by Haynes & Boone. Report, Deposition. Case filed 7/26/17.

FOX Factory, Inc. v. SRAM, LLC and Sandleford, Ltd. Cases No. 1:18-cv-00130-WJM and 1:18-cv-00127-WJM. US District Court of the District of Colorado. Retained by Finnegan. Report, Deposition. Case filed 1/17/18.

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In the Matter of Certain Submarine Telecommunication Systems and Components Thereof. United States International Trade Commission. Retained by Fish & Richardson P.C. (representing Complainant). Report, Deposition. Case filed 7/11/18.

Zimmer Surgical, Inc. and Dornoch Medical Systems, Inc. v. Stryker Corporation et al. and Counterclaims. Case No. 16-679-RGA-MP., US District Court of Delaware. Retained by Finnegan Henderson. Reports, Deposition. Case filed 8/8/16.

Nexxon Limited v. Eaglepicher Technologies, LLC and OneD Material, LLC. Case No.:15-955 (RGA) US District Court of Delaware. Retained by Nixon Peabody. Report. Case filed 10/21/15.

In the Matter of Certain Electrochemical Glucose Monitoring Systems and Components Thereof. United States International Trade Commission. Retained by Dentons LLP (representing Complainant Dexcom). Report, Deposition. Case filed 9/18/17.

Sabre GLBL, Inc. v. Melody Shan, aka Shan Melody Xiaoyun. JAMS Ref. #1310022477. Retained by LeClair Ryan, LLP. Arbitration Testimony.

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Blast Motion, Inc. v Zepp Labs, Inc. Case No.: 15-cv-0700-JLS-NLS. US District Court, Southern District of California. Retained by Fenwick & West. Reports, Deposition. Case filed 3/31/15.

The Node Firm, LLC, Node Source, LLC, Nodesource, Inc., Daniel Shaw, and Joe McCann v. YLD Limited and Nuno Job and Counter Complaint. Case No.: 3:16-cv-00399- VC. US District Court, Northern District of California. Retained by Kramer Levin. Report, Deposition. Case filed 5/28/15 (Transferred from US District Court Southern District of New York.).

Sealant Systems International Inc., Illinois Tool Works v. TEK Global S.R.L. and TEK Corporation. Case No. CV 11-0774. U.S. District Court, Northern District of California, Retained by Keker, Van Nest and Peters, Reports, Deposition, Trial. Case filed 4/7/11.

Symantec Corporation v. RPost Holdings, Inc. at al. Case No. 3:14-CV-00238, US District Court Northern District of California. Retained by Fenwick & West. Report. Case filed 1/15/14.

Liqwd, Inc. and Olaplex LLC v. L'Oréal USA et al. Case No: 17-cv-00014-SLR, US District Court for the District of Delaware. Retained by Quinn Emanuel Urquhart & Sullivan. Declarations, Deposition. Case re-filed January 2017.

VH Noodle House, Inc. v. Vuong. ADR Services, California Court. Retained by the Law Offices of Mattaniah Eytan and Bowles & Verna, LLP. Oral and written opinions. Case filed November 2016. (neutral expert)

Cloud9 eSports, Inc., v. Twitch Interactive, Inc. JAMS Ref. No. 1100082764, Judicial Arbitration and Mediation Services, San Francisco. Retained by Fenwick & West. Report. Case filed 3/18/16.

Actifio, Inc. v. Delphix Corporation. Case No:1:14-cv-13247-DJC, US District Court for the District of Massachusetts, Boston Division. Retained by Fenwick & West. Report. Case filed 4/14/15.

Versata Software, Inc. F/K/A/ Trilogy Software, Inc.; and Versata Development Group, Inc. F/K/A Trilogy Development Group, Inc. v. Zoho Corporation D/B/A ManageEngine. Case No: 1:13-CV-003711-SS US District Court of the Western District of Texas. Retained by Tyz Marton & Schumann LLP. Report, Deposition. Case filed 5/3/13.

Vir2us, Inc. v. Invincea, Inc. and Invincea Lab, LLC. Case No. 2:15-cv-00162 HCM-LRL, US District Court for the Eastern District of Virginia, Norfolk Division. Retained by Bunsow Demory Smith and Allison LLP. Report. Deposition. Case filed 10/23/15.

In the Matter of Certain Activity Tracking Devices, Systems, and Components Thereof. Inv. No. 337-TA-963. United States International Trade Commission. Retained by Gibson Dunn and Crutcher LLP (representing Respondents FitBit and Flextronics). Report. Deposition. Trial (written and oral). Case filed 7/7/15.

Avid Technology, Inc. v. Media Gobbler, Inc. Case No: 2:14-cv-13746 PBS, U.S. District Court for the District of Massachusetts. Retained by Perkins Coie LLP. Report. Deposition. Case filed 1/16/15.

Finisar Corporation v. Nistica, Inc. Case No: CV 13 3345-BLF, U.S. District Court for the Northern District of California. Retained by Dentons. Report. Deposition. Trials. Case filed 7/17/13.

EXHIBIT 19A

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-669 (GBW)
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-1635 (GBW)
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	

**PLAINTIFF'S MOTION IN LIMINE NO. 1 TO PRECLUDE NATERA FROM
CONTESTING VALIDITY UNDER 35 U.S.C. § 101**

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Dated: February 9, 2024

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Pursuant to Federal Rules of Evidence 401, 402, and 403, Invitae seeks to preclude Natera from presenting argument or evidence regarding patent eligibility of the Asserted Patents under § 101. The Court has already spoken on patent eligibility and has ruled that the Asserted Patents are directed to eligible subject matter. D.I. 28 at 4, 7. That ruling is the law of the case.

I. THE ISSUE OF PATENT ELIGIBILITY HAS BEEN DETERMINED

On June 30, 2021, Natera sought to dismiss this case under Rule 12(b)(6), contending that Invitae’s ’799 patent—which includes claims very similar to those of the other two Asserted Patents—claimed ineligible subject matter under § 101. D.I. 8, 9. After fully considering the motion, Judge Stark found as a matter of law in analyzing *Alice* step one that the ’799 Patent is “directed to a specific solution to a technological problem in the field of sequence assembly” and not an abstract idea. D.I. 28 at 4. Judge Stark further found that there was “no need” to evaluate *Alice* step two. *Id.* at 7. This is the law of the case.

Under the law of the case doctrine, when a court reaches a decision regarding an issue of law, “that decision should continue to govern the same issues in subsequent stages in the same case.” *Pepper v. U.S.*, 562 U.S. 476, 506 (2011). This doctrine “promotes the finality and efficiency of the judicial process by protecting against the agitation of settled issues.” *Christianson v. Colt Industries Operating Corp.*, 486 U.S. 800, 816 (1988). The doctrine applies here to the already decided issue of patent eligibility to achieve the same goal here.

The inquiry at “*Alice* step one presents a legal question that can be answered based on the intrinsic evidence.” *CardioNet, LLC v. InfoBionic, Inc.*, 955 F.3d 1358, 1372-73 (Fed. Cir. 2020). Here, the Court found the claims of the ’799 Patent are not directed to an abstract idea at *Alice* step one and that it was “not necessary” to evaluate *Alice* step two. D.I. 28 at 4, 7. When a court has made such a finding at *Alice* step one in ruling on a 12(b)(6) motion to dismiss, it is appropriate

for that court to apply the finding as the law of the case. *See Savvy Dog Sys., LLC v. Pennsylvania Coin, LLC*, No. 3:19-cv-01470, 2022 WL 4349829, at *5 (M.D. Pa. Sept. 19, 2022) (unnecessary to revisit a court’s prior *Alice* step one ruling where there is “no extraordinary circumstance”); *Kove IO, Inc. v. Amazon Web Servs., Inc.* No. 18 C 8175, 2024 WL 450028, at *17-19 (N.D. Ill. Feb. 6, 2024) (invoking law of the case, explaining that “[b]ecause this Court did not proceed to the second step of the *Alice* inquiry in its previous section 101 analysis, its eligibility decision was a legal determination and thus should not be disturbed absent clear error or another compelling justification.”).

The Court’s ruling of patent eligibility should be applied with equal force to the ’308 and ’863 Patents. The ’308 and ’863 Patents are continuations of the ’799 Patent and share the same specification. The claims of the ’308 and ’863 Patents are also directed to similar patent-eligible subjects as the ’799 Patent, teaching, among other things, concrete steps describing “a specific solution to a technological problem in the field of sequence assembly.” D.I. 28 at 4; *see* D.I. 1-1 (’799 Patent) at cl. 1; *see also* D.I. 57-4 (’308 Patent) at cl. 1; *see also* D.I. 57-3 (’863 Patent) at cl. 1. Like the ’799 Patent, the claims of the ’308 and ’863 Patents claim steps of (1) obtaining sequence reads; (2) assembling the sequence reads into contigs; (3) placing the contigs along the reference genome; (4) comparing a number of contigs with a reference genome; (5) aligning reads to a number of contigs; and (6) genotyping. *See* D.I. 1-1 (’799 Patent) at cl. 1; *see also* D.I. 57-4 (’308 Patent) at cl. 1; *see also* D.I. 57-3 (’863 Patent) at cl. 1. These limitations are far from abstract. Even Natera’s own expert describes the ’308 and ’863 Patents as “largely repeat[ing] the limitations of the ’799 Patent claims” and similar for the purposes of the § 101 patent eligibility test. D.I. 245-1, Ex. D ¶¶ 214, 215.

Thus, the issue of patent eligibility has been decided by the Court for all Asserted Patents.

A. Natera Presents No New Arguments

Natera’s purported new arguments are insufficient to overcome the law of the case. *See In re Pharmacy Benefit Mgrs. Antitrust Litig.*, 582 F.3d 432, 439 (3d Cir. 2009) (the law of the case doctrine applies except in “extraordinary circumstances . . . where (1) new evidence is available or (2) a supervening new law has been announced.”). For the purely legal issue of patent eligibility under § 101, “dueling expert testimony” in the record does not in and of itself raise a relevant factual dispute. *Mortg. Grader, Inc. v. First Choice Loan Servs. Inc.*, 811 F.3d 1314, 1325 (Fed. Cir. 2016). The Court’s claim construction findings are irrelevant as the parties agreed claim construction was not necessary to rule on patent eligibility. D.I. 28 at 7.

To the extent Natera contends that its expert may present new arguments regarding patent eligibility, this is simply wrong. Natera’s expert opinions are simply a repackaging of its arguments already presented to this Court. Dr. Metzker describes the claims of the ’799 Patent as reciting an algorithm, the argument Natera made in its 12(b)(6) motion to dismiss. *See* D.I. 245-1, Ex. D ¶ 193; *see also* D.I. 9 at 1. As discussed above, Natera itself represents that for the purposes of patent eligibility, the ’308 and ’863 Patents are subject to the same arguments as the ’799 Patent. D.I. 245-1, Ex. D ¶ 215. Thus, Dr. Metzker’s report does not constitute new evidence sufficient to create an extraordinary circumstance where the law of the case should be ignored.

For the above reasons, Invitae respectfully requests the Court preclude Natera from contesting the eligibility of the Asserted Patents under 35 U.S.C. § 101.

Dated: February 9, 2024

Respectfully submitted,

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CERTIFICATE OF SERVICE

I, Brian E. Farnan, hereby certify that on February 9, 2024, a copy of PLAINTIFF INVITAE CORPORATION'S MOTION IN LIMINE NO. 1 TO PRECLUDE NATERA FROM CONTESTING VALIDITY UNDER 35 U.S.C. § 101 was served on the following as indicated:

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**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

NATERA’S OPPOSITION TO LABCORP’S MOTION *IN LIMINE* NO. 1

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Labcorp seeks to preclude Natera from “contesting the eligibility of the Asserted Patents under 35 U.S.C. § 101” before this Court, at trial or otherwise. Labcorp’s motion overreaches. It asks the Court to make a dispositive ruling on the subject-matter eligibility of three patents when Judge Stark (to whom this case was previously assigned) did no more than deny a Rule 12(b)(6) motion directed at only **one** of those patents and when the full case record, as developed during discovery, shows the ineligibility of **all three** Asserted Patents.

To be clear, Natera does not seek to ask the jury to decide the legal issue of whether the Asserted Claims are patent ineligible under Section 101. But there is no reason why the **Court** cannot decide that issue after trial, in view of the evidence presented. Labcorp does not even attempt to explain why such evidence would be irrelevant, prejudicial, or otherwise prohibited under the Federal Rules of Evidence, and, as Natera shows below, it is not.

I. ARGUMENT

Issues of subject matter eligibility may be decided after trial. *See, e.g., Chamberlain Grp., Inc. v. Techtronic Indus. Co.*, 935 F.3d 1341, 1344–45, 1349 (Fed. Cir. 2019); *Intell. Ventures I LLC v. Symantec Corp.*, 838 F.3d 1307, 1311–12 (Fed. Cir. 2016). That the Court denied Natera’s Rule 12(b)(6) motion that the claims of the ’799 Patent are patent ineligible is not a basis to preclude Natera from introducing evidence regarding the subject-matter ineligibility of that patent, let alone the other two Asserted Patents. *See, e.g., Smartflash LLC v. Apple Inc.*, 680 F. App’x 977, 978, 980–81 (Fed. Cir. 2017) (reversing denial of JMOL of patent ineligibility, which the district court decided after its summary judgment ruling on the same issue). Indeed, Chief Judge Connolly has rejected such arguments, holding that a prior ruling that patents were not ineligible at *Alice* step one does not automatically dispose of the issue. *See* Ex. 1 at 73:2–77:10 (defendant could present Section 101 defense at trial, despite the Court having denied summary judgment at *Alice* step one); *see also Natera, Inc. v. CareDx, Inc.*, 705 F. Supp. 3d 258, 266 (D. Del. 2023).

Labcorp's cases are either inapt or cut against it. None prohibited the presentation of new evidence of patent ineligibility after a motion-to-dismiss denial based on *Alice* step one. *CardioNet, LLC v. InfoBionic, Inc.* says only that *Alice* step one "**can** be answered based on the intrinsic evidence," not that it must be, and says nothing about step two. 955 F.3d 1358, 1372–73 (Fed. Cir. 2020) (emphasis added). *Kove IO* and *Savvy Dog Sys.* both demonstrate why Labcorp's motion should be denied. In *Kove IO v. Amazon Web Servs., Inc.*, the Court granted a summary judgment motion of Section 101 eligibility, finding "there are no changed circumstances or new facts in the record that warrant departing from the law of the case doctrine." No. 18-C-8175, 2024 WL 450028, at *17–19 (N.D. Ill. Feb. 6, 2024). The court in *Savvy Dog Sys., LLC v. Pennsylvania Coin, LLC* declined to reconsider its motion-to-dismiss holding on the same basis. No. 19-01470, 2022 WL 4349829, at *5 (M.D. Pa. Sept. 19, 2022). But even assuming there was "law of the case" based on a **denial** of a Rule 12(b)(6) motion (there is not), Labcorp seeks to bar Natera from even **presenting** evidence that would allow the Court to determine whether there are "changed circumstances or new facts in the record." *Kove IO*, 2024 WL 450028, at *18. If Labcorp wanted a dispositive ruling under Section 101, it should have moved for summary judgment and afforded Natera the opportunity to present the full evidentiary record supporting its defense. Instead, Labcorp's motion presumes a summary judgment victory it never even sought.

Natera previews here just a few examples of the record evidence it would have marshaled had Labcorp timely sought summary judgment against Natera's Section 101 defense: First, the patents' inventor has now admitted that the patents are directed to an abstract idea. Dr. Porreca testified that he invented "a computational algorithm," *see* Ex. 2 at 60:11–61:14, the inventive aspect of which "is the combination of multiple steps together," *see id.* at 70:7–23. *See also id.* at 102:23–103:1, 105:5–6. Dr. Porreca also contradicted Labcorp's allegation in its Complaint, core

to its Section 101 argument and Judge Stark’s ruling, that an advantage of the claimed method is “computational tractability,” testifying that any such advantage is achieved from an unclaimed element of his invention. *See id.* at 141:4–143:16; D.I. 13 at 4–5; D.I. 28 at 4–5. Labcorp, too, later jettisoned that motion-to-dismiss argument, persuading the Court during *Markman* that the patented method could be performed with as few as two sequence reads, which would impose no computational burden at all. *See* D.I. 72 at 30 (the claims are satisfied using “some ‘sequence reads’”); D.I. 84 at 9–11; D.I. 28 at 4–5.

In deciding Natera’s motion to dismiss, the Court was required to accept the allegations in Labcorp’s (then, Invitae’s) complaint. The complete evidentiary record demonstrates that those allegations are incorrect. Natera should be permitted to present that evidence. That includes the testimony of the inventor, Dr. Porreca, and Natera’s expert Dr. Metzker, who addressed Section 101 in his reports. *See* Ex. 3 ¶¶ 189–229; Ex. 4 ¶¶ 32–53. Labcorp’s expert will have the opportunity to respond with his opinions, disclosed in his report. *See* Ex. 5 ¶¶ 108–131.

Not one of Labcorp’s cases addressed a motion *in limine*. And Labcorp is not arguing that Natera’s evidence is irrelevant or prejudicial. Labcorp’s sole argument is that the Court’s denial of a motion to dismiss on one patent is law of the case as to the claims of all three patents, despite evidence later emerging showing their ineligibility. Labcorp cites no law or case precluding the Court from deciding Natera’s Section 101 defense after trial, based on evidence presented at trial.

Labcorp’s motion has nothing to do with the Federal Rules of Evidence. Instead, in the guise of an *in limine* motion, Labcorp asks the Court to rule on an untimely summary judgment motion that each Asserted Claim is patent-eligible under Section 101. Natera respectfully requests that the Court deny Labcorp’s motion, hear both parties’ arguments and evidence, and **then** decide, on a post-trial motion, if Natera established the ineligibility of the Asserted Claims.

EXHIBIT 1

IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

NATERA, INC.,)
)
Plaintiff,) C.A. No. 20-038 (CFC)
)
v.)
)
CAREDX, INC.,)
)
Defendant.)

Thursday, January 11, 2024
3:00 p.m.
Pretrial Conference

844 King Street
Wilmington, Delaware

BEFORE: THE HONORABLE COLM F. CONNOLLY
United States District Court Judge

APPEARANCES:

MORRIS NICHOLS ARSHT & TUNNELL
BY: DEREK J. FAHNESTOCK, ESQ.

-and-

APPEARANCES CONTINUED:

QUINN EMANUEL URQUHART & SULLIVAN, LLP
BY: KEVIN P.B. JOHNSON, ESQ. (via telephone)
BY: SANDRA L. HABERNY, ESQ.
BY: ANDREW M. HOLMES, ESQ.
BY: VALERIE LOZANO, ESQ. (via telephone)
BY: JEFF NARDINELLI, ESQ. (via telephone)
BY: ANDREW BRAMHALL, ESQ.
BY: ABIGAIL CLARK, ESQ.
BY: BIANCA FOX, ESQ.

Counsel for the Plaintiff

FARNAN LLP
BY: BRIAN E. FARNAN, ESQ.

-and-

WEIL, GOTSHAL & MANGES LLP
BY: EDWARD R. REINES, ESQ.
BY: DEREK C. WALTER, ESQ.
Counsel for the Defendant

- - - - -

P R O C E E D I N G S

(Proceedings commenced in the courtroom beginning at
3:00 p.m.)

THE COURT: All right. Please be seated.

Mr. Fahnestock, welcome.

MR. FAHNESTOCK: Good afternoon, Your Honor.

It's Derek Fahnestock from Morris Nichols on behalf of
plaintiff, Natera.

I'll just introduce the team here, all from
Quinn Emanuel. Sandra Haberny --

MS. HABERNY: Good afternoon, Judge.

MR. FAHNESTOCK: Andrew Bramhall --

MR. BRAMHALL: Good afternoon.

MR. FAHNESTOCK: Drew Holmes --

MR. HOLMES: Good afternoon.

MR. FAHNESTOCK: Abigail Clark, Bianca Fox,
and Tara Srinivasan, I apologize --

MS. SVINIVASAN: Good afternoon.

MR. FAHNESTOCK: -- and on the phone. And we
thank Your Honor for that accommodation because they were
unable to get here based on flights; our lead counsel,
Kevin Johnson and Valerie Lozano, as well as Jeff
Nardinelli

THE COURT: All right. You want to just --

MR. JOHNSON: Good afternoon, Your Honor.

THE COURT: Okay. Good afternoon. Thanks.

All right. Thank you.

MR. FARNAN: Good afternoon, Your Honor.

Brian Farnan on behalf of CareDx. And with me is
Edward Reines --

MR. REINES: Good afternoon.

MR. FARNAN: -- and Derek Walter from Weil,
Gotshal & Manges.

THE COURT: All right. Thank you.

MR. FARNAN: Thank you.

THE COURT: Had you all thought about how you
want to proceed, in what order?

MR. FAHNESTOCK: We haven't actually discussed
it, Your Honor, but, you know, maybe we could just
discuss a couple of basic procedural trial issues first,
like the time of trial and phasing, if that's okay.

MR. REINES: Whatever is best for the Court,
frankly.

THE COURT: All right. Well, I think you
asked for 13, you asked for 11.

MR. FAHNESTOCK: That's right.

THE COURT: I was thinking what about 12 each,
and then we don't count closings, and then you each get
an hour or closing. What do you think?

1 **THE COURT:** I denied the motion, but you
2 better tie it up.
3 **MR. BRAMHALL:** Yeah, understood.
4 **THE COURT:** All right. Next?
5 **MR. FAHNESTOCK:** Your Honor, I think
6 Mr. Bramhall has an issue. We still have an issue where
7 Your Honor's order, of course, to meet and confer and
8 narrow the case, we still have issue with the number of
9 defenses that we think that they want to run.
10 **THE COURT:** Okay. You want to do that next?
11 We have Dauberts. We have to hurry. Let's go.
12 **MR. BRAMHALL:** Thank you, Your Honor. Andrew
13 Bramhall, again, and I have another visual aid, if that's
14 possible for me to hand up.
15 **THE COURT:** Sure. It's possible.
16 **MR. BRAMHALL:** May I approach?
17 **THE COURT:** Sure.
18 **MR. BRAMHALL:** Thank you, Your Honor.
19 So, your Honor, at this stage, on the Natera
20 side we've substantially narrowed our case.
21 What I've handed you is a document that's
22 showing you at the top our remaining asserted claims. So
23 we're down to five, which is two independent claims,
24 three dependent. We're not hearing any argument from the
25 other side that that's too much or can't be tried in the

amount of time we have or amount of days.
2 Now, on the other hand, if you take a look at
3 what CareDx still has available to them or have not
4 narrowed on their invalidity arguments, and I'm happy to
5 be corrected on any of this from counsel, if there's
6 something on here that shouldn't be. But we have vastly
7 more arguments -- and, in particular, Your Honor, our
8 focus --
9 **THE COURT:** I'm not going to limit them.
10 They've got 12 hours. They will have to get it in. They
11 think they can do this in 12 hours, good for them.
12 **MR. BRAMHALL:** If I may, Your Honor, the risk
13 for us is we have all of these defenses we need to now
14 prepare for. Inevitably, to Your Honor's point, some of
15 them are going to fall out, but that's after we've used
16 our time in a prejudicial way.
17 **THE COURT:** No, but here's what I'm going to
18 do. I'm going to make them assert these defenses in
19 front of the jury. So if they withdraw them, I'm going
20 to tell the jury. I'm going to tell the jury. They've
21 got to pursue them. They've got to pursue the defenses.
22 They cannot withdraw the defenses.
23 Now, what I'm going to do is, I will give them
24 to -- what date do you want to pick your final defenses?
25 **MR. REINES:** I think we are comfortable with

1 these, but if you want to give us until at least tomorrow
2 so we can discuss it.
3 **THE COURT:** I just think you have to decide.
4 Because this is the way -- I just did this in another
5 trial, and it worked great is, you are stuck. You must
6 go forward with every defense. The jury will be
7 instructed that you asserted these defenses. And if you
8 withdraw them, I'm going to tell the jury that they
9 asserted these defenses. And I'm going to tell the jury
10 I ruled against them. Because you're not allowed to
11 withdraw them. If you're not going to pursue them, I'm
12 going to tell them.
13 You cannot blindsides people. It's not fair.
14 It's the crappy kind of lawyer behavior I don't like, and
15 it's not right. So pick your defenses.
16 How long do you want? How much time do you
17 need? You want 24 hours? You want 36 hours? What do
18 you want?
19 **MR. REINES:** Twenty-four hours. We skinned
20 it down, so we're comfortable.
21 **THE COURT:** And I understand that. You might
22 be able to try all of these. Go for it. But what you
23 can't do is you can't walk in and say, we withdrew four
24 of them. Unfair.
25 **MR. REINES:** Right. I don't think there's

any --
2 **THE COURT:** And, by the way, same thing with
3 them. Because if they really think they're going to try
4 five claims, that's a stretch. And so same thing. You
5 can't withdraw any claims. You are stuck.
6 So give me the deadline you want, and I will
7 pick it, and you're both stuck.
8 **MR. BRAMHALL:** Same timeline works for us,
9 Your Honor; i.e., 24 hours.
10 **THE COURT:** 24 hours. You have until 5:00
11 tomorrow night.
12 **MR. BRAMHALL:** Fantastic, Your Honor.
13 **THE COURT:** And what you -- final assertion of
14 claims, final assertion of defenses. All right. Next?
15 **MR. BRAMHALL:** Thank you, Your Honor.
16 **MR. REINES:** Thank you.
17 I think the next thing, with Your Honor's
18 prompting, is the *Daubert*.
19 **THE COURT:** Can I just ask you one thing on
20 the 101s?
21 **MR. REINES:** Yes.
22 **THE COURT:** There was this statement in the
23 letter.
24 Do you have the letter? I have it here. I
25 want you to look at this one, and I'll find my other

copy. That's it, right?

Okay. Mr. Reines, I was going to ask you this. You write in this letter, which is D.I. 423. It's dated January 5th, quote, "With respect to the 101 defense on the '544 patent specifically, CareDx further notes that in view of the rationale of the Court's summary judgment opinion, it understands that this issue is no longer available to be presented to the jury and will seek confirmation on this point at the pretrial conference," unquote.

MR. REINES: Thank you. Yes.

So we're just --

THE COURT: I'm not giving you confirmation because that's not at all the case. I did not make that defense unavailable to you by my ruling.

MR. REINES: Okay. So here's what our rationale was, Your Honor, just so you understand where we're coming from. It wasn't -- our understanding was because you found it a method of preparation, that that was a failure to meet Step 1, and we understood -- I think understand, as Your Honor pointed out the law is not pristine in this area, but that Step 1, I'm never aware of anyone saying that that's a factual-based step, that that's a purely legal step.

Now, you've corrected me on 101 law before,

so -- but on this one, on Step 1 -- so our understanding is since Your Honor -- we're not seeking to lose a defense, right, so it was just -- we want the definitive ruling so were, you know, preserving the record.

So our -- because Your Honor said, "I found it a method of preparation, Step 1 is not satisfied," that we can't go --

THE COURT: Do you have my opinion? I don't remember distinguishing Step 1.

I don't think I made any reference at all to it. I just referred to the fact that the Federal Circuit case law makes clear what the result was.

Does somebody have my opinion? Want to hand it up to me?

MS. HABERNY: Your Honor, what I recall the opinion saying is that it was found that you denied the Section 101 motion under *Illumina*. And the *Illumina* precedent found that a method of preparation was patentable subject matter at Step 1, and said that, from that, you don't need to go to Step 2 to determine issues of fact as to what's routine and conventional.

And so based on that, and I think we had the same understanding, under the *Illumina* precedent, whether the steps are routine and conventional is no longer at issue because the claim was found to be directed to

patentable subject matter at Step 1, method of preparation.

THE COURT: Okay. So I think this is a --

MS. HABERNY: And I do have Your Honor's order here, if you would like me to --

THE COURT: Yeah. Can you hand it up to me?

MS. HABERNY: I, unfortunately, have it on a computer.

MR. REINES: E-mail it.

THE COURT: Hold up.

MS. HABERNY: Docket Number 402, Page 13. And I could read the relevant portion.

THE COURT: Hold on.

Does anybody have a copy of *Illumina* with them?

MR. REINES: We can bring it up on the screen. I don't know if that helps.

THE COURT: You pointed out to me something I wish I had written better, which is my opinion. And it's funny because I've recently clarified this exact issue in another opinion.

I should never have said that they are patent eligible in that sentence in the first or second paragraph of this opinion, which is located at D.I. 402. They can be patent eligible.

And so, in other words, courts don't engage and they don't find summary judgment to say that a patent is valid and nor do they engage in determining that a patent subject -- or a patent is eligible under 101. It's a mistake on my part. And what it is, is a patent could be eligible.

So, in other words, it's not, per se ineligible. So I did not mean to preclude or make unavailable the defendants from asserting a 101 defense. They can.

So, again, I just wrote this opinion in the last week or two.

MS. CLARK: Yeah, you did, Your Honor. In *CR Bard v. AngioDynamics*.

THE COURT: Right. And I made the point there, and I didn't find a case that actually says, pointblank, that courts don't declare patents eligible, but they don't. It doesn't make any sense that they would, that you would only do as you do in the invalidity context as a Court, you would only rule that a patent had been proven, by clear and convincing evidence, to be invalid.

Likewise, I would only grant summary judgment that a patent is ineligible, like *Bard* -- like in the *Bard* case, I would not say, per se, as a matter of law, a

patent is eligible under 101. Courts don't engage in that.

So to the extent my opinion fairly -- unfortunately, I did not word it as well as I should have in this case, because the issue was not in front of me to think about it that way. But you, the defendants, are allowed to pursue your 101 defense at trial. I did not declare as a matter of law that that patent is ineligible for 101, and then whether it's eligible or not is a question that remains before me.

MS. HABERNY: Then, Your Honor, we have a question about how this will be presented to the jury because what a patent is directed to, and under *Illumina*, being directed to a method of preparation is a question of law, not a question of fact.

And so that -- I'm presuming now because Your Honor did find that the patent claims were directed to a method of preparation, then I'm not entirely sure what could be presented to the jury after that.

THE COURT: So you're going to argue that you're going to look at the factual basis for Step 2 in front of the jury.

MS. HABERNY: Well, if, under *Illumina*, the inquiry did not proceed to Step 2, I'm not sure how this can be presented to the jury.

THE COURT: It's not like it's estoppel,

right?

MS. HABERNY: I mean, let's just say, suppose --

THE COURT: Who were the parties in *Illumina*? Was anybody here a party to that case?

MR. REINES: Yes, Your Honor.

THE COURT: Okay. Sorry. Were you --

MR. REINES: On that one, I was successful, Your Honor.

THE COURT: You won?

MR. REINES: Yes.

THE COURT: Yeah. So when you say you, personally, was CareDx a party to that case?

MR. REINES: No.

THE COURT: Oh, okay. So my --

MR. REINES: Oh, I'm sorry. Me, personally. I'm sorry.

THE COURT: Yeah. CareDx -- neither CareDx nor Natera was a party to that case?

MS. HABERNY: Correct.

THE COURT: So there's no estoppel.

MR. REINES: So, Your Honor, I think the issue -- and I have to say I agree with Ms. Haberny to this effect. Your Honor did rule, as a legal matter, as

I understood it -- I don't want you to have --

THE COURT: Yeah.

MR. REINES: But that the way we understand it is that there's not -- it's not claiming -- it's not directed to a natural law or legal principle because it's directed towards a preparation. Okay? Let's just hypothetically say that's what you ruled. If that's what you ruled, then --

THE COURT: What I should have ruled is this, to be very clear. What I said in my opinion at Page 1 into Page 2, I said, quote, "Methods for preparing a fraction of cell-free DNA that is enriched in fetal DNA to make possible the observation of DNA however are patent eligible under Section 101."

What I should have said, "Methods for preparing a fraction of cell-free DNA that is enriched in fetal DNA to make possible the observation of DNA, however, can be patent eligible under 101."

That's what I should have put. All right? And that's because -- in other words, I don't think -- or, and what I would have to think about more is whether we should have -- well, it may be that a Court could rule that the Federal Circuit could rule that methods of preparation are always directed to subject matter that is patent eligible. That could be -- and I'd have to think

about that.

And, in fact, I will tell you if you parse the *Bard* opinion. In *Bard*, I was actually asked by both sides to engage in exegesis of an unprecedential opinion issued by the Federal Circuit in a *Bard* case. And in that opinion -- again, it's nonprecedential, the Federal Circuit actually did say both that the patents in question were not directed to subject matter eligibility. And then about a sentence or two later, the Federal Circuit said "The patents are eligible under 101."

And one of the parties asked me to focus on those two sentences to say that the Federal Circuit has declared as a matter of law that the patents asserted in that case, which were asserted in the case before me, are valid or are eligible under 101 as a matter of law. And I said I can't do that. But I agreed that those two sentence supported the argument that that's what the Federal Circuit had done.

I also said that if you look up at a couple of sentences before those two sentences, you will see where the Federal Circuit defined what was the question before it, which supported the other party's position. All right?

But the bottom line, what I did is I only made reference in my opinion to the sentence that talked about

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THE COURT: Anything else I can resolve now?

No. Okay.

Then the jury is coming in at -- now, you are going to set up the courtroom beforehand. You are coming in earlier that morning. And then they are going to come in right at 9:00, and we can pick them really quick. And then we'll get to the *Daubert* motions. All right?

And then we'll start on Monday, sharp, 8:30. Go right at it. You get 12 hours, each side.

We should be doing closing arguments Thursday afternoon, you know. Maybe we slate it for Friday morning. But I'm assuming we will probably be closing, you know, Thursday.

MR. FAHNESTOCK: Phase II?

THE COURT: Okay. That's right. Because we're going to break it in phases. I forgot. And I didn't figure out -- thank you for reminding me that.

Because in terms of closing arguments, how is that going to work? Well, you just have to split it. Okay.

How long do you think you plan the first phase goes?

MS. HABERNY: Probably three days.

THE COURT: Three days? So damages -- so, really, we're just going to have damages. That's going

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to be the only thing that's different. Is that right?

MR. FAHNESTOCK: That seems to be the only thing in the second phase. No willfulness, no inducement.

THE COURT: So the reason why I separate these is because of -- mainly because of undue prejudice with willfulness, it seems to me. And kind of injecting issues into the case unnecessarily. We will still do it this way. It's really worked.

Actually, didn't we do it in your case? In the last case, did we do damages separately?

MR. REINES: No, we didn't.

THE COURT: It's worked out fine. We did it in *Personal Audio*, and it worked out well, you know.

MR. FARNAN: Yes, Your Honor.

THE COURT: Okay. All right. Great. Anything else?

MR. REINES: That's it, Your Honor.

THE COURT: All right. Thanks very much. I will see you.

(The proceedings concluded at 5:34 p.m.)

CERTIFICATE OF COURT REPORTER

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I hereby certify that the foregoing is a true and accurate transcript from my stenographic notes in the proceeding.

/s/ Bonnie R. Archer
Bonnie R. Archer
Official Court Reporter
U.S. District Court

EXHIBIT 2

Page 1

VOLUME: I
PAGES: 1-326
EXHIBITS: 1-33

UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE
NO. 1:21-cv-01635-LPS

INVITAE CORPORATION,)
Plaintiff,)
vs.)
NATERA, INC.,)
Defendant.)

VIDEOTAPED DEPOSITION OF INVITAE
CORPORATION BY GREGORY J. PORRECA, PhD, called as a
witness by and on behalf of the Defendant, pursuant
to the applicable provisions of the Federal Rules
of Civil Procedure, Rule 30(b)(6), before P. Jodi
Ohnemus (remotely), RPR, RMR, CRR, CA-CSR #13192,
NH-LSR #91, MA-CSR #123193, and Notary Public,
within and for the Commonwealth of Massachusetts,
at Cambridge, Massachusetts, on Friday, April 28,
2023, commencing at 9:47 a.m.

<p style="text-align: right;">Page 58</p> <p>1 A. Yes. This would be the first diagram of 2 the algorithm. 3 Q. Let's look at Exhibit 5 to your 4 deposition, and then I'm going to want a break in a 5 minute 'cause I can hear my voice going. But let's 6 look at Exhibit 5 for a moment. 7 (Exhibit 5, Invention Disclosure Form, 8 ML-PORRECA000000068-74.) 9 A. Okay. 10 Q. Doctor Porreca, I've placed before you 11 what I've marked as Exhibit 5 to your deposition, 12 which bears the Bates numbers ML-PORRECA 68 through 13 74. It's a document entitled "Invention Disclosure 14 Form." 15 Do you see that there? 16 A. I do. 17 Q. It lists as the -- people who conceived of 18 and/or reduced to practice the invention, yourself 19 and Doctor Kennedy; correct? 20 A. That is correct. 21 Q. And then there is a section entitled 22 "Description of the Invention"? 23 A. Yes. 24 Q. And that continues on for a couple of 25 pages; and on page 4 of this document actually has</p>	<p style="text-align: right;">Page 60</p> <p>1 A. Tom Meyers was our IP attorney at the time 2 for the company. 3 Q. In house or outside counsel? 4 A. Outside counsel. 5 Q. And it says (as read): 6 "On what date did you make such a 7 disclosure?" 8 Answer: "September 28, 2011." 9 You see that? 10 A. I do see that. 11 Q. Fair to say, then, that you had the idea 12 on September 27, 2011, and were in a position to 13 disclose the idea to your lawyer the next day? 14 A. That's what this document indicates. 15 Q. Is it right? 16 A. As far as I can remember, I believe it is 17 correct. 18 Q. On the top of the next page it says (as 19 read): 20 "When did you first do any experimental 21 work towards carrying out the invention?" 22 You see that there? 23 A. I do. 24 Q. And the answer is "N/A." 25 A. Yes.</p>
<p style="text-align: right;">Page 59</p> <p>1 the photograph of the whiteboard; correct? 2 A. That is correct. 3 Q. Then it says (as read): 4 "When did you first think of this 5 invention?" 6 Answer: "September 27, 2011." 7 Is that right? 8 A. That's correct. 9 Q. And I guess I should ask two questions: 10 That's what it says. And it's accurate; correct? 11 A. That is what it says. And that is 12 accurate. 13 Q. Thank you. And it says (as read): 14 "What record do you have to substantiate 15 this date?" 16 Then it says (as read): 17 "This disclosure, email from Greg to Caleb 18 with photo of whiteboard outlining method." 19 You see that? 20 A. I do see that. 21 Q. And it says (as read): 22 "To whom did you first disclose this 23 invention?" 24 And the answer is "Tom Meyers." 25 Who's that?</p>	<p style="text-align: right;">Page 61</p> <p>1 Q. Is that meaning not applicable? 2 A. Correct. 3 Q. And the reason that that's your answer is 4 that you didn't do any experimental work towards 5 carrying out the invention; correct? 6 A. That's correct, because it was a 7 computational algorithm. 8 Q. Right. The -- the invention is a 9 computational algorithm. It's not something that 10 you do physically; correct? 11 A. It's not something that -- I -- I think 12 the way I answered that question was it's not some 13 kind of a wet lab technique. It's a computational 14 algorithm. 15 Q. And then you say, (as read): 16 "When did you first make written 17 description of the invention?" 18 Answer: "September 27, 2011." 19 You see that there? 20 A. I do. 21 Q. Now, on every page of this document you 22 and Doctor Kennedy have signed it and dated it 23 November 7, 2011, other than the last page; is that 24 correct? 25 A. So there's a signature -- there are two</p>

<p style="text-align: right;">Page 62</p> <p>1 signatures and dates on every page at the bottom. 2 I think that's what you're referring to. That -- 3 those signatures are mine and someone named Mark 4 Umbarger. That's not Caleb Kennedy's signature. 5 Mark -- 6 Q. So -- go ahead. Please continue. 7 A. Mark was the person who witnessed this. 8 Q. Okay. So I was obviously wrong about 9 that. With no disrespect to Mr. Umbarger, those 10 lines could be essentially any name. So I'm going 11 to start over and just get it correct. I have no 12 interest in having you tell me something that isn't 13 true. So thank you. Withdrawn. 14 If we direct you to the bottom of the 15 first page, we see your signature dated November 16 7th, 2011, and the signature of somebody named Mark 17 Umbarger, who is acting as the witness; correct? 18 A. That's correct. 19 Q. Who is Mr. or Doctor Umbarger? 20 A. Doctor Umbarger was another person who 21 worked for me in the R&D department at Good Start. 22 He was a Good Start employee. 23 Q. I want to try to understand the sequence 24 in which things happened. 25 If you turn to the last page of this</p>	<p style="text-align: right;">Page 64</p> <p>1 what happened or why it looks that way. 2 Q. All right. That's fair. And whatever -- 3 but do you understand that to be Mr. Umbarger's 4 signature? 5 A. I do, yes. 6 Q. All right. And to the right of it it says 7 November 7th, 2011? 8 A. Yes, it does. 9 Q. And then you and Mr. or Doctor -- forgive 10 me -- Umbarger signed all the other pages of this 11 document on November 7th, 2011? 12 A. Yeah. That's the -- that's the date. 13 Q. Do you have an understanding of how that 14 happened? So it looks like you signed it on the 15 28th and he witnessed it. And then, you know, a 16 month and a half later -- or whatever that is -- 17 Doctor Kennedy signed it and you signed every page. 18 How'd that all happen? 19 A. I don't recall. 20 Q. Okay. That's fair. 21 MR. STONE: I'm going to ask that we take 22 a ten-minute break here because I obviously need 23 some water. We've been going a little while. Is 24 that okay with everyone else? 25 THE WITNESS: Yes.</p>
<p style="text-align: right;">Page 63</p> <p>1 document. 2 A. Yes. 3 Q. Am I right that the first inventor 4 signature is Gregory Porreca. That's you? 5 A. That's correct. 6 Q. And it's dated September 28, 2011. 7 You see that? 8 A. I do. 9 Q. And, then, five lines down under "Witness 10 signature," there's what I think is Mark Umbarger's 11 signature; correct? 12 A. That is correct. 13 Q. Also dated September 28, 2011; correct? 14 A. That is correct. 15 Q. Is the second signature on the page Caleb 16 Kennedy? 17 A. I believe it is, yes. 18 Q. And it's dated 7 November 2011; correct? 19 A. Yes. Correct. 20 Q. And, then, I think what's happening in the 21 second "Witness Signature" is that Mr. Umbarger 22 wrote his name, for whatever reason didn't like the 23 way it looked, crossed it out, and wrote it again. 24 Is that what you see there? 25 A. I see a bunch of scribbling. I don't know</p>	<p style="text-align: right;">Page 65</p> <p>1 VIDEO OPERATOR: We're now going off the 2 record at approximately 10:58 a.m. 3 (Recess was taken.) 4 VIDEO OPERATOR: This is the beginning of 5 media No. 2. We're going back on the record at 6 approximately 11:16 a.m. 7 Go ahead, sir. 8 Q. Dr. Porreca, when we broke we were looking 9 at the invention disclosure form for the invention 10 that became the '799 patent; correct? 11 A. That is correct. 12 Q. All right. Let's -- let's look at it 13 again together. I want to start with just, sort 14 of, geography. Directing you to the "Description 15 of the Invention" section, the first paragraph 16 there that says "Please provide a concise 17 description," that paragraph is part of the form 18 that you fill in; correct? 19 A. That is correct. 20 Q. All right. And then the stuff that you 21 filled in begins with the words "Analysis of 22 sequence data"; correct? 23 A. That's correct. 24 Q. And if you look at that part of the first 25 page and then into the second page, you'll see on</p>

<p>Page 66</p> <p>1 the second page there's a paragraph that says (as 2 read): 3 "The invention described here." 4 You see that? 5 A. Yes. 6 Q. Am I correct that the text in that section 7 above the words "the invention described here" that 8 is the paragraph that begins "Analysis of sequence 9 data" and the two numbered paragraphs under it and 10 the paragraph that begins "The advantage of this 11 approach" and the three numbers -- numbered 12 paragraphs after it, all of that is your 13 description of the prior art of what was known 14 before; correct? 15 A. (Witness reviews document.) I'm reviewing 16 it now. 17 Q. Of course. You should. 18 A. (Witness reviews document.) So I think 19 that text is a description of certain aspects of 20 the prior art that we thought were relevant and 21 that, in part, motivated the invention. 22 Q. And, then, the part that is a description 23 of the invention, unsurprisingly, is the part that 24 begins with the words "The invention described 25 here."</p>	<p>Page 68</p> <p>1 Do you see that there? 2 A. I do see that. 3 Q. And then it says (as read): 4 "The process is as follows." 5 And there are six numbered paragraphs 6 below that; correct? 7 A. Yes, there are. 8 Q. And is it fair to describe those six 9 numbered paragraphs as each being a step of the 10 process? 11 MR. PEPE: Object to form. 12 A. (Witness reviews document.) Yeah. These 13 are the high-level -- look like -- steps of the 14 process to me. 15 Q. Step 1 is (as read): 16 "Assemble a set of reads into one or more 17 contigs." 18 You see that there? 19 A. I do see that. 20 Q. Your invention is not -- strike that. 21 There are a number of different algorithms 22 that one can use to assemble reads into contigs; 23 correct? 24 MR. PEPE: Object to form. 25 A. Yeah, I don't think this specifies what</p>
<p>Page 67</p> <p>1 A. (Witness reviews document.) This -- this 2 is a description of the algorithm. 3 When we say a description of the 4 invention, that sounds a little precise to me. I 5 think this is -- this was -- our intent here was to 6 describe the algorithm that we had come up with. 7 Q. Okay. I -- I'm -- I'm not looking to use 8 the words in a limiting way. I'm looking to 9 understand the structure of the document. So maybe 10 we can do it this way -- withdrawn. 11 The words before "The invention described 12 here" are your attempts to describe aspects of the 13 prior art and some of the problems with those 14 aspects of the prior art. And the words that begin 15 with "The invention described here" and flow onto 16 the next page are a description of the algorithm 17 that you have come up with and how it helped solve 18 those problems; is that fair? 19 A. Yes, that's fair. 20 Q. And you write (as read): 21 "The invention described here is a method 22 to reliably detect indels of increased length as 23 well as substitutions located in cis with indels or 24 with multiple other substitutions that prevent 25 alignment."</p>	<p>Page 69</p> <p>1 algorithm you would use to do that assembly 2 process. 3 Q. I don't either, but you're two questions 4 ahead of me. We're going to get there in a moment. 5 Just stay -- stay with me. I -- I don't think any 6 of this is going to be a surprise. I don't even 7 think we disagree about it, but let's just go one 8 question at a time if we could. Okay? 9 A. Okay. 10 Q. At the time of your invention on September 11 27 of 2011 there were multiple algorithms already 12 known in the art for how to combine reads into 13 contigs; correct? 14 A. Yes, that's correct. 15 Q. Right. And you don't purport to have 16 invented a new algorithm for combining reads into 17 contigs. Your invention can be practiced with any 18 of those algorithms; correct? 19 MR. PEPE: Object to form. 20 A. The invention can use different assembly 21 algorithms. It was conceived at the time to use 22 assembly as a generic process. 23 Q. And just to be -- withdrawn. 24 You didn't invent a new assembly algorithm 25 for assembling reads to contigs as part of this</p>

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<p>1 invention; correct?</p> <p>2 A. We did not invent a new assembly algorithm</p> <p>3 to assemble reads. The assembly algorithm sits</p> <p>4 inside of the larger GATA algorithm.</p> <p>5 Q. And let's talk about that for a second.</p> <p>6 GATA is a set of -- strike that.</p> <p>7 The GATA algorithm has a number of steps</p> <p>8 within it; correct?</p> <p>9 A. That is correct.</p> <p>10 Q. And your contention is that the overall</p> <p>11 algorithm is inventive; correct?</p> <p>12 A. That is correct.</p> <p>13 Q. But some of the steps that are performed</p> <p>14 as part of that algorithm are things that people</p> <p>15 were already doing, like assembling reads into</p> <p>16 contigs; correct?</p> <p>17 A. That is correct.</p> <p>18 Q. And you're not -- it's not your contention</p> <p>19 that every step of the algorithm is individually</p> <p>20 inventive. What's inventive is the overall</p> <p>21 algorithm; correct?</p> <p>22 A. That is correct. The inventive part of</p> <p>23 this is the combination of multiple steps together.</p> <p>24 Q. And I am going to ask you as we go through</p> <p>25 the steps some -- whether some of them were already</p>	<p>1 The step of the GATA algorithm that is the</p> <p>2 '799 patent, one step of that requires assembling</p> <p>3 reads into contigs; correct?</p> <p>4 A. Yes.</p> <p>5 Q. And there may be many ways in which one</p> <p>6 can do that as one step of the GATA process;</p> <p>7 correct?</p> <p>8 A. That's correct.</p> <p>9 Q. And the GATA algorithm doesn't require any</p> <p>10 particular means of assembling reads into contigs.</p> <p>11 It just requires that reads be assembled into</p> <p>12 contigs; correct?</p> <p>13 A. I don't know that -- I don't know that I</p> <p>14 would say it doesn't require any particular means.</p> <p>15 I think it -- it does require reads to be assembled</p> <p>16 into contigs. I'm sure there are assembly methods</p> <p>17 that -- well, I would imagine there are assembly</p> <p>18 methods that wouldn't work with this process.</p> <p>19 Q. What the GATA -- strike that.</p> <p>20 What the GATA algorithm of the '799 patent</p> <p>21 requires in this step is that the reads be</p> <p>22 assembled into the contigs, but it doesn't dictate</p> <p>23 a particular means of doing that; correct?</p> <p>24 A. That is correct.</p> <p>25 Q. And, then, in step 2 of the GATA algorithm</p>
Page 71	Page 73
<p>1 known in the art, and when I do that, I'm not</p> <p>2 suggesting that means the overall algorithm was</p> <p>3 known in the art. I'm just going to ask you about</p> <p>4 each individual step because I want to figure out</p> <p>5 what the pieces are. And that -- that's the reason</p> <p>6 I'm asking. So withdrawn.</p> <p>7 As of September 27, 2011, the idea of</p> <p>8 assembling reads into contigs, assembling reads</p> <p>9 into contigs was known in the art; correct?</p> <p>10 A. Yes, it was.</p> <p>11 Q. And you don't purport to have invented a</p> <p>12 new way of assembling reads into contigs; correct?</p> <p>13 A. That is correct.</p> <p>14 Q. Your GATA algorithm can be performed with</p> <p>15 any method of assembling reads into contigs. It</p> <p>16 simply requires that reads be assembled into</p> <p>17 contigs; correct?</p> <p>18 A. I don't know if it can be performed with</p> <p>19 any method. It can be --</p> <p>20 Q. That's a very --</p> <p>21 A. -- performed with different -- with</p> <p>22 multiple methods.</p> <p>23 Q. Okay. You know, that's totally fair. So</p> <p>24 I'm going to ask it that way. Withdrawn.</p> <p>25 Your GATA algorithm -- withdrawn.</p>	<p>1 as set forth in this invention disclosure, you (as</p> <p>2 read):</p> <p>3 "Determine the genomic position of each</p> <p>4 contig generated in step 1 and identify any</p> <p>5 differences between that contig and the reference</p> <p>6 genome (substitutions and indels)."</p> <p>7 Do you see that there?</p> <p>8 A. I do see that.</p> <p>9 Q. And it says that (as read):</p> <p>10 "This can be done using BWA-long."</p> <p>11 You see that?</p> <p>12 A. I do.</p> <p>13 Q. BWA-long is a software algorithm that</p> <p>14 existed before September 27, 2011; correct?</p> <p>15 A. That is correct.</p> <p>16 Q. And the idea of aligning contigs -- strike</p> <p>17 that.</p> <p>18 The idea of aligning contigs to a</p> <p>19 reference genome and identifying differences</p> <p>20 between the contig and the reference genome was</p> <p>21 known in the prior art before September 27, 2011;</p> <p>22 correct?</p> <p>23 A. I don't know that it's true that the idea</p> <p>24 of taking reads, assembling -- assembling them into</p> <p>25 a contig, and then aligning them to a reference</p>

<p style="text-align: right;">Page 98</p> <p>1 A. Yes.</p> <p>2 Q. First off, am I correct that each of these</p> <p>3 is a file format for computer data which is why</p> <p>4 they begin with a period?</p> <p>5 A. That is correct. This looks like -- yes,</p> <p>6 this looks like a -- an attempt to indicate what</p> <p>7 our internal file formats were for each step.</p> <p>8 Q. The first one, ".fq," is something that</p> <p>9 was known in the art as FASTQ, F-A-S-T-Q; correct?</p> <p>10 A. That is correct.</p> <p>11 Q. And that's not a file format that you</p> <p>12 invented as part of the GATA algorithm in the '799</p> <p>13 patent. That was in the prior art; correct?</p> <p>14 A. Correct.</p> <p>15 Q. The second one is ".fa," that's FASTA,</p> <p>16 F-A-S-T-A; correct?</p> <p>17 A. Yes. I believe that's correct.</p> <p>18 Q. And that also is an algorithm -- strike</p> <p>19 that.</p> <p>20 That also is a file format that was known</p> <p>21 in the prior art. You didn't invent that as part</p> <p>22 of this; correct?</p> <p>23 A. Correct.</p> <p>24 Q. Do you know what "Remove base qualities"</p> <p>25 is in step 1?</p>	<p style="text-align: right;">Page 100</p> <p>1 A. The base quality is how good each -- each</p> <p>2 letter in the read is.</p> <p>3 Q. Right. And -- and just to close off that</p> <p>4 loop, there's no alignment information in any of</p> <p>5 that; correct?</p> <p>6 A. That is correct. There's no -- those base</p> <p>7 qualities do not encode alignment information. The</p> <p>8 FASTQ file has not been -- is not the output of an</p> <p>9 alignment algorithm.</p> <p>10 Q. And so we see FASTQ information, the</p> <p>11 unaligned reads being assembled into read -- strike</p> <p>12 that.</p> <p>13 I -- I want to ask a question -- I'm going</p> <p>14 to come back to that in a second.</p> <p>15 Where it says "Assemble reads," No. 2?</p> <p>16 A. Yeah.</p> <p>17 Q. It's referring to assembling reads into</p> <p>18 contigs, not assembling letters into reads;</p> <p>19 correct?</p> <p>20 A. That is correct.</p> <p>21 Q. All right. So now I can go back to where</p> <p>22 I was, but I want to just make sure I understood</p> <p>23 that. Thank you for bearing with me. Withdrawn.</p> <p>24 And so on the left part of this flow chart</p> <p>25 we see unaligned reads being assembled into a</p>
<p style="text-align: right;">Page 99</p> <p>1 A. It may be that the assembly tool that we</p> <p>2 were using needed an input format that didn't</p> <p>3 contain the base qualities, but I -- I don't know</p> <p>4 for sure.</p> <p>5 Q. Okay. The -- whatever it is, it is the</p> <p>6 difference between the prior art FASTQ format and</p> <p>7 the prior art FASTA format; correct?</p> <p>8 A. I think that this is indicating that the</p> <p>9 steps line up with the boxes, with the arrows --</p> <p>10 Q. Uh-huh.</p> <p>11 A. -- between the boxes. I think that's what</p> <p>12 this is indicating.</p> <p>13 Q. Right. And so whatever "remove base</p> <p>14 qualities" is, it's a description of how you</p> <p>15 convert a FASTQ into a FASTA; correct?</p> <p>16 A. That seems like a reasonable explanation.</p> <p>17 As far as I know, a FASTA does not include base</p> <p>18 qualities.</p> <p>19 Q. And what are base qualities?</p> <p>20 A. Those are characters in the file that</p> <p>21 describe the accuracy of the base calls or the</p> <p>22 letters, the A, Cs, Gs, and Ts in that file.</p> <p>23 Q. And just to be clear, that's not alignment</p> <p>24 information. The reads are unaligned. The base</p> <p>25 quality is how good a read is this; correct?</p>	<p style="text-align: right;">Page 101</p> <p>1 contig in step 2; correct?</p> <p>2 A. Yes.</p> <p>3 Q. We then see that contig made from the</p> <p>4 unaligned raw reads being aligned to the reference</p> <p>5 genome in step 3; correct?</p> <p>6 A. That's correct.</p> <p>7 Q. We then see the generation of an indexed</p> <p>8 reference, which is how does the contig compare to</p> <p>9 the reference genome in terms of where on the</p> <p>10 genome is it and how are they different from each</p> <p>11 other, if at all; correct?</p> <p>12 A. No. I think that that step is referring</p> <p>13 to something that has to happen before you can use</p> <p>14 BWA-short on the read data. BWA-short is an</p> <p>15 algorithm that takes a reference genome as an input</p> <p>16 and a set of reads as another input.</p> <p>17 Q. Right.</p> <p>18 A. But reference genome has to be converted</p> <p>19 into something called an index first.</p> <p>20 Q. Got it.</p> <p>21 A. So I think what this diagram is showing is</p> <p>22 that those contigs had to be turned into an index</p> <p>23 before they could be used as a reference genome for</p> <p>24 BWA-short.</p> <p>25 Q. Okay. And then at the top of -- well,</p>

<p style="text-align: right;">Page 102</p> <p>1 strike that.</p> <p>2 I want to make sure I understand the way</p> <p>3 the diagram works.</p> <p>4 What the flow chart is showing us is that</p> <p>5 the FASTQ data becomes a FASTA file, then a contig,</p> <p>6 then a .sam file, then a FASTA file again, and then</p> <p>7 it goes back up to the top and it gets rejoined</p> <p>8 with the FASTQ data to become a BAM file; correct?</p> <p>9 A. I think the diagram is a little confusing,</p> <p>10 actually, because that step 4, "Generate an indexed</p> <p>11 reference," I don't think the output of that</p> <p>12 indexing process would be a FASTA file.</p> <p>13 Q. I was going to ask that next.</p> <p>14 Generally what this is trying to show us</p> <p>15 is that the raw reads get converted into a</p> <p>16 contig -- strike that.</p> <p>17 Generally what this diagram is claiming is</p> <p>18 the invention or part -- I'm having a hard one</p> <p>19 here. Give me a moment. Withdrawn.</p> <p>20 We're looking at the invention disclosure</p> <p>21 for what became the '799 patent; correct?</p> <p>22 A. Yes.</p> <p>23 Q. And we're looking at a flow chart that</p> <p>24 attempts to summarize the algorithm of the '799</p> <p>25 patent; correct?</p>	<p style="text-align: right;">Page 104</p> <p>1 Q. Well, to be -- to be fair, the</p> <p>2 algorithm -- the patent goes on to then claim using</p> <p>3 genotyping.</p> <p>4 So I -- I don't mean it in -- you know</p> <p>5 what? Let -- I -- that's -- that's a fair answer,</p> <p>6 and we're going to come to that.</p> <p>7 Withdrawn.</p> <p>8 Step 6 of this diagram within the</p> <p>9 invention disclosure for the '799 patent is to</p> <p>10 genotype; correct?</p> <p>11 A. That's correct.</p> <p>12 Q. The input to that genotyping process is</p> <p>13 shown as being a BAM file; correct?</p> <p>14 A. That's correct.</p> <p>15 Q. And the output is shown as being a .vcf</p> <p>16 file; correct?</p> <p>17 A. That's correct.</p> <p>18 Q. And a .vcf file is one of the file formats</p> <p>19 that was known in the prior art as the output from</p> <p>20 a genotype caller -- a variant caller; correct?</p> <p>21 A. That's correct.</p> <p>22 Q. And, again, you don't purport to have</p> <p>23 invented the VCF file format or the BAM file format</p> <p>24 or any particular variant calling software as part</p> <p>25 of the '799 patent; correct?</p>
<p style="text-align: right;">Page 103</p> <p>1 A. Yes.</p> <p>2 Q. And what it is showing us is raw unaligned</p> <p>3 reads are combined to form a contig. That contig</p> <p>4 is aligned to the reference genome to see how the</p> <p>5 contig differs, if at all, from the genome and</p> <p>6 where it aligns; and then that information is</p> <p>7 combined with the raw reads again to interpret how</p> <p>8 do the raw reads align to the reference genome and</p> <p>9 how are they different than the reference genome,</p> <p>10 if at all; correct?</p> <p>11 A. I think at a high level that summary is</p> <p>12 correct, yes.</p> <p>13 Q. And all of the steps that precede the</p> <p>14 genotyping step are steps that result in a BAM</p> <p>15 file; correct?</p> <p>16 A. Those steps result in a number of files,</p> <p>17 but a BAM file is one of them. And the BAM file</p> <p>18 would -- would reflect the output of that final</p> <p>19 alignment step.</p> <p>20 Q. So one way of encoding the output of the</p> <p>21 '799 patent algorithm is as a BAM file; correct?</p> <p>22 A. I would need to review the '799 patent. I</p> <p>23 don't know if that's -- I can't remember if that's</p> <p>24 where the algorithm ends that's claimed in that</p> <p>25 patent.</p>	<p style="text-align: right;">Page 105</p> <p>1 MR. PEPE: Object to form.</p> <p>2 Q. Go ahead.</p> <p>3 A. We don't purport to have invented the VCF</p> <p>4 file format.</p> <p>5 I would consider the overall algorithm to</p> <p>6 be a variant calling algorithm.</p> <p>7 Q. Let's look at the patent together. It's</p> <p>8 Exhibit 2.</p> <p>9 A. Okay.</p> <p>10 Q. I want you to look at first column 5?</p> <p>11 A. Okay.</p> <p>12 Q. You'll see in the middle of column 5 sort</p> <p>13 of lower middle, a section called "Brief</p> <p>14 Description of the Drawings."</p> <p>15 A. Yes.</p> <p>16 Q. No. 1 says (as read):</p> <p>17 "Figure 1 is a diagram of methods of the</p> <p>18 invention."</p> <p>19 Do you see that?</p> <p>20 A. I do.</p> <p>21 Q. Let's go look at figure 1 together. Flip</p> <p>22 back a few pages.</p> <p>23 A. Okay.</p> <p>24 Q. Do you see here a -- a different flow</p> <p>25 chart?</p>

<p style="text-align: right;">Page 106</p> <p>1 A. I do.</p> <p>2 Q. You'll notice on the left that each of the</p> <p>3 six items in the flow chart has a number assigned</p> <p>4 to it.</p> <p>5 You see those?</p> <p>6 A. I do.</p> <p>7 Q. And I will represent -- and we'll look</p> <p>8 together -- that the patent from time to time</p> <p>9 refers to each of these steps by these numbers.</p> <p>10 Do you know where the numbers came from?</p> <p>11 Like why it's 101, 105 as opposed to 102?</p> <p>12 A. (Witness reviews document.)</p> <p>13 I think I could review the patent and tell</p> <p>14 you.</p> <p>15 Q. Okay. If you see something along the way</p> <p>16 that -- we're going to go through a fair bit of the</p> <p>17 patent. So if you see something along the way, let</p> <p>18 me know. But why don't we start by looking at</p> <p>19 column 12 together.</p> <p>20 A. Okay.</p> <p>21 Q. It says at around line 34 (as read):</p> <p>22 "Figure 1 is a diagram of methods of the</p> <p>23 invention. Methods include obtaining 101 sequence</p> <p>24 reads and assembling 105 then into a contig, which</p> <p>25 is then aligned 109 to a reference. Differences</p>	<p style="text-align: right;">Page 108</p> <p>1 A. -- and in that case you're not obtaining a</p> <p>2 nucleic acid sample.</p> <p>3 Q. Okay. Let's look at column 5, line 60.</p> <p>4 It says (as read):</p> <p>5 "Nucleic acid in a sample can be any</p> <p>6 nucleic acid, including, for example, genomic DNA</p> <p>7 in a tissue sample, cDNA amplified from a</p> <p>8 particular target in a laboratory sample, or mixed</p> <p>9 DNA from multiple organisms."</p> <p>10 Do you see that there?</p> <p>11 A. I do.</p> <p>12 Q. And I want you to look now at column 9.</p> <p>13 A. Okay.</p> <p>14 Q. And specifically at line 52 where it says</p> <p>15 (as read):</p> <p>16 "After any processing steps (for example,</p> <p>17 obtaining, isolating fragmenting, or</p> <p>18 amplification), nucleic acid can be sequenced</p> <p>19 according to certain embodiments of the invention."</p> <p>20 You see that there?</p> <p>21 A. I do.</p> <p>22 Q. I want you to just run your eyes along</p> <p>23 columns -- this section of the patent from column</p> <p>24 5, line 60 to column 9, line 54 -- or 55, wherever</p> <p>25 that ends, and look at the description of how one</p>
<p style="text-align: right;">Page 107</p> <p>1 are identified by comparison 113. The raw reads</p> <p>2 are aligned 117 to the contigs and positional and</p> <p>3 variant information is mapped to the reads from the</p> <p>4 reference via the contig allowing genotyping 121 to</p> <p>5 be performed."</p> <p>6 You see that there?</p> <p>7 A. I do.</p> <p>8 Q. That paragraph is using the numbers in</p> <p>9 figure 1; correct?</p> <p>10 A. Yes.</p> <p>11 Q. Does it do anything to trigger a</p> <p>12 recollection as to why those were the numbers?</p> <p>13 A. No, it doesn't.</p> <p>14 Q. Okay. I want to walk through where the</p> <p>15 patent talks about each of the steps of the method.</p> <p>16 So let's start in column 5, the detailed</p> <p>17 description.</p> <p>18 A. Okay.</p> <p>19 Q. Okay. Will you agree with me that in</p> <p>20 order to obtain reads you have to first start with</p> <p>21 a nucleic acid sample?</p> <p>22 A. I -- maybe. I think -- I mean, you</p> <p>23 could -- you could go to the internet and download</p> <p>24 reads --</p> <p>25 Q. True.</p>	<p style="text-align: right;">Page 109</p> <p>1 goes about obtaining nucleic acid samples for</p> <p>2 purposes of carrying out the invention as</p> <p>3 described.</p> <p>4 Take a minute to just look at those</p> <p>5 sections.</p> <p>6 A. (Witness reviews document.) Okay.</p> <p>7 Q. All right. Have you had an opportunity to</p> <p>8 look at the parts of the '799 patent that are</p> <p>9 between column 5, line 60 where it begins talking</p> <p>10 about nucleic acid, and column 9, line 55 where it</p> <p>11 stops talking about nucleic acids?</p> <p>12 A. Yes, I have.</p> <p>13 Q. And is it fair to say that everything in</p> <p>14 that section of the patent, from column 5, line 60</p> <p>15 to column 9, line 55, was known in the prior art?</p> <p>16 MR. PEPE: Object to form.</p> <p>17 A. I haven't had a chance to review that.</p> <p>18 I -- I don't think I can say that after scanning</p> <p>19 all of that text.</p> <p>20 Q. Is there anything that you think you</p> <p>21 invented about nucleic acid preparation as part of</p> <p>22 the invention of the '799 patent?</p> <p>23 MR. PEPE: Same objection.</p> <p>24 A. I don't -- I don't think so. I'm not sure</p> <p>25 I understand your question.</p>

<p style="text-align: right;">Page 138</p> <p>1 the court reporter's. 2 VIDEO OPERATOR: Let's go off the record. 3 We're now going off the record at 12:50 p.m. 4 (Whereupon the deposition recessed at 5 12:50 p.m.) 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25</p>	<p style="text-align: right;">Page 140</p> <p>1 if you feed it ten times as much information, it 2 would take 100 times as long. 3 Q. So let's look at the '799 patent again, 4 Exhibit 2 to your deposition, and let's look at 5 column 2 together. 6 A. Sorry. Which exhibit was that again? 7 Q. I believe the patent is Exhibit 2. 8 A. Okay. 9 Q. It is, yes. 10 A. And what column? 11 Q. Column 2. And remember the columns start 12 after the drawings. 13 A. Right. Okay. 14 Q. Okay. There's a section in column 2 15 entitled "Summary." 16 You see that there? 17 A. Yes. 18 Q. And you know from your experience as an 19 inventor on patents that that section is generally 20 at a high level a summary of the invention claimed 21 in the patent; correct? 22 A. Yes. 23 Q. I'd like to direct you to lines 39ish in 24 that paragraph, the words at the right side say, 25 "By assembling."</p>
<p style="text-align: right;">Page 139</p> <p>1 AFTERNOON SESSION (1:39 p.m.) 2 VIDEO OPERATOR: This is the beginning of 3 media 3. We're now going back on the record at 4 approximately 1:40 p.m. 5 Go ahead, sir. 6 Q. Welcome back, Doctor Porreca. 7 I'd like to talk to you about something 8 called computational tractability. Have you ever 9 heard of the terms computational tractability 10 before? 11 A. Yes. 12 Q. And what, generally, is your understanding 13 of what computational tractability is? 14 A. When I hear that I think about the idea 15 that there are algorithms that, because of the way 16 they're designed, can take so long to run on large 17 datasets that they're impractical to use. 18 Q. The math is too hard or too -- 19 A. It's not that the math is too hard. It's 20 that the -- usually what happens is the number of 21 times the computer has to cycle through something 22 grows much faster than the amount of input data 23 coming in. 24 So, you know, if you feed it twice as much 25 information, it would take four times as long. And</p>	<p style="text-align: right;">Page 141</p> <p>1 Do you see that? 2 A. I do. 3 Q. It says (as read): 4 "By assembling reads into contigs or 5 contigs as well as aligning the individual reads to 6 the contigs, the need to compare each of the reads 7 to all of the others is avoided, providing 8 computational tractability." 9 Do you see that there? 10 A. I do. 11 Q. And is it your view that one of the 12 advantages of the '799 algorithm is that it is more 13 computationally tractable than the methods that it 14 improves upon? 15 A. I think that's an element, yes. 16 Q. And that's one advantage of it -- 17 A. Yeah. 18 Q. -- correct? Okay. 19 Why would you -- strike that. 20 In the prior art methods that the '799 21 algorithm is being compared to here it talks about 22 the need to compare each of the reads to all of the 23 others. 24 You see that? 25 A. I do.</p>

<p style="text-align: right;">Page 142</p> <p>1 Q. Why would you compare each of the reads to 2 all of the other reads in the prior art methods? 3 MR. PEPE: Object to form. 4 Q. You can answer. 5 A. I think that this is getting at the idea 6 that when the assembly is done here the assembly is 7 not performed on all of the reads from the 8 experiment. It's only performed on the -- the 9 group of reads that came from a specific region in 10 the target genome. And as a result of that, you're 11 able to limit the amount of computation that's 12 required to perform the assembly. 13 My recollection is that a lot of these 14 assembly algorithms, including the one that -- that 15 we were contemplating here, the -- the runtime 16 grows exponentially with, I think, kind of the 17 number of reads or the length, the total length of 18 what's being assembled; and so by keeping that 19 narrower and performing the assembly in chunks, 20 you're able to get around that problem. 21 Q. Could we turn to the claim of -- of the 22 patent, assuming that you have a PDF version, you 23 should be able to go to the last page and then back 24 up one. I'd like you to look at the second-to-last 25 page of the exhibit.</p>	<p style="text-align: right;">Page 144</p> <p>1 The -- the '799 algorithm does not require 2 that the reads be aligned to the reference genome 3 before they are turned into contigs; correct? 4 MR. PEPE: Object to form. 5 A. It doesn't require that, and that's not -- 6 that's not how reads were being grouped prior 7 assembly. There was no alignment process 8 occurring. 9 Q. Okay. That was my understanding as well. 10 So I want to just be clear on that. 11 So -- withdrawn. 12 What happens here is (as read): 13 "A method for assembling sequence reads, 14 the method comprising" -- I want to read together. 15 Are you with me? 16 A. Uh-huh. 17 Q. (As read): 18 "...obtaining a sample comprising template 19 nucleic acid; sequencing the template nucleic acid 20 to generate a plurality of sequence reads." 21 Plurality, as you know, is a group of more 22 than one. 23 A. Yes. 24 Q. (As read): 25 "...inputting a reference genome and said</p>
<p style="text-align: right;">Page 143</p> <p>1 A. Yeah. 2 Q. All right. You're in column 26? 3 A. I am. 4 Q. What is claimed -- you see at the bottom 5 "What is claimed is" and then there's claim 1? 6 A. Yes. 7 Q. You just told us that the method of the 8 invention involves performing assembly only on a 9 group of reads that come from a specific region in 10 the target genome. 11 Where is that in claim 1? Where does it 12 tell us that? 13 MR. PEPE: Object to form. 14 A. I don't know that I said that -- that -- 15 that's something that we did when we implemented 16 it. Right. 17 Q. Okay. 18 A. And what it's saying here again -- I'm 19 no -- I'm not a patent attorney; so I could be 20 wrong, but when we say inputting a reference genome 21 in a plurality of sequencing reads, that doesn't 22 mean that every read that was generated by the 23 sequencer has to be assembled together. 24 Q. All right. So let's -- let's take that in 25 pieces.</p>	<p style="text-align: right;">Page 145</p> <p>1 plurality of sequence reads into a computer 2 system." 3 You see that? 4 A. Yes. 5 Q. (As read): 6 "...the computer system has a processor 7 coupled to nontransitory memory --" 8 You see that? 9 A. Yes. 10 Q. (As read): 11 -- "to perform the steps of: assembling a 12 contig from at least some of the plurality of 13 sequence reads." 14 A. Right. 15 Q. You see that there? 16 So let's -- let's talk about that. 17 We agree that not all of the reads need to 18 find their way into the contig. The contig can be 19 assembled from at least some of the raw reads; 20 correct? 21 MR. PEPE: Object to form. 22 A. Well, the way I interpret this is that the 23 assembly doesn't need to be performed using all of 24 the reads. 25 Q. Okay.</p>

Page 324

1 DEPONENT'S ERRATA SHEET
2 AND SIGNATURE INSTRUCTIONS
3
4
5 The original of the Errata Sheet has
6 been delivered to Mitchell Matorin, Esq.
7 When the Errata Sheet has been
8 completed by the deponent and signed, a copy
9 thereof should be delivered to each party of record
10 and the ORIGINAL delivered to Eric Stone, Esq., to
11 whom the original deposition transcript was
12 delivered.

17 After reading this volume of your
deposition, indicate any corrections or changes to
18 your testimony and the reasons therefor on the
Errata Sheet supplied to you and sign it. DO NOT
19 make marks or notations on the transcript volume
itself.

Page 325

1 Commonwealth of Massachusetts
2 Middlesex, ss.
3
4
5 I, P. Jodi Ohnemus, Notary Public
6 in and for the Commonwealth of Massachusetts,
7 do hereby certify that there came before me
8 (remotely) on the 28th day of April, 2023, the
9 deponent herein, who was duly sworn by me; that the
10 ensuing examination upon oath of the said deponent
11 was reported stenographically by me and transcribed
12 into typewriting under my direction and control;
13 and that the within transcript is a true record of
14 the questions asked and answers given at said
15 deposition.

11 I FURTHER CERTIFY that I am neither
attorney nor counsel for, nor related to or
12 employed by any of the parties to the action
in which this deposition is taken; and, further,
13 that I am not a relative or employee of any
attorney or financially interested in the outcome
14 of the action.
15

IN WITNESS WHEREOF I have hereunto set my
16 hand and affixed my seal of office this
30th day of April, 2023, at Waltham.

Patricia Jode Okemus

P. Jodi Ohnemus, RPR, RMR, CRR,
CSR, Notary Public,
Commonwealth of Massachusetts
My Commission Expires:
3/3/2028

EXHIBIT 3

UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

INVITAE CORPORATION,

)

)

Plaintiff,

)

Case No. 21-cv-669-GBW

)

**HIGHLY CONFIDENTIAL –
ATTORNEY’S EYES ONLY**

v.

)

)

NATERA, INC.

)

)

Defendant.

)

)

INVITAE CORPORATION,

)

)

Case No. 21-cv-01635-GBW

)

**HIGHLY CONFIDENTIAL –
ATTORNEY’S EYES ONLY**

Plaintiff,

)

v.

)

)

NATERA, INC.

)

)

Defendant.

)

)

**OPENING EXPERT REPORT OF MICHAEL METZKER, PH.D. REGARDING
INVALIDITY OF U.S. PATENT NOS. 10,604,799; 11,155,863; AND 11,149,308**

185. Craig (2008)³⁹⁷ describes a generalized framework for multiplexed resequencing of targeted regions of the human genome on the Illumina Genome Analyzer using degenerate indexed DNA sequence barcodes ligated to fragmented DNA prior to sequencing.³⁹⁸

186. Craig (2008) describes attaching barcode sequences to template nucleic acid and assigning the reads to subsets based on the barcode sequences, including attaching barcode sequences to template nucleic acid during sequencing so that multiple samples can be sequenced at once and then demultiplexed, meaning the resulting sequence reads can be grouped by the samples from which they were generated.³⁹⁹

O. Wiseman (2009)

187. Wiseman (2009)⁴⁰⁰ describes pyrosequencing of complementary DNA–PCR amplicons as a general approach to determine specific genotypes in nonhuman primates.⁴⁰¹

188. Wiseman (2009) describes grouping reads into subsets based on their barcode sequences and assembling contigs using those barcodes.⁴⁰²

IX. SECTION 101 Analysis

189. Counsel have informed me that there is a two-step test for distinguishing patent claims that claim patent-ineligible laws of nature, natural phenomena, and abstract ideas from those that claim patent-eligible applications of those concepts. Step One asks whether the patent claims are directed to ineligible subject matter. If the claims are drawn to ineligible subject matter, then at step two the question is whether the claims include an inventive concept sufficient to transform the claim into a patent-eligible application. Where the additional features recite nothing more than well-understood, routine, or conventional activity, the patent claims directed to an ineligible subject matter remain patent-ineligible. I have also been informed and understand that the typical question at Step One for computer-related claims is whether the claims are directed to an improvement to computer functionality versus being directed to an abstract idea.

190. I have been asked to analyze whether the asserted patent claims satisfy the requirements for patentability under 35 U.S.C § 101.

A. Invalidity of the '799 Patent Under Section 101

191. In my opinion, the Asserted Claims are directed to an abstract idea, and do not add anything more than well-known, routine, and conventional steps to that abstract idea.

192. In particular, the Asserted Claims are directed to the abstract idea of organizing and comparing genomic data. These data are derived from sequencing biological material, which is then translated into data and analyzed within a computer. The methods for organizing

³⁹⁷ Produced as NTRA-INV-T-00001151.

³⁹⁸ See Craig (2008) at 887.

³⁹⁹ *Id.*

⁴⁰⁰ Produced as NTRA-INV-T-00001151.

⁴⁰¹ See Wiseman (2009), produced as NTRA-INV-T-00009951, at 1322.

⁴⁰² *Id.* at 1322, 1327.

and comparing genomic data recited in the Asserted Patents could even be done by hand or visually, although doing so would not be practically feasible given the sheer volume of data obtained in genomic bioinformatic methods. For example, one could use an integrative genomic viewer (“IGV”) to visually inspect how and where sequences of genomic data differ.⁴⁰³ The Asserted Patents identify this method as being within the prior art.⁴⁰⁴

193. The claimed methods themselves simply recite a particular algorithm—a compilation of steps—for carrying out the claimed methods for organizing and comparing genomic data. The claims do not recite unique technological hardware or software for carrying out this algorithm, and the results obtained from the algorithm for organizing and comparing the data are inherent in the properties of the biological material that is sequenced or used to create the reference genome. For example, whether any mutations or differences between two sequences are present is due not to the algorithm but to whether biological material itself contains a mutation or errors due to the sequencing process.

194. I also understand that the Court made a ruling early in this case where it held that Claim 1 of the ’799 patent, as being representative of the asserted patent claims for purposes of analyzing Section 101, was not directed to an abstract idea at Step One, but rather “to a specific solution to a technological problem in the field of sequence assembly. The claimed process enables the identification of mutations with positional accuracy in a computationally tractable manner.”⁴⁰⁵

195. I respectfully disagree with the Court’s assessment. In my opinion, the Asserted Claims merely use the computer as a tool to implement an abstract idea, rather than being directed to a technological improvement itself. Facts now in evidence that were not available to the Court at the time, including deposition testimony of a named inventor of all three Asserted Patents, Dr. Gregory Porreca, and Invitae’s bioinformatics scientists, Dr. Joshua Paul and Dr. Andrea Velenich, support my opinion that the Asserted Claims are not directed to eligible subject matter. Dr. Porreca testified that the invention claimed in the Asserted Patents is “an algorithm for making genotype calls” that could be used with “commercially available genotyping software.”⁴⁰⁶ In other words, the ’799 Patent claims merely recite applying algorithms to two data sets in order to obtain a new form of that same data. Dr. Joshua Paul, who is the former Head of Bioinformatics at Invitae, testified that that the method described in the Asserted Patents to combine outputs of two sets of alignments (contigs:reference and reads:contigs to yield reads:reference) was “a high level, philosophical approach to the problem” and that the method, as described, was not “sufficiently specific to make any assessment on what the outcome would be.”⁴⁰⁷ Dr. Andrea Velenich, who is a Principal Bioinformatics Scientist at Invitae, testified that the Asserted Claims contain only “a very high-level description of the method” for the claimed invention.⁴⁰⁸

⁴⁰³ See Robinson *et al.*, *Integrative genomics viewer*, NATURE BIOTECHNOLOGY 9:24-26 (2011) (“Robinson (2011)”).

⁴⁰⁴ E.g., ’799 Patent at 20:22–31; Robinson (2011).

⁴⁰⁵ D.I. 128 at 4.

⁴⁰⁶ Porreca Dep. Tr. at 57:3–58:2; *see also id.* at 66:12–70:4; 92:24–97:19, 110:1–137:16.

⁴⁰⁷ Paul Dep. Tr. at 66:21–67:10, 67:20–68:3.

⁴⁰⁸ Velenich Dep. Tr. at 95:3–95:9.

196. In fact, the claimed method could be and was performed manually, such as in Morin (2011) Supplemental Information:

Reads from the individual RNA-seq libraries were assembled using ABySS as previously described using multiple values of k. Iterative pairwise alignments of the contigs from the individual kmer assemblies resulted in a merged contig set that was aligned against the reference Human genome (hg18) using BLAT as described. Putative fusions were identified from contigs that had alignments to two distinct genomic locations. The putative events were filtered using evidence from alignment of reads to contigs using Bowtie and alignments of reads to the genome using BWA. Those events with at least four read pairs from the reads-to-genome alignment and two supporting reads from the reads-to-contig alignment (i.e., across the fusion breakpoint) were manually curated to produce a final list of putative fusions. The genomic breakpoints for the transcriptome predicted events were identified manually from the alignments of the reads to the genome using IGV. The genomic breakpoints were later confirmed by assembly using ABySS and these results are summarized in Supplementary Table S3.

Putative indels were identified from alignment of the contigs to hg18 using BLAT when contiguous unmatched base(s) were found in either the contig (insertion) or reference (deletion) sequences. The events were filtered for read support with events requiring three or more reads to be considered in the filtered set. The filtered set was then screened against dbSNP130 to find putative novel events. **The resulting set was manually inspected using read alignments (against both the genome and contigs) to visually confirm candidates. This approach revealed the deletion in GNA13 shown in Supplementary Figure. S4.**

The splicing alterations in MLL2 (Fig. 3B and C) and GNA13 (Supplementary Figure S4) were identified from pairwise alignments of the contigs to hg18 using BLAT. The contig alignments were then matched against the four known gene models to identify novel splice junctions. The putative novel splice junctions were filtered where two or more reads were required across the novel junction for the event to be considered. **Manual inspection using read alignments (against both the genome and contigs) was performed to visually confirm candidates.**⁴⁰⁹

197. Morin (2011) Supplemental Information discloses the steps of assembly, alignment, and combining information from alignments to identify putative mutations, as described *supra* at Section VIII.H. Morin (2011) Supplemental Information discloses manually performing the step in which mutations are identified and genotyping is performed: “The resulting set was manually inspected using read alignments (against both the genome and contigs) to visually confirm candidates. This approach revealed the deletion in GNA13 shown in Supplementary Fig. S4. . . . Manual inspection using read alignments (against both the genome and contigs) was performed to visually confirm candidates.”⁴¹⁰

198. As Morin (2011) Supplemental Information demonstrates, the final “combining” step of Claim 1 of the ’799 Patent could be and was performed manually. Morin (2011)

⁴⁰⁹ Morin (2011) Supplemental Information at 13–14 (internal citations omitted) (emphases added).

⁴¹⁰ *Id.*

discloses that once one has obtained an assembled contig, a contig:reference alignment, and read:contig alignments, all of which, the Asserted Patents explain, are done using prior-art methods, one could simply look at each alignment and compare them to one another to identify the variants as they exist in the reads relative to the reference genome. The alleged inventors of the Asserted Patents have done nothing more than claim an automated version of a simple visual comparison of data. As discussed *supra*, merely applying a generic computer to the patent-ineligible abstract idea of data manipulation does not render the claimed invention patent-eligible. This supports my opinion that the Examiner's withdrawal of the rejection of the '891 Application under Section 101 was mistaken. While the Applicant argued to the Examiner the impossibility of assembling and comparing millions of reads by hand, Invitae argued to the court, and the court agreed, that the claims encompass assembly and alignment of just two reads.⁴¹¹ Further, under the Court's claim construction, the claimed method covers any "plurality of sequence reads,"⁴¹² *i.e.*, even a very small number of reads. It is my opinion that the computational steps of the claimed method can be performed manually, without a computer, if the number of sequence reads is small enough. As an example, if the "plurality of sequence reads" includes only a few reads, one of ordinary skill in the art would have known how to perform the steps of the claimed method by hand, without the use of a computer, which supports my opinion that the addition of the use of a computer to the claimed method did not render the claims patent-eligible.

199. The prosecution history of the Asserted Patents also supports my opinion that the claims are directed to an abstract idea. The Examiner rejected the claims for non-statutory double-patenting over U.S. Patent Nos. 8,209,130 ("130 Patent") and 8,738,300 ("300 Patent").⁴¹³ In response, rather than contending that the Asserted Patents are patentably distinct from those two prior patents, the Applicant filed a terminal disclaimer.⁴¹⁴

200. The only difference between the independent claims of the '130 Patent and the '799 Patent is that the Applicant added limitations requiring that the claimed method be performed using a generic computer. By issuing a non-statutory double patenting rejection, the Examiner made the determination that the performance of the claimed method using a computer was an obvious variation of the algorithm itself, *i.e.*, the computer requirements do not add any patentable weight to the claim. This further supports my opinion that the District Court wrongly determined that the Asserted Claims of the '799 Patent are patent eligible. In my opinion, it cannot be the case that the alleged invention improves the functioning of a computer itself, if the performance of the claimed invention using a computer is patentably indistinct from the performance of the claimed invention without the use of a computer. This opinion is further supported by the fact that Dr. Porreca himself testified that the Asserted Patents, as well as the '130 Patent, are all "versions of the GATA algorithm," and that "they're all reflecting the same underlying idea."⁴¹⁵

201. Further, I have reviewed the Asserted Patents, their common specification, and the prosecution history of the patents, and I do not find any support for the alleged improvement

⁴¹¹ *Id.* at Invitae0000002461–0000002465; D.I. 84 at 16–19.

⁴¹² '799 Patent, Cl. 1.

⁴¹³ *See* Invitae0000000001 at Invitae0000002450, 2454–2455.

⁴¹⁴ *Id.* at Invitae0000002335.

⁴¹⁵ Porreca Dep. Tr. at 158:1–159:8.

in computational tractability provided by the Asserted Claims. For example, the Asserted Claims themselves do not recite any precise methods for *how* sequences should be assembled or aligned against each other. Even at the outset of the claims, where some or all of the sequence reads are to be assembled into contigs, the claims do not explain what methods, mathematics, or algorithms should be used to determine precisely which reads should be assembled into contigs. Such precise detail would, at a minimum, be a necessary (but not sufficient) requirement for a process that “enables the identification of mutations with positional accuracy in a computationally tractable manner.” Further, I have found no evidence to support the assertion that the claimed methods provide for a more computationally tractable method for assembling sequences. The claims on their face and in light of the specification simply reflect the abstract idea of how genomic data can be organized and compared. Any potential benefit of greater positional accuracy or computational tractability is entirely hypothetical and would, at best, be due to the abstract idea reflected in the claims itself, rather than any claim elements related to how this abstract idea-algorithm is applied or implemented in a computer. The testimony of Dr. Porreca supports my opinion that the Asserted Claims do not claim any improvement in computational tractability. Dr. Porreca testified that when the assembly is performed on “the group of reads that came from a specific region in the target genome,” the user is “able to limit the amount of computation that’s required to perform the assembly,”⁴¹⁶ but the Asserted Claims do not require that the assembly be performed only on a group of reads from a specific region in the target genome. Rather, the Asserted Claims require only “assembling a contig from at least some of the plurality of sequence reads.”⁴¹⁷ In other words, Dr. Porreca’s assertion about what makes the claimed method more computationally tractable than methods in the prior art is nowhere in the Asserted Claims.

202. The Patent Office examiner rejected draft claims that set forth special hardware or software for carrying out the claimed methods on the basis that these claims were not supported by the written description for the patents.⁴¹⁸ I believe this is further evidence of the fact that, even to the extent the Asserted Claims in theory enable greater positional accuracy or computational tractability, that property is not a technological improvement but simply a theoretical efficiency of the algorithm itself. There is no data or evidence in the Asserted Patents, or in the record of this case as far as I am aware, that the claimed methods of the Asserted Patents, without more, result in an improvement to computer functionality. The Asserted Patents also repeatedly make reference to the use of well-known, prior art methods for performing each of steps of the claimed algorithm. The Examiner eventually withdrew the Section 101 rejection on the ground that the claimed method could not be performed in the human mind.⁴¹⁹ In my opinion, the Examiner was mistaken, because the Asserted Claims merely use the computer as a tool to implement an abstract idea, which could be performed manually, such as through comparing sequences by manual inspection, as described *infra*.

203. In my opinion, nothing significantly more is claimed in the Asserted Patents because the Asserted Claims do not recite any inventive concept that is not an abstract idea. The ’799 Patent admits that every other feature of the claimed method other than the abstract idea

⁴¹⁶ Porreca Dep. Tr. at 141:3–142:20.

⁴¹⁷ ’799 Patent, Cl. 1.

⁴¹⁸ See Invitae0000000001 at Invitae0000002450, Invitae0000002454– Invitae0000002455.

⁴¹⁹ *Id.* at Invitae0000002477.

itself was well understood, routine, and conventional. Aside from the algorithmic steps of assembling, aligning, and combining data, the only limitations left are “obtaining” a sample comprising DNA and “sequencing” the DNA to generate the sequence reads. Therefore, the ’799 Patent merely claims an abstract idea applied to well understood, routine, and conventional elements.

204. The ’799 Patent specifies that both of the steps of “obtaining” a sample comprising DNA and “sequencing” the DNA to generate sequence reads were conventional and well known in the art. The ’799 Patent describes that it was well-understood in the prior art how to obtain a DNA sample,⁴²⁰ and does not purport to improve on the prior art in this regard. The ’799 Patent also states that DNA-sequencing can be accomplished “by any method known in the art,”⁴²¹ and recounts the many established DNA-sequencing techniques that could be employed to practice the claims,⁴²² while not purporting to have advanced that prior art at all. The Asserted Claims do not explain or show how sequence data comparison is improved, except by using already-existing computer and sequencing technology.

205. The ’799 Patent states that sequence reads and a reference genome are input into an standard, general-purpose computer system,⁴²³ to perform the steps of:

- a. assembling a contig from at least some of those sequence reads, using any method known in the art⁴²⁴;
- b. aligning the contig to the reference genome to create contig:reference descriptions of mutations, “using any suitable computer program known in the art,”⁴²⁵;
- c. aligning the sequence reads to the contig using methods known in the art to create read:contig descriptions,⁴²⁶; and
- d. combining the contig:reference “descriptions” with the read:contig “descriptions” to produce read:reference “descriptions,”⁴²⁷ to map positional and variant information of mutations found in the individual reads relative to the reference genome.⁴²⁸

206. As the Asserted Claims read in light of the specification demonstrate, all of the methods described in the specification for obtaining a DNA sample, sequencing the DNA, assembling the DNA into contigs, aligning the contigs to the reference genome, aligning the sequence reads to the contig, and describing positional and variant information produced by performing a DNA alignment are routine and conventional methods that were well understood in

⁴²⁰ *E.g.*, ’799 Patent at 5:60–63; 6:16–18, 6:30–36,

⁴²¹ ’799 Patent at 9:56.

⁴²² *Id.* at 9:56–67; 10:5–12:23

⁴²³ ’799 Patent at 2:65–3:42, 12:33–34, FIG. 2.

⁴²⁴ *Id.* at 13:4–16:29, FIG. 1 (step 105), FIG. 2 (step 1)

⁴²⁵ *Id.* at 19:11–13; *see also id.* at 16:54–17:3, 20:35–39, FIG. 1 (steps 109, 113), FIG. 2 (step 2).

⁴²⁶ *Id.* at 20:54–21:11, FIG. 1 (step 117), FIG. 2 (step 3)

⁴²⁷ *Id.* at 21:18–21, FIG. 2 (step 4),

⁴²⁸ *Id.* at 21:22–24; *see generally* ’799 Patent, Cl. 1; ’863 Patent, Cl. 1; ’308 Patent, Cl. 1, 20.

the art.

207. The '799 Patent allegedly teaches a novel choice of which data to compare and the order in which to compare them. The other steps of the method described in the patent are well understood, routine, and conventional, as the '799 Patent explicitly directs the skilled artisan to use unimproved, prior-art DNA sequencing equipment to determine the nucleotide sequence of the sample, and to use unimproved, prior-art hardware and software to generate sequence reads and contigs and to align them to the reference genome. The only thing allegedly new is the abstract idea of the order in which to compare those data.

208. Even if the Asserted Claims achieved the purported solution of providing a novel choice of which data to compare and the order in which to compare them, the Asserted Claims only use generic functional language to do so and require nothing other than conventional computer and network components operating according to their ordinary functions (*e.g.*, “a computer processor,” “a computer program,” “any traditional assembly algorithm,” etc.).

209. Although the Asserted Claims include “parameters,” the claims fail to specify precisely what the parameters *are*, and the parameters at most concern abstract data manipulation—alignment of DNA sequences relative to one another. The '799 Patent itself confirms that the invention is meant to utilize “existing computer power,”⁴²⁹ and nothing in the Asserted Claims, understood in light of the specification, requires anything other than off-the-shelf, conventional computer, sequencing, assembly, and alignment technology and algorithms for performing comparisons between sequence data and presenting the desired information.

210. In my opinion, the dependent Asserted Claims are also ineligible for patenting. The dependent Asserted Claims all proceed from the same abstract idea: an algorithmic method of manipulating and combining genetic sequence data using an intermediate data set.

211. The dependent Asserted Claims all recite the same well understood, routine, conventional steps of obtaining a DNA sample and sequencing it. The dependent Asserted Claims also all require a generic computer to perform the algorithmic method. Some of the Asserted Claims specify a particular prior-art DNA-sequencing technique,⁴³⁰ and/or math or algorithm, which is itself an abstract idea,⁴³¹ or require the identification of one or more naturally occurring mutations based on the math work.⁴³² Neither the Asserted Claims nor the specification explain what the claimed parameters are or how they should be manipulated, and do not appear to be more than manipulating data in such a way that is abstract.⁴³³

212. None of the dependent Asserted Claims adds an inventive concept because the dependent Asserted Claims do nothing more than limit the application of the abstract idea to specific conventional, routine operations, which does not render the dependent Asserted Claims patent-eligible. Therefore, for the same reasons why Claim 1 of the '799 Patent is directed to patent-ineligible subject matter, the dependent Asserted Claims are also directed to a patent-

⁴²⁹ '799 Patent at 4:52–57.

⁴³⁰ '799 Patent, Cl. 2–5, 13, 14.

⁴³¹ '799 Patent, Cl. 3, 4, 6, 7, 15, 16.

⁴³² '799 Patent, Cl. 8–12.

⁴³³ '799 Patent, Cl. 15–16.

ineligible abstract idea.

213. Thus, it is my opinion that the Asserted Claims of the '799 Patent do not claim a patent-eligible invention. The inventors of the '799 Patent claim to have discovered that information from DNA datasets—reads and contigs—can be compared and combined using existing, prior-art computers and software into a new form that is better than prior-art analyses. That is not a patentable invention. It is, at best, an improved abstract idea. It is my opinion that nothing about the patent claims adds an inventive concept sufficient to save the claims.

B. Invalidity of '308 and '863 Patents Under Section 101

214. The '863 and '308 Patents—both continuations of the '799—largely repeat the limitations of the '799 Patent claims. It is my understanding that the parties agree that Claim 1 of each of the '799, '308, and '863 Patents are representative.⁴³⁴

215. It is my opinion that the Asserted Claims of the '308 and '863 Patents have the same patent-eligibility problems as the '799 Patent described *supra*.

216. Like Claim 1 of the '799 Patent, the independent Asserted Claims of the '308 and '863 Patents are generally directed to methods of organizing and comparing genomic data using a computer. The additional limitations and dependent Asserted Claims in the '308 and '863 Patents are also ineligible for patenting. The Asserted Claims all proceed from the same abstract idea: an algorithmic method of manipulating and combining genetic sequence data using an intermediate data set. The dependent Asserted Claims all recite the same well understood, routine, conventional steps of obtaining a DNA sample and sequencing it. And the dependent Asserted Claims all require a generic computer to perform the algorithmic method.

217. Some of the additional limitations and dependent Asserted Claims recited in the '308 and '863 Patents specify a particular prior-art DNA-sequencing technique and/or algorithm, which is itself abstract⁴³⁵), or require the identification of one or more naturally occurring mutations based on the math work.⁴³⁶ But none of additional elements or dependent Asserted Claims them adds an inventive concept. Rather, the dependent Asserted Claims do nothing more than limit the application of an abstract idea to specific conventional, routine operations. For the same reasons that the independent Asserted Claims of the '308 and '863 Patents are directed to a patent-ineligible abstract idea, the dependent Asserted Claims are also patent-ineligible.

218. It is my opinion that, like the Asserted Claims of the '799 Patent, the Asserted Claims of the '308 and '863 Patents merely recite methods for analyzing and comparing digital information extracted from DNA, which is an abstract idea. The purported novelty of both the '308 and '863 Patents remains aligning contigs to the reference genome and reads to contigs. There is no change to either (a) the basic steps of obtaining a DNA sample, sequencing it, and inputting sequence data into a computer, or (b) assembling the reads into contigs, aligning the contigs to the reference genome, aligning the reads to the contig, and combining these two alignments. No new laboratory processes for preparing the genetic sample for analysis are claimed, and no new, unconventional, or non-routine steps are claimed to perform the

⁴³⁴ See Case No. 1:21-cv-00669, D.I. 1, ¶ 15; Case No. 1:21-cv-01635, D.I. 1, ¶¶ 16–17.

⁴³⁵ '863 Patent, Cl. 2–6, 9; '308 Patent, Cl. 2–4, 15–19.

⁴³⁶ '863 Patent, Cl. 7, 8; '308 Patent, Cl. 5–14.

computerized analyses. The only differences between the independent Asserted Claims of the '308 and '863 Patents and Claim 1 of the '799 Patent are (i) the addition of prior-art steps in the sequencing process and (ii) superficial elaboration on the ineligible abstract idea at the core of the '799 Patent claims.

219. The Asserted Claims of the '308 and '863 Patents do not add anything to render the claimed inventions any more patent-eligible. The Asserted Claims each add limitations that fall into three categories, none of which can confer patent eligibility: (i) limitations that are known in the art according to the patents' common specification, *i.e.*, methods for sequencing DNA, methods for sequencing DNA,⁴³⁷ methods for aligning those sequences,⁴³⁸ and methods for storing those alignments on a computer;⁴³⁹ (ii) additional abstract ideas, *i.e.*, specific mathematical algorithms for analyzing the sequences; and (iii) both natural phenomena and elements known in the art, *i.e.*, types of genetic material to analyze and types of mutations to detect.

220. None of the limitations added by the Asserted Claims of the '308 and '863 Patents transforms the claims into an improvement to computer functionality. Adding prior-art limitations on how to prepare the DNA for sequencing (the "attaching the fragments . . ." and "amplifying . . ." limitations) do not qualify as a technological improvement and are conventional and routine.⁴⁴⁰ The data comparison methods claimed are nothing but unpatentable abstract ideas.

221. The Asserted Claims of the '308 and '863 Patents do not recite any improvement in the functionality or operation of a computer, but instead involve using prior-art, unimproved hardware and prior-art, unimproved software and invoke generic computers as tools.⁴⁴¹ The limitations added by the Asserted Claims of the '308 and '863 Patents do not alter the claims' essential character of using a computer as a tool to perform an abstract idea. The Asserted Claims do not change or improve anything about the computer itself, the dependent Asserted Claims simply include more detail on what the user instructs the generic computer to do.

222. Instead of identifying a potentially patentable specific improvements in the capabilities of a computer, the '863 Patent identifies only a desirable result or function that can be achieved using existing computers. The Asserted Claims do not describe improvements to the way computers store information or otherwise function, but instead merely rely on their ordinary storage and transmission capabilities and apply that ordinary functionality in the specific context of comparing sequence data. Thus, even if the data comparisons of the '863 Patent had the incidental benefit of freeing up the prior-art computer processor to perform more computations, that would not make the data comparison itself anything other than an unpatentable abstract idea.

223. No other limitations—individually or as an ordered combination and apart from those embodying the ineligible subject matter itself—establish an inventive concept that transforms the abstract idea into patent eligible subject matter. The alleged invention of

⁴³⁷ '799 Patent at 9:56–67; 10:5–12:23.

⁴³⁸ *Id.* at 19:11–20:21

⁴³⁹ *Id.* at 20:43–48.

⁴⁴⁰ *E.g.*, '308 Patent at 15:11–16:32; 17:65–18:64; 19:12–20:23; 21:36–22:16.

⁴⁴¹ '308 Patent at 13:23–16:38; 16:56–20:32; 20:50–64; '863 Patent at 13:26–16:34; 16:59–20:27; 20:49–56.

combining the contig-based sequence assembly approach with an individual alignment base sequence assembly approach is the abstract idea at the core of the alleged invention.

224. The additional limitations found in the Asserted Claims of the '308 and '863 Patents merely describe well understood, routine, and conventional elements and techniques. Indeed, the other steps of the method are well understood, routine, and conventional, as the '308 and '863 Patents explicitly direct the skilled artisan to use unimproved, prior-art DNA sequencing equipment to determine the nucleotide sequence of the sample, and to use unimproved, prior-art hardware and software to generate sequence reads and contigs and to align them to the reference genome. Like for the '799 Patent, the only thing allegedly new that is claimed in the '308 and '863 Patents is the abstract idea of the order in which to compare those data.

225. Aside from the algorithmic steps of assembling, aligning, and combining data, the only limitations left are “obtaining” a sample comprising DNA and “sequencing” the DNA to generate the sequence reads. But the '308 and '863 Patents admit that both of those steps were conventional and well known in the art. The '308 and '863 Patents devote over a column of text to recycling the prior art about how to obtain a DNA sample,⁴⁴² and do not purport to improve on the prior art in this regard. Likewise, the shared Asserted Patent specification states that DNA-sequencing can be accomplished “by any method known in the art,”⁴⁴³ and recounts the many established DNA-sequencing techniques that could be employed to practice the claims,⁴⁴⁴ while not purporting to have advanced that prior art at all.

226. The added limitations found in the Asserted Claims of the '308 and '863 Patents add superficial elements to the algorithmic steps of the '799 Patent’s process, but, as discussed *supra*, the common specification acknowledges that these elements, too, are routine and conventional.

227. The '308 Patent adds no new elements outside the limitations describing the analysis of digital information. The Asserted Claims simply repackage the invention of the '799 Patent, adding only statistical formulae—*i.e.*, a token elaboration on the ineligible abstract idea itself. *See* '610 application.

228. The '863 Patent adds, in Claim 1, (i) “amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the template nucleic acid in one of the channels in the flow cell” and (ii) “attaching the fragments to a surface of channels in a flow cell.” But, these elements are routine and conventional and add nothing inventive to the claimed invention.⁴⁴⁵

⁴⁴² *E.g.*, '799 Patent at 5:60–63, 6:16–18, 6:30–36; '308 Patent at 5:60–63; 6:16–18, 6:30–36; '863 Patent at 5:60–63, 6:16–18

⁴⁴³ *Id.* at 9:56

⁴⁴⁴ *E.g.*, *id.* at 9:56–67; 10:5–12:23

⁴⁴⁵ '587 Appl., ¶ 37 (“The amplification reaction may be any amplification reaction known in the art that amplifies nucleic acid molecules, such as polymerase chain reaction, nested polymerase chain reaction, polymerase chain reaction-single strand conformation polymorphism, ligase chain reaction.”) (emphasis added); '587 Appl., ¶ 53 (“Another example of a sequencing

229. For at least these reasons, it is my opinion that all of the Asserted Claims are directed to an abstract idea and do not add an inventive concept.

X. SECTIONS 102 AND 103 ANALYSIS

230. In **Appendix A**, I set forth a chart showing the references and combinations of references for each of the Asserted Claim. My analysis of those references and combinations is below.

231. As I state throughout my Report, I believe the written description of the Asserted Patents and their prosecution histories support my opinions about the invalidity of the Asserted Claims, and I cite to them as part of my analysis. These citations and analysis are not meant to suggest that it is my opinion that the disclosures of the Asserted Patents, and their prosecution histories, themselves would provide one of ordinary skill in the art with a particular motivation or reasonable expectation of success in achieving the claimed invention based on the prior art. As I discuss throughout my Report, the prior art itself provides such motivations and reasonable expectation of success. However, the Asserted Patents provide additional support for my opinions that one of ordinary skill would have had, based on the prior art, the pertinent motivations, as well as knowledge, disclosures, and basis, for forming a reasonable expectation of successfully achieving the claimed invention, and I believe that one of ordinary skill would have applied that existing knowledge within the context of developing a sequence assembly and alignment process or technique.

A. HaploTypeCaller (2011) Anticipates and/or Renders Obvious All Asserted Claims

232. It is my understanding that Invitae accuses Natera's use of an implementation of Mutect2, Sentieon's TNseq software, of infringing the Asserted Claims.⁴⁴⁶ I further understand from GATK documentation, Invitae's infringement contentions, and conversations with Dr. Banks and Mr. Poplin that the particular functions Invitae accuses of infringement are the same in Mutect2 and HaploTypeCaller.

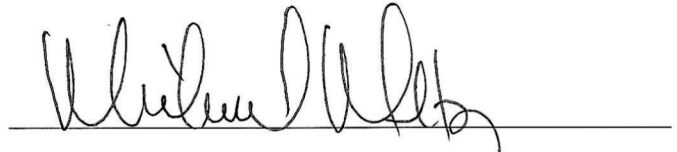
233. It is my opinion that if Sentieon's alleged implementation of Mutect2 is found to infringe any Asserted Claim, HaploTypeCaller (2011) invalidates that claim because it was invented and used before the earliest alleged priority date of the Asserted Claims, September 27, 2011. I have been informed and understand that a product that would infringe the Asserted Claims if developed after their priority date anticipates the Asserted Claims if developed earlier. My opinions on the invalidity of the Asserted Claims in light of HaploTypeCaller (2011) are consistent with Invitae's infringement contentions. Nothing in this opinion should be construed as any admission or opinion on any issues of infringement.

technology that can be used in the methods of the provided invention is Illumina sequencing. Illumina sequencing is based on the amplification of DNA on a solid surface using fold-back PCR and anchored primers. Genomic DNA is fragmented, and adapters are added to the 5' and 3' ends of the fragments. mDNA fragments that are attached to the surface of flow cell channels are extended and bridge amplified." (emphasis added)).

⁴⁴⁶ See *Plaintiff Invitae Corporation's Final Infringement Contentions*, dated December 19, 2022 ("Final Infringement Contentions"); see also at Final Infringement Contentions, Appendix A; Final Infringement Contentions, Appendix B; Final Infringement Contentions, Appendix C.

I declare under penalty of perjury that the foregoing is true and correct.

Dated: June 16, 2023



Michael L. Metzker Ph.D.

EXHIBIT 4

UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

INVITAE CORPORATION,

)

)

Plaintiff,

)

Case No. 21-cv-669-GBW

)

**HIGHLY CONFIDENTIAL –
ATTORNEY’S EYES ONLY**

v.

)

)

NATERA, INC.

)

)

Defendant.

)

)

INVITAE CORPORATION,

)

)

Plaintiff,

)

Case No. 21-cv-01635-GBW

)

**HIGHLY CONFIDENTIAL –
ATTORNEY’S EYES ONLY**

v.

)

)

NATERA, INC.

)

)

Defendant.

)

)

)

REPLY EXPERT REPORT OF MICHAEL METZKER, PH.D. REGARDING
INVALIDITY OF U.S. PATENT NOS. 10,604,799, 11,155,863, AND
11,149,308

VI. SECTION 101 ANALYSIS

32. I have been asked by counsel for Natera to respond to Dr. Krane's opinions about my analysis of the validity of the Asserted Claims under Section 101.⁸⁷

33. Counsel has informed me that there is a two-step test for distinguishing patent claims that claim patent-ineligible laws of nature, natural phenomena, and abstract ideas from those that claim patent-eligible applications of those concepts. Step One asks whether the patent claims are directed to an ineligible subject matter. If the claims are drawn to an ineligible subject matter, then at Step Two, the question is whether the claims include an inventive concept sufficient to transform the claim into a patent-eligible application. Where the additional features recite nothing more than well-understood, routine, or conventional activity, the patent claims directed to an ineligible subject matter remain patent-ineligible. I have also been informed and understand that the typical question at Step One for computer-related claims is whether the claims are directed to a technological improvement to the computer functionality extending beyond improving the accuracy of a mathematically calculated statistical prediction, versus being directed to an abstract idea such as simply computerized mathematical calculations.

34. I incorporate by reference my analysis of the invalidity of the Asserted Claims under Section 101 from the Metzker Op. Report.⁸⁸ It is my opinion that the Asserted Claims do not satisfy the requirements for patentability under 35 U.S.C. § 101 because the Asserted Claims are directed to an abstract idea, and do not add anything more than well-known, routine, and conventional steps to that abstract idea.

A. Invalidity of the '799 Patent Under Section 101

⁸⁷ See Krane Reb. Report at Section IX.

⁸⁸ See Metzker Op. Report at Section IX.

35. Nothing in the Krane Reb. Report alters my conclusion that the Asserted Claims are directed to abstract data manipulation—alignment of DNA sequences relative to one another—using a generic computer and prior art sequencing, assembly, and alignment technology and algorithms to perform comparisons between sequences and present the desired information.⁸⁹

36. Dr. Krane and I disagree on the correctness of the Court’s prior Section 101 ruling.⁹⁰ For the reasons explained in the Metzker Op. Report and herein, I respectfully disagree with the Court’s assessment of the validity of the Asserted Patents under Section 101.⁹¹ In particular, additional information, including deposition testimony of one of the inventors and Invitae’s claim construction arguments, that was not available to the Court at the time of its Section 101 ruling confirms that the Asserted Claims are directed to an abstract idea (computer data manipulation) for detecting a natural phenomenon (mutations in nucleic acid sequences) using routine and conventional methods, and are therefore invalid under Section 101.

37. Dr. Krane contends that the claimed methods could not be performed by hand or visually and asserts that the claimed method has “the benefits of reduced computational requirements and increased accuracy,” but never explains what it is about the claimed method that gives it these benefits.⁹² Dr. Krane also asserts that I stated in the Metzker Op. Report that it is “impossible” to perform the claimed method visually or by hand.⁹³ Dr. Krane is mistaken. In

⁸⁹ *Id.*

⁹⁰ *See* Krane Reb. Report at ¶¶ 113, 118, 120; *see also* Metzker Op. Report at ¶¶ 194–195.

⁹¹ *See* Metzker Op. Report at ¶¶ 194–195.

⁹² *See* Krane Reb. Report at ¶ 114.

⁹³ *Id.*, citing to the Metzker Op. Report at ¶ 192. Dr. Krane mischaracterizes “impossible” with my statement that “doing so would not be practically feasible.”

the Metzker Op. Report, I explained that performing the claimed method by hand with a very large number of reads might “not be practically feasible,” not that doing so was impossible. In fact, performing genotyping by visual inspection is possible if the number of sequence reads being compared is small enough. I also explained in the Metzker Op. Report that Morin (2011) performs the “combining” step of the claimed method by visual analysis.⁹⁴ Dr. Krane misreads Morin (2011), appearing to suggest that Morin (2011) only discloses aligning sequence reads directly to a reference genome,⁹⁵ but Morin (2011) also discloses the steps of the claimed method.⁹⁶ That is, Morin (2011) discloses generating a read:reference alignment by first aligning contigs to a human reference genome and also aligning the sequence reads to those contigs, using those alignments to visually confirm candidate indels, as well as performing the other steps of the Asserted Claims.⁹⁷ My Op. Report, which is incorporated herein by reference, contains my analysis of why, in light of Morin (2011) and the other references I detail therein, the Asserted Claims do not teach a “completely new alignment” over the prior art,⁹⁸ contrary to Dr. Krane’s assertion.⁹⁹

38. To rebut my analysis concerning whether the claimed method can be performed visually or manually, Dr. Krane asserts that “a POSITA, reading the claims and the specification, would understand the patent claims are not directed to a small set of sequence reads.”¹⁰⁰ I

⁹⁴ See Metzker Op. Report at ¶¶ 196–198.

⁹⁵ See Krane Reb. Report at ¶¶ 121–122.

⁹⁶ See Metzker Op. Report at Sections IX.A, X.H; *see also* Morin (2011) Supplemental Information at 13–14.

⁹⁷ *Id.*

⁹⁸ See Metzker Op. Report at Section X.H; *see generally id.* at Section X.

⁹⁹ See Krane Reb. Report at ¶ 123.

¹⁰⁰ *Id.*

disagree. I note that this also appears to be inconsistent with Invitae’s attorneys’ arguments during the claim construction proceedings, where Invitae’s counsel stated that the Asserted Claims encompass performing the method using any number of sequence reads.¹⁰¹ Regardless, the Asserted Claims of the ’799 Patent do not specify or require a large number of reads, nor do they specify the length of the sequence reads. Moreover, Dr. Krane stops short of asserting that the claimed method improves on the prior art by rendering feasible the alignment of millions of reads. Instead, the Krane Reb. Report asserts that the Examiner correctly allowed the Asserted Claims to issue because “the length of the reference genome” makes it difficult to perform the claimed alignment method by hand.¹⁰² The Krane Reb. Report does not argue that performing the allegedly inventive step of combining contig:reference and read:contig alignment information to yield read:reference alignments is impossible to perform manually, nor can Dr. Krane, because that is exactly what Morin (2011) discloses.¹⁰³ Assuming for the sake of argument that Dr. Krane meant that because the length of the reference genome,¹⁰⁴ it is impossible to perform the contig:reference alignment by hand, that does not alter my conclusion that the Asserted Claims are directed to the abstract idea of organizing and comparing genomic data. Fundamentally, what is claimed is still the abstract idea of comparing sequences using a generic computer and prior art sequencing, assembly, and alignment technology and algorithms. Moreover, as acknowledged by the Asserted Patents, it was known in the art to align contigs to a reference

¹⁰¹ See D.I. 72 at 31, 44–45; see also D.I. 84 at 9–10.

¹⁰² See Krane Reb. Report at ¶ 124 (citing Invitae0000000001–0000002508 at Invitae0000002477).

¹⁰³ See Metzker Op. Report at ¶¶ 196–198.

¹⁰⁴ See Krane Reb. Report at ¶ 124 (citing Invitae0000000001–0000002508 at Invitae0000002477).

genome,¹⁰⁵ and therefore, that limitation cannot provide the inventive concept required under Section 101.

39. Further, even if it is the case that performing genotyping visually or manually is more error-prone than doing it with a computer, the proposition that a computer can perform a mathematical operation more accurately than a human can perform the same mathematical operation by hand is not a remarkable proposition. Dr. Krane asserts but does not explain how “[t]he inventions of the Asserted Patents improve the reliability of sequence assembly”¹⁰⁶ as compared with the visual genotyping method used in Morin (2011), other than by employing a generic computer to perform the steps of the claimed method. As I opined in the Metzker Op. Report, applying a generic computer to perform an abstract idea without claiming any technological improvement on the process of comparing sequence alignment information, as the Asserted Patents do, does not render the underlying abstract idea of data comparison patent-eligible.¹⁰⁷

40. In response to my analysis that the Asserted Claims do not recite any technological improvement in computational tractability nor precise methods for how sequences should be assembled or aligned against each other,¹⁰⁸ Dr. Krane asserts that the Asserted Claims need not recite the advantages of the invention in order to be patent-eligible.¹⁰⁹ I have been informed by counsel and understand that a patent need not recite the advantages of the invention in the claims themselves, but an invention’s advantages are distinct from the invention itself,

¹⁰⁵ See ’799 Patent at 1:38–2:6.

¹⁰⁶ See Krane Reb. Report at ¶ 114.

¹⁰⁷ See Metzker Op. Report at ¶¶ 192–193, 195, 201–204, 206–209.

¹⁰⁸ *Id.* at ¶ 201.

¹⁰⁹ See Krane Reb. Report at ¶ 126.

which must still pass muster under the two-step inquiry. As described in the Metzker Op. Report, the problem with the Asserted Claims is not that they fail to recite the advantages of the invention, but rather that the Asserted Claims do not claim an invention that results in an inventive technological improvement over the prior art.¹¹⁰ Further, Dr. Krane asserts that my analysis “oversimplif[ies] the claimed invention as a combination of alignments,”¹¹¹ but this contradicts Dr. Krane’s own opinions in the sections of his report dealing with the analysis of the Asserted Claims under Sections 102 and 103, wherein he refers repeatedly to the “two-step alignment” of the claimed method as what is missing from the prior art and what makes the Asserted Claims “novel and inventive.”¹¹² Regardless, as I previously explained, merely combining data and presenting it in a different form is not inventive.¹¹³

41. Dr. Krane and I agree that Dr. Porreca testified that prior art methods can be used to perform certain steps of the claimed methods.¹¹⁴ The Krane Reb. Report, however, overlooks the importance of Dr. Porreca’s testimony that the invention claimed in the Asserted Patents is “an algorithm for making genotype calls” that can be used with “commercially available genotyping software.”¹¹⁵ Dr. Porreca’s testimony directly supports my opinion that the Asserted Claims are directed to an abstract idea: an algorithm for obtaining and combining data from two sets of alignments (contigs:reference and reads:contigs) to identify mutations or differences.

¹¹⁰ See Metzker Op. Report at ¶¶ 195, 202, 220. As I acknowledged in the Metzker Op. Report, the specification of the Asserted Patents does recite the alleged advantages of the invention over the prior art. *E.g.*, ’799 Patent at 1:44–67, 2:1–6.

¹¹¹ See Krane Reb. Report at ¶ 124.

¹¹² See Krane Reb. Report at ¶¶ 182, 238, 337, 342, 514, 813, 1022, 1248, 1334.

¹¹³ See Metzker Op. Report at ¶¶ 201–209.

¹¹⁴ See Krane Reb. Report at ¶ 118; Metzker Op. Report at ¶ 195.

¹¹⁵ See Porreca Dep. Tr. at 57:3–58:2; *see also id.* at 65:12–70:4; 92:24–97:19, 110:1–137:16; Metzker Op. Report at ¶ 195.

Those individual steps can be performed using prior art methods of obtaining a nucleic acid sample, sequencing nucleic acids, assembling the sequence reads, and performing alignments.¹¹⁶ Rather than identify any supposed technological improvement claimed by the Asserted Patents, the Krane Reb. Report relies on the Court’s prior determination that the claims are patent-eligible under Section 101, with which I respectfully disagree. Neither the Court nor Dr. Krane states what the “practical technological improvements” the Asserted Claims recite,¹¹⁷ because there are none.

42. The Krane Reb. Report misses the point that the Asserted Claims recite only an algorithm for manipulating sequence data.¹¹⁸ It is not my opinion that the mere fact that the claims are “algorithmic” necessarily renders them patent-ineligible. To the contrary, I have been informed and understand that the Asserted Claims are patent-ineligible under Section 101 if they are directed to an abstract idea and merely invoke the use of a generic computer without reciting any inventive concept or technological improvement.¹¹⁹ Here, that abstract idea is an algorithmic method for manipulating sequence data. Invoking a computer as a tool to implement an abstract idea does not render the underlying abstract idea a technological improvement over the prior art, as previously explained.¹²⁰ In other words, it is not the quality of the claimed method as being “algorithmic” that renders the Asserted Claims patent-ineligible, but rather that the Asserted Claims are directed to an abstract idea without reciting any technological improvement.

¹¹⁶ See Metzker Op. Report at ¶¶ 195, 204–206.

¹¹⁷ See Krane Reb. Report at ¶ 118; D.I. 28 at 6.

¹¹⁸ See Krane Reb. Report to Metzker at ¶¶ 115, 127.

¹¹⁹ See Metzker Op. Report at ¶¶ 192–193, 195, 201–204, 206–209.

¹²⁰ See Metzker Op. Report at ¶¶ 200–202.

43. Dr. Krane seems to suggest that the testimonies of Drs. Paul and Velenich are irrelevant. I disagree. For example, the Krane Reb. Report summarizes Dr. Paul as being “familiar with the high-level operations of how variant callers work, but not the details,”¹²¹ and Dr. Velenich as being “insufficiently familiar with the inner workings of callers such as HaplotypeCaller.”¹²² Based on Drs. Paul and Velenich’s testimonies, the Krane Reb. Report asserts that these statements are “an endorsement of the inventiveness of the Asserted Claims” because they understand how the Asserted Claims “work at a high level.”¹²³ The Krane Reb. Report takes these statements out of context. For example, Dr. Krane ignores the fact that Drs. Paul and Velenich were each answering the question of whether the Asserted Claims, as written, contained enough detail for one of ordinary skill in the art to have understood how it works and perform the claimed method. Moreover, Dr. Paul and Velenich each answered that question in the negative. Dr. Paul testified that the Asserted Claims are a “high level, philosophical approach to the problem” for which it would be “a leap” to make “any statement about quality” as an improved method of variant-calling.¹²⁴ Dr. Velenich made the same conclusion, testifying that the Asserted Claims were a “high level description of the method” that lacked “implementation details” necessary to perform the claimed method.¹²⁵ It is of no matter that Drs. Paul and Velenich testified that they are unfamiliar with the inner workings of different variant callers, particularly in light of the fact that both appear to meet the qualifications of one of ordinary skill in the art under my and Dr. Krane’s proposed definitions.

¹²¹ See Krane Reb. Report at ¶ 119, citing to Paul Dep. Tr. at 68:5–19.

¹²² *Id.*, citing to Velenich Dep. Tr. at 93:13–18.

¹²³ *Id.* at ¶ 119.

¹²⁴ See Paul Dep. Tr. at 66:21–67:10.

¹²⁵ See Velenich Dep. Tr. at 94:13–95:8.

44. The Krane Reb. Report asserts that “the applicant correctly argued that the sequence reads were transformed by the methods, and thus not an abstract idea.”¹²⁶ Here, the Krane Reb. Report is referencing the file history wherein the Applicant argued that the method transforms sequence reads, which are “not directly readable as the subject’s genome” when they come off the sequencer, into something usable, *i.e.*, a contig aligned to a reference genome.¹²⁷ Dr. Krane ignores that the Court construed the term “sequence reads” to mean “raw reads as generated by the sequencing instrument.”¹²⁸ In fact, the Krane Op. Report argues that Natera infringes the Asserted Claims even though Signatera uses as an input reads that have been pre-aligned to a reference genome in the form of a BAM file.¹²⁹ In light of these statements, it appears that Dr. Krane views the claimed method as the same whether it is performed with reads as they come off the sequencer (*i.e.*, raw reads) or with aligned reads (*i.e.*, pre-processed or pre-aligned). Yet, the Krane Reb. Report appears to assert that the claimed method “transform[s]” sequence reads in some way.¹³⁰ If the use of pre-aligned reads to perform the claimed method is equivalent to the use of sequence reads as they come off the sequencer, it cannot be that the claimed method “transforms” the sequence reads in any manner. This reinforces my conclusion that the Asserted Claims are directed to a patent-ineligible abstract idea of sequence read data manipulation without any technological improvement.

45. The Krane Reb. Report references the prosecution history of the Asserted Claims

¹²⁶ See Krane Reb. Report at ¶ 12.

¹²⁷ See Invitae0000000001–0000002508 at Invitae0000002335–0000002338.

¹²⁸ See D.I. 84; D.I. 85.

¹²⁹ See, *e.g.*, Krane Op. Report at ¶¶ 80–87.

¹³⁰ See Krane Reb. Report at ¶ 12.

to say that finding them valid was a “condition of their issuance.”¹³¹ Dr. Krane, however, fails to rebut my analysis concerning how the prosecution history supports my conclusion that the Asserted Claims are not patent-eligible. Further, as discussed in the Metzker Op. Report, the Applicant filed a terminal disclaimer in response to a non-statutory double-patenting rejection over the ’130 Patent—showing the Examiner thought the claimed method is nothing more than an obvious variation of the high-level algorithm, to which the computer requirements added nothing of patentable weight—rather than contend the ’799 Patent was patentably distinct from the ’130 Patent.¹³² This demonstrates that the use of a computer added nothing of patentable weight to the Asserted Claims. Dr. Porreca’s testimony that the Asserted Patents and the ’130 Patent are all “versions of the GATA algorithm”¹³³ further supports this conclusion, which the Krane Reb. Report does not dispute.¹³⁴

46. The Krane Reb. Report also misconstrues my analysis regarding the inherent properties of the biological material.¹³⁵ My opinion is that the Asserted Claims are directed to an abstract idea that uses prior art methods to detect mutations or differences that are inherent in the properties of the biological material that is sequenced or used to create the reference genome.¹³⁶ Further, it is my understanding that, contrary to the Krane Reb. Report’s suggestion otherwise, the Court did not “reject[]” any argument that the Asserted Claims are directed to inherent

¹³¹ *Id.* at ¶ 110.

¹³² *See* Metzker Op. Report at ¶¶ 199–200.

¹³³ *See* Porreca Dep. Tr. at 158:1–159:8.

¹³⁴ *See* Metzker Op. Report at ¶ 200.

¹³⁵ *See* Krane Reb. Report at ¶ 116.

¹³⁶ *See* Metzker Op. Report at ¶ 193.

properties of biological material.¹³⁷ As I have been informed by counsel, neither party made such an argument in connection with the Court’s earlier decision on Section 101.¹³⁸

47. The Krane Reb. Report simply disagrees with my analysis of the dependent claims “for the reasons stated for the independent claims.”¹³⁹ Obviously, Dr. Krane does not challenge my conclusions that the dependent claims all proceed from the same abstract idea claimed in the independent claims, also require a generic computer to perform the algorithmic method, and only limit the abstract idea to the use of particular prior art methods.¹⁴⁰

B. Invalidity of the ’308 and ’863 Patents Under Section 101

48. Dr. Krane’s cursory rebuttal to my analysis of the invalidity of the ’308 and ’863 Patents under Section 101 lacks any substantive response to my analysis that the Asserted Claims of the ’308 and ’863 Patents are directed to an abstract idea and do not recite an inventive concept.¹⁴¹

49. In particular, the Krane Reb. Report fails to rebut my analysis demonstrating that nothing about the additional limitations and dependent claims of the ’308 and ’863 Patents renders them patent-eligible over the ’799 Patent.¹⁴² As I explain in detail in the Metzker Op. Report, the additional limitations and dependent claims recited in the ’308 and ’863 Patents do not add an inventive concept, but rather merely limit the application of an abstract idea to specific conventional, routine operations.¹⁴³ Dr. Krane asserts, without elaboration, that “the

¹³⁷ See Krane Reb. Report at ¶ 117.

¹³⁸ See D.I. 28.

¹³⁹ See Krane Reb. Report at ¶ 128.

¹⁴⁰ See Metzker Op. Report at ¶¶ 210–213.

¹⁴¹ See Krane Reb. Report at ¶¶ 130–131.

¹⁴² See Metzker Op. Report at ¶¶ 215–229.

¹⁴³ *Id.*

Asserted Claims of the '308 and '863 Patents are, as described for the '799 Patent, patent eligible and do not suffer from any of the alleged shortcomings Dr. Metzker offers in his opinion.”¹⁴⁴

Nowhere does the Krane Reb. Report explain why the Asserted Claims of the '308 and '863 Patents “do not suffer from any of the alleged shortcomings” I identified in the Metzker Op. Report or why “the dependent claims do add further inventive concepts.”¹⁴⁵

50. In particular, the Krane Reb. Report makes no attempt to respond to my conclusion that the independent Asserted Claims of the '308 and '863 Patents recite the same abstract idea of an algorithmic method of manipulating and combining genetic sequence data.¹⁴⁶ This is because the independent Asserted Claims of the '308 and '863 Patents do not change the basic steps of the method claimed in the '799 Patent nor recite any new methods of sample preparation or analysis that are unconventional or non-routine steps to perform the computerized analysis.¹⁴⁷ The Krane Reb. Report does not rebut my conclusion that the only differences between then independent Asserted Claims of the '308 and '863 Patents and the '799 Patent are (i) the addition of prior art methods and (ii) non-substantive elaboration on the abstract idea claimed in the '799 Patent.¹⁴⁸ Dr. Krane also does not refute that the limitations added in the '308 and '863 Patents merely recite prior art methods of sequencing a nucleic acid sample, aligning those sequences, storing those alignments on a computer, and analyzing those alignments using specific mathematical algorithms, and describe natural phenomena and

¹⁴⁴ See Krane Reb. Report ¶ 131.

¹⁴⁵ *Id.*

¹⁴⁶ See Metzker Op. Report at ¶¶ 215–229.

¹⁴⁷ *Id.*

¹⁴⁸ *Id.*

elements known in the art.¹⁴⁹ The Krane Reb. Report also does not respond to my conclusion that the added limitations of the Asserted Claims of the '308 and '863 Patents do not claim any improvement to computer functionality but instead recite only conventional and routine steps using prior art, unimproved hardware and prior art, unimproved software invoking generic computers as tools.¹⁵⁰

51. In the Krane Reb. Report, Dr. Krane spends a single sentence responding to my analysis that the dependent Asserted Claims of the '308 and '863 Patents are also patent-ineligible, saying only that “the dependant [*sic*] claims do add further inventive concepts.”¹⁵¹ The Krane Reb. Report makes no effort to say what “further inventive concepts” Dr. Krane alleges the dependent Asserted Claims of the '308 and '863 Patents add,¹⁵² or to respond to my conclusion that the dependent claims simply add known elements regarding how a generic computer is to perform the claimed method for comparing sequence data without describing any improvements to how a generic computer stores information or functions.¹⁵³

52. In particular, the Krane Reb. Report does not respond to my conclusion that the dependent Asserted Claims are directed to a patent-ineligible abstract idea because they recite the same well understood, routine, conventional steps of obtaining a DNA sample and sequencing it using conventional, routine, prior art methods, and require a generic computer to perform the algorithmic method.¹⁵⁴ Similarly, the Krane Reb. Report did not respond to my

¹⁴⁹ *Id.*

¹⁵⁰ *Id.* (citing to '308 Patent at 13:23–16:38; 16:56–20:32; 20:50–64; '863 Patent at 13:26–16:34; 16:59–20:27; 20:49–56.).

¹⁵¹ *See* Krane Reb. Report at ¶ 131.

¹⁵² *Id.*

¹⁵³ *See* Metzker Opening Report at ¶¶ 215–229.

¹⁵⁴ *Id.*

conclusion that the dependent Asserted Claims of the '308 and '863 Patents do not add an inventive concept because they either (i) merely limit the application of an abstract idea to specific conventional, routine operations using prior art DNA sequencing techniques and/or algorithms or (ii) require the identification of one or more naturally occurring mutations based on mathematical operations.¹⁵⁵

53. For at least the same reasons I identified in the Metzker Op. Report—reasons that the Krane Reb. Report has done little to refute—it is my opinion that all of the Asserted Claims are directed to an abstract idea and do not add an inventive concept.¹⁵⁶

VII. SECTIONS 102 AND 103 ANALYSIS

54. Nothing in the Krane Reb. Report causes me to change the opinions rendered in the Metzker Op. Report, and I incorporate those opinions herein. In this Section, I address the arguments raised by the Krane Reb. Report, and where Dr. Krane incorporates his analysis of other claims or claim limitations into his analysis of a certain claim limitation, I do, as well. I do not address the invalidity of claim limitations that the Krane Reb. Report does not dispute, as I assume that Dr. Krane agrees with my opinions. My analysis of each independent Asserted Claim applies equally to the claims depending from them. I also note that in several instances, Dr. Krane only opines that certain dependent claims are not anticipated, and does not offer any opinion, or rebuttal to the Metzker Op. Report as to obviousness of those claims.¹⁵⁷ I therefore understand that Dr. Krane's opinions as to these claims are limited to his opinion that they are not anticipated. However, in the event Dr. Krane provides an opinion as to non-obviousness, I

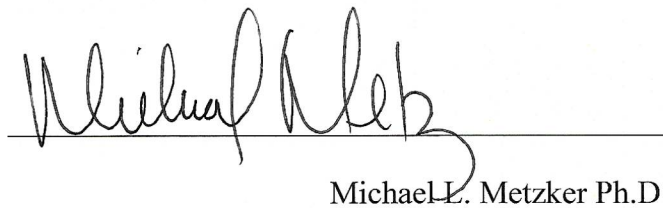
¹⁵⁵ *Id.* at ¶¶ 216–217, 221.

¹⁵⁶ *See* Metzker Op. Report at Section IX.

¹⁵⁷ *See, e.g.,* Krane Reb. Report at ¶¶ 624–625, 1042, 1044–1045, 1056–1057, 1249, 1251–1252.

I declare under penalty of perjury that the foregoing is true and correct.

Dated: August 11, 2023

A handwritten signature in black ink, appearing to read "Michael Metzker", is written over a horizontal line. The signature is fluid and cursive, with the first name "Michael" and last name "Metzker" clearly distinguishable.

Michael L. Metzker Ph.D.

EXHIBIT 5

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

INVITAE CORPORATION,

Plaintiff,

v.

NATERA, INC.

Defendant.

Case No. 21-cv-669-GBW

JURY TRIAL DEMANDED

**HIGHLY CONFIDENTIAL –
OUTSIDE ATTORNEYS’ EYES
ONLY**

INVITAE CORPORATION,

Plaintiff,

v.

NATERA, INC.

Defendant.

Case No. 21-cv-1635-GBW

JURY TRIAL DEMANDED

**HIGHLY CONFIDENTIAL –
OUTSIDE ATTORNEYS’ EYES
ONLY**

**REBUTTAL EXPERT REPORT OF DAN E. KRANE TO THE OPENING EXPERT
REPORT OF MICHAEL METZKER, PHD**

Dated: July 21, 2023

By: 

Dr. Dan E. Krane

105. Craig (2008) merely discloses using barcodes on fragmented DNA and using the wholly irrelevant Bayes factors. *Id.* Dr. Metzker's description is very specific and overreaching for the amount of information Craig (2008) actually discloses, those conclusions cannot be drawn from what Dr. Metzker has cited. Metzker Opening Report ¶ 186.

O. Wiseman (2009)

106. Wiseman (2009) discloses "pyrosequencing of complementary DNA-PCR amplicons as a general approach to determine comprehensive MHC class I genotypes in nonhuman primates." Wiseman (2009) at 1322.

107. Wiseman (2009) discloses using barcoding on amplicons and grouping those amplicons into four sets. Wiseman (2009) at 1322. It also discloses creating contigs from the amplicons, but does not disclose using the barcodes using contig construction. Wiseman (2009) at 1327.

IX. SECTION 101 ANALYSIS

108. As discussed in Section V, counsel has informed me and I understand the two-step test for determining patentable claims under Section 101. *See supra* discussion.

109. I have been asked to analyze the Asserted Claims as well as Dr. Metzker's analysis. Metzker Opening Report ¶¶ 189-213.

110. As a preliminary matter, I understand that the Asserted Claims have already been found valid under Section 101 by the USPTO as a condition of their issuance. Further, I also understand that the Court has already ruled once on the validity under Section 101 of Claim 1 of the '799 Patent, as representative of the Asserted Claims, and has also ruled that the Asserted Claims are valid under Section 101.

A. Validity of the '799 Patent Under Section 101

111. In my opinion, the Asserted Claims are not directed to an abstract idea, and, regardless, add more than well-known, routine, and conventional steps.

112. Specifically, the Asserted Claims are directed to a specific technological problem, that of assembling DNA sequences, and they explain on a specific basis how to solve this problem in a better way than existed in the prior art at the time.

113. Having reviewed Dr. Metzker's opinion as well as, with attorney assistance, the Court's earlier Section 101 ruling on Claim 1 of the '799 Patent, I do not believe Dr. Metzker raises any substantive new argument in his opinion that was not already addressed by the Court in its previous ruling, nor do I believe he provides any evidence sufficiently novel to shed a different light upon these already-litigated arguments. I agree with the Court's previous ruling. D.I. 28.

114. The Asserted Claims are directed to the concrete steps of sequence assembly, with the benefits of reduced computational requirements and increased accuracy. Dr. Metzker claims that the methods of the Asserted Patents could be done by hand or visually, but then immediately states that this is impossible. Metzker Opening Report ¶ 192. The inventions of the Asserted Patents improve the reliability of sequence assembly, and taking Dr. Metzker's visual approach only introduces more errors into the assembly.

115. Dr. Metzker first opines that the Asserted Claims recite an algorithm, and that they are invalid upon that basis. Metzker Opening Report ¶ 193. As I have been informed by Invitae's attorneys and as I understand from the Court's previous Section 101 ruling, the mere labelling of something as "algorithmic" does not preclude patent eligibility. D.I. 28 at 6 ("By contrast, here, Claim 1 *not only recites an algorithmic method* of manipulating and combining genetic sequence data..."). Nor does Dr. Metzker's opinion that the claims are invalid for "not recit[ing] unique

technological hardware or software” weigh any heavier, as Invitae described the inventions as “directed to a concrete *technique*” in its prior Section 101 briefing to the Court, and the Court agreed, ruling that the Asserted Claims “recite[] the application of the method.” *Id.* at 6.

116. Dr. Metzker then opines that the Asserted Claims claim inherent properties of biological material. Metzker Opening Report ¶ 193. As I explain further in Section X, I disagree with this opinion. *See infra*. The Asserted Patents do not claim the *existence* of mutations, but rather *an inventive and improved method for detecting them*. Dr. Metzker’s argument here conflates the two issues and amounts to opining that a patent for a new and improved type of microscope for biological samples is actually claiming every disease contained within said biological samples. As discussed throughout this Report, the claimed methods do not merely “organiz[e] and compar[e] genomic data,” the claimed methods combine methods for detecting mutations in an inventive manner, creating a new method that decreases computational requirements and increases accuracy.

117. Additionally, Dr. Metzker’s “inherent properties” opinion has also already been rejected by the Court. In its previous ruling, the Court stated that the invention “is directed to a specific solution to a technological problem in the field of sequence assembly. *The claimed process enables the identification of mutations* with positional accuracy in a computationally tractable manner.” D.I. 28 at 4.

118. Nor does the deposition testimony of Drs. Porreca, Paul, and Velenich support Dr. Metzker’s opinion, contrary to his assertions. Metzker Opening Report ¶ 195. First, his characterization of Dr. Porreca’s testimony is incorrect at best. Dr. Porreca does not describe the invention as used with commercially available genotyping software, merely that it could be used *for one particular step*, and that the invention is the entire method, which contains within it some

steps which may be performed by known algorithms. *See, e.g.* Porreca Depo at 57:11-19; 66:12–70:4; 92:24–97:19, 110:1–137:16. This line of argument, too, was already raised by Natera in its prior briefing to the Court, where it argued that the Asserted Claims simply recited “well understood, routine, and conventional elements” already known in the art. D.I. 9 at 11-12. The Court rejected this argument when it ruled that the Asserted Claims were patent eligible, noting that the Asserted Claims “recite applying the new and improved computerized methods to practical technological improvements.” D.I. 28 at 6. I see no new justification in Dr. Metzker’s report for its reconsideration now.

119. Second, Dr. Metzker’s citations to the testimony of Drs. Paul and Velenich lack context. Dr. Paul testified that he is familiar with the high-level operations of how variant callers work, but not the details. *See, e.g.* Paul Depo at 68:5-19. Thus, his answer that he understands the Asserted Claims to work at a high level which Dr. Metzker cites is in fact an endorsement of the inventiveness of the Asserted Claims to the extent of his ability to answer. Dr. Velenich gives similar testimony that she is insufficiently familiar with the inner workings of callers such as HaplotypeCaller. *See, e.g.,* Velenich Depo at 93:13-18.

120. Dr. Metzker then recites yet another already-rejected argument, that “the ’799 Patent claims merely recite applying algorithms to two data sets in order to obtain a new form of that same data.” Metzker Opening Report ¶ 195. The Court has already explained the error of this position in its previous ruling, and I see no support cited by Dr. Metzker sufficiently novel to justify revisiting this argument. D.I. 28 at 6 (“When Natera says that the claims before me are directed to *just a mathematical result* or simply involve using computers as tools rather than any improvement in computers or other technology, *I disagree.*”)

121. Dr. Metzker then references his analysis of Morin (2011). Metzker Opening Report ¶ 196. I discuss Dr. Metzker’s analysis of Morin (2011) in Section X.H, and incorporate it by reference here accordingly. *See infra*.

122. As shown in the very excerpt of Morin (2011) Supplemental Information quoted by Dr. Metzker, Morin (2011) describes little more than the prior art already acknowledged in the Asserted Patents. For instance, Morin (2011) Supplemental Information discloses read-to-reference alignments as “alignments of reads to the genome using BWA” and “at least four read pairs from the reads-to-genome alignment.” Metzker Opening Report ¶ 196. The direct alignment of reads to references to identify mutations is well established prior art as explained in, *inter alia*, the specification of the Asserted Patents themselves, as well as Invitae’s prior Section 101 briefing, which the Court ruled in favor of.

123. In contrast to Morin (2011), the Asserted Claims teach a new and inventive solution to the problem of sequence assembly involving creating a completely new alignment through the combination of the read:contig and contig:reference alignments. While the comparatively primitive process detailed in Morin (2011) was performed manually, the method of the Asserted Patents cannot be performed in the human mind. Dr. Metzker disagrees, describing a hypothetical (and *purely* hypothetical, for such a project is a gross oversimplification of the problem relative to the practical application of the method to actual sequence reads) project which involves aligning only two sequence reads. Dr. Metzker opines that in such a project, the number of sequence reads is few enough and gives a contig that is short enough that a person could, potentially, align that relatively small amount of nucleotide sequence information in some period of time. Metzker Opening Report ¶ 198. However, a POSITA, reading the claims and the specification, would

understand that the patent claims are not directed to a small set of sequence reads. See, e.g., '799 Patent at 1:28-37, 2:39-43, 9:56-12:23.

124. Additionally, even misunderstanding and oversimplifying the claimed invention as a combination of alignments, as Dr. Metzker has done, as the Examiner noted in the Reasons for Allowance, it is not the number of sequence reads that makes alignment by hand impossible, *it is the length of the reference genome*. Invitae0000002477. Even for the simplest of organisms such as *E. coli*, its genome contains between 4.5 and 5.5 million base pairs, depending on the strain being considered. For more complex organisms, such as humans, the complexity rises geometrically. For example, human chromosome 21, the *smallest* of the *twenty-three* chromosome pairs in humans and representing a mere 1.5% of the human genome, is an *order of magnitude larger* than the entire *E. coli* genome. As noted by the Examiner and misunderstood by Dr. Metzker, the claimed methods cannot be performed by hand not just because of the number of base pairs one is attempting to align, but because of the number of base pairs one is attempting to *align against*.

125. Dr. Metzker proceeds to argue that because Morin (2011) showed the “combining” step could be performed manually, because the '130 and '799 Patents differ only in that the '799 recites the use of a computer, and because the Examiner issued the '799 Patent with a terminal disclaimer, thus the '799 patent must be invalid. Metzker Opening Report ¶¶ 198-200. However, as demonstrated above, Dr. Metzker’s entire argument fails at its first step, as Morin (2011) does not, in fact, show that the methods of the Asserted Patents could be performed manually.

126. Dr. Metzker next opines that the “Asserted Claims do not claim any improvement in computational tractability,” stating that “the Asserted Claims themselves do not recite any precise methods for *how* sequences should be assembled or aligned against each other.” Metzker

Opening Report ¶ 201. However, I understand from the Court’s prior ruling that the claims themselves do not need to articulate the advantages of the claimed combinations or of the invention in order to be patent eligible. D.I. 28 at 6 (“We know from cases like *Uniloc*, as well as . . . last week’s decision *Mentone Solutions LLC v. Digi International Inc.*, . . . that ***the claims themselves do not need to necessarily articulate the advantages of the claimed combinations or of the invention in order to be patent eligible.***”) Instead, such articulation may also be found in the specification, drawings, or be inherent in the patent’s disclosure due to the skill in the art at the time.

127. Regarding Dr. Metzker’s opinion that “the Asserted Claims merely use the computer as a tool to implement an abstract idea, which could be performed manually, such as through comparing sequences by manual inspection” (Metzker Opening Report ¶ 202) I have already explained his error. *See supra* discussion of Morin (2011). Regarding his opinion that the Asserted Claims are “algorithmic” and thus invalid, as I state *supra*, I understand from the Court’s prior ruling on this topic that something being “algorithmic” does not render it unpatentable.

128. Dr. Metzker proceeds to analyze the dependent claims, and opines that they, too, are unpatentable under Section 101. Metzker Opening Report ¶ 204-12. I disagree for the reasons stated for the independent claims.

129. It is my opinion that the Asserted Claims of the ’799 Patent do claim a patent-eligible invention. The inventors of the ’799 Patent claim a novel method of sequence assembly that employs a strategy/approach that improves the computational tractability of the problem that cannot be completed by a human mind alone.

B. Validity of '308 and '863 Patents Under Section 101

130. The '863 and '308 Patents are continuations of the '799 Patent and share a common specification. It is also my understanding that the parties agree that Claim 1 of each patent is representative, as Dr. Metzker states in his report. Metzker Opening Report ¶ 214.

131. It is my opinion that the Asserted Claims of the '308 and '863 Patents are, as described for the '799 Patent, patent eligible and do not suffer from any of the alleged shortcomings Dr. Metzker offers in his opinion. *See supra* analysis. It is my opinion that none of the Asserted Claims are directed to an abstract idea and the dependant claims do add further inventive concepts.

X. SECTIONS 102 AND 103 ANALYSIS

132. I have reviewed the chart provided by Dr. Metzker as Appendix A of his Opening Report.

133. I have reviewed Dr. Metzker's opinions in his Opening Report and respectfully disagree. I do not believe the Asserted Claims or the Asserted Patents are invalid. They disclose inventions for sequence assembly and alignments that were novel at the time of the inventions. The Asserted Patents' disclosures, as well as the state of the prior art, show that this is true.

A. HaplotypeCaller (2011) Does Not Anticipate and/or Render Obvious All Asserted Claims

134. Dr. Metzker opines that the asserted claims of the Asserted Patents are anticipated by HaplotypeCaller (2011), or rendered obvious alone or in combination with information known to skilled artisans at the time of the invention and/or other references disclosed in Dr. Metzker's report, as well as common sense and the general state of the art. Metzker Opening Report ¶ 234. I disagree.

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	C.A. No. 21-669 (GBW)
)	
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	
<hr/>		
LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	C.A. No. 21-1635 (GBW)
)	
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	

**PLAINTIFF'S REPLY IN SUPPORT OF ITS MOTION *IN LIMINE* NO. 1: TO
PRECLUDE NATERA FROM CONTESTING VALIDITY UNDER 35 U.S.C. § 101**

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Dated: August 13, 2025

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Natera seeks to introduce evidence regarding patent eligibility of the Asserted Patents under §101 in an effort to persuade the Court to revisit its prior ruling on this issue. Opp. at 1.

As the Federal Circuit explained in *CardioNet, LLC v. InfoBionic, Inc.*, however, “*Alice* step one presents a legal question that can be answered based on the intrinsic evidence” and the Court’s “analysis at *Alice* step one involves examining the patent claims in view of the plain claim language, statements in the written description, and the prosecution history, if relevant.” 955 F.3d 1358, 1372-73 (Fed. Cir. 2020). This Court was not required to consider other extrinsic evidence at *Alice* step one. And unlike the court in Natera’s cited *Smartflash LLC v. Apple Inc.*, once this Court decided Natera failed *Alice* step one, there was no need to proceed to step 2.

Even if the Court were to consider extrinsic evidence, none of the evidence cited in Natera’s opposition rises to the level “extraordinary circumstances” that would require this Court to revisit its *Alice* step one ruling. See *Savvy Dog Sys., LLC v. Pennsylvania Coin, LLC*, No. 3:19-cv-01470, 2022 WL 4349829, at *5 (M.D. Pa. Sept. 19, 2022). Natera’s citation to Dr. Porreca’s testimony regarding “a computational algorithm” ignores this Court prior ruling that labelling something as “algorithmic” does not on its own preclude patent eligibility. Opp. at 2; D.I. 28 at 6 (“By contrast, here, Claim 1 not only recites an algorithmic method of manipulating and combining genetic sequence data...”). Natera’s argument regarding “computational tractability” is similarly unpersuasive as it ignores the Court’s prior ruling that the claims themselves do not need to articulate the advantages of the claimed combinations or of the invention in order to be patent eligible. Opp. at 2-3, D.I. 28 at 6 (“We know from cases like *Uniloc* . . . that the claims themselves do not need to necessarily articulate the advantages of the claimed combinations or of the invention in order to be patent eligible.”).

This Court’s prior ruling regarding patent eligibility under §101 should be upheld.

August 13, 2025

Respectfully submitted,

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CERTIFICATE OF SERVICE

I, Brian E. Farnan, hereby certify that on August 13, 2025, a copy of PLAINTIFF'S REPLY IN SUPPORT OF ITS MOTION IN LIMINE NO. 1: TO PRECLUDE NATERA FROM CONTESTING VALIDITY UNDER 35 U.S.C. § 101 was served on the following as indicated:

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EXHIBIT 19B

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-669 (GBW)
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-1635 (GBW)
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	

**PLAINTIFF'S MOTION IN LIMINE NO. 2: TO EXCLUDE EVIDENCE AND
ARGUMENT REGARDING THE PRIOR LITIGATION BETWEEN INVITAE AND
NATERA**

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Dated: February 9, 2024

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Pursuant to Federal Rules of Evidence 402, 403, and 404, Invitae moves to preclude Natera, from offering prejudicial argument, evidence, or testimony regarding the prior litigation between the parties, namely *Natera, Inc. v. ArcherDX, Inc. et al.*, C.A. No. 20-125-GWB (D. Del.) (the “prior litigation”). This includes, but is not limited to, the outcome of the jury trial or allegations that the instant case is an attempt by Invitae to retaliate against Natera for the prior litigation. Indeed, the unfair prejudice caused by allowing Natera to cast Invitae as engaging in retaliatory litigation would be great and would be counterbalanced by no probative value whatsoever.

While the parties agree that a discrete subset of the damages evidence in the prior litigation may relate to a reasonable royalty analysis in this case, all of the other issues – whether technical, equitable, business, or other – are irrelevant. The limited relevant damages evidence does not require additional surrounding prejudicial context or details to provide its full probative value. Invitae proposed the parties simply refer to the relevant damages evidence as from a previous litigation, without mention of the parties involved or circumstances. But Natera, intent on painting Invitae in a bad light, refused.

I. PRIOR LITIGATION HISTORY IS IRRELEVANT, UNFAIRLY PREJUDICIAL, AND IMPERMISSIBLY GOES TO CHARACTER

As a rule, evidence regarding litigation history and the outcome of previous lawsuits are “generally inadmissible.” *Johns Hopkins University v. Alcon Labs. Inc.*, C.A. No. 15-525, 2018 WL 4178159, at 42-43 (D. Del. Aug 30, 2018). Such evidence “has, at best, miniscule probative value, and this is significantly outweighed by the potential for confusion of the issues that would result from admission of the evidence.” *10X Genomics, Inc., et al. v. Nanostring Technologies, Inc.*, C.A. No. 21-653-MFK, D.I. 277, at 3 (D. Del. Nov 2, 2023). Even when minimal relevance exists, courts in this district still exclude litigation history evidence “as its probative value is substantially outweighed by the danger of unfair prejudice.” *AVM Technologies LLC v. Intel*

Corporation, C.A. No. 15-33-RGA, D.I. 637, at 1-2 (D. Del. Apr. 19, 2017); *see also Willis Electric Co., Ltd. v. Polygroup Limited et al.*, C.A. No. 15-3443 (JNE/DTS), D.I. 930, at 15-17 (D. Minn Jan. 5, 2024) (“Accordingly, Polygroup is precluded from presenting any evidence or argument regarding the prior lawsuits, ***even if Willis Electric references intellectual property issues***, under Federal Rules of Evidence 402, 403 and 404(b).”); *Cosmos Granite (W.), LLC v. Minagrex Corp.*, No. 19-cv-1697, 2021 WL 5140226, at *2 (W.D. Wash. Nov. 4, 2021); *CellTrust Corp. v. Ionlake, LLC*, No. 19-cv-2855, 2023 WL 3052733, at *4-6 (D. Minn. Apr. 23, 2023).

These cases squarely address the issue Invitae now raises. A few discrete and self-contained facts from the prior litigation, which both parties’ damages experts in this case have addressed in their reports, pertain solely to the calculation of a reasonable royalty for damages. This, however, should not open the door to laissez-faire presentation of every single scrap of prejudicial evidence or argument regarding the prior litigation, as Natera seemingly contends is warranted. Indeed, Natera’s apparent motive for its position, namely a trial strategy centered on depicting Invitae as a vengeful litigator in search of an opportunity to retaliate against Natera for the prior litigation, is, as the above cases show, ***precisely*** why courts preclude such evidence as irrelevant, unfairly prejudicial, and improper character evidence.

II. REASONABLE ROYALTY DOES NOT REQUIRE IDENTIFYING PRIOR LITIGATION INFORMATION TO ESTABLISH

Even where, as here, discrete facts and evidence from a prior lawsuit are relevant to a later case, courts ***still*** preclude prejudicial evidence and argument regarding litigation history and prior litigation outcomes. *Willis Electric*, D.I. 930, at 15-17 (“Accordingly, Polygroup is precluded from presenting any evidence or argument regarding the prior lawsuits, ***even if Willis Electric references intellectual property issues***, under Federal Rules of Evidence 402, 403 and 404(b).”).

In this case, both parties referenced certain contained facts from the prior litigation pertaining solely to damages in their damages expert reports. Invitae, understanding these facts are amenable to redaction of identifying information without diminishing their probative value, proposed exactly that solution when meeting and conferring with Natera regarding prospective motions *in limine*. Natera, however, refused, thus necessitating this motion.

Notably, Natera's refusal was not predicated upon any faults in Invitae's suggested solution, but merely upon the misguided notion that Invitae's prior litigation history and the outcome of the prior litigation is relevant. As documented above, however, the law is squarely to the contrary.

For these reasons, Invitae respectfully requests the Court preclude evidence and argument from Natera regarding the prior litigation, aside from the discrete damages evidence raised in both parties' damages expert reports, and preclude evidence and argument regarding said damages evidence intended to prejudicially leverage the outcome of the prior litigation.

Dated: February 9, 2024

Respectfully submitted,

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CERTIFICATE OF SERVICE

I, Brian E. Farnan, hereby certify that on February 9, 2024, a copy of PLAINTIFF INVITAE CORPORATION'S MOTION IN LIMINE NO. 2: TO EXCLUDE EVIDENCE AND ARGUMENT REGARDING THE PRIOR LITIGATION BETWEEN INVITAE AND NATERA was served on the following as indicated:

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IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

NATERA’S OPPOSITION TO LABCORP’S MOTION *IN LIMINE* NO. 2

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Labcorp seeks to exclude argument and evidence regarding *Natera, Inc. v. ArcherDX, Inc. et al.*, No. 20-125 (D. Del.) (the “*ArcherDX* Case”), but that case is relevant to multiple issues in this case, including obviousness and damages. A blanket prohibition on all references to the *ArcherDX* Case is unwarranted and belied by Labcorp’s own conduct. Labcorp concedes that evidence from the *ArcherDX* Case is relevant to its claims for damages. And Labcorp moved this Court for production of materials from the *ArcherDX* Case, and as part of this Pretrial Order, is submitting deposition designations from the *ArcherDX* Case (to which Natera has objected).

I. THE RELEVANT FACTS

How Invitae ended up owning the Asserted Patents, and the timing of it, is directly relevant to the hypothetical negotiation and whether the patented invention is commercially successful. Neither Labcorp nor Invitae invented what is claimed by the Asserted Patents. At the time that Dr. Gregory Porreca conceived of the claimed invention, he led Good Start Genetics, which he had founded. [REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED] Ex. 2 at 283:18–21, 284:15–285:19, 301:25–304:6. There is no dispute that evidence of these transactions is relevant and admissible.

The ’799 Patent issued on March 31, 2020, which is the date of the hypothetical negotiation in this case. In October 2020, Invitae acquired ArcherDX, a competitor to Natera. At that time, ArcherDX was a defendant in a lawsuit brought by Natera, the *ArcherDX* Case.

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED] See Ex. 3 at Invitae00003205–Invitae00003206; Ex. 1 at 261:14–262:6, 267:8–272:5, 274:12–23, 277:11–281:11, 282:15–289:23, 302:16–308:6. Invitae then sued Natera in this case using the patent family it re-purchased from Dr. Porreca.

II. ARGUMENT

Labcorp agrees that the history by which, and the prices at which, Invitae purchased, sold, then re-purchased the Asserted Patent family is relevant in this case. But that history is incomplete without evidence of the circumstances in which Invitae purchased the Asserted Patent family in 2021. The **complete** transaction history is relevant to at least two disputed issues in this case.

Damages: As the parties agree, the hypothetical negotiation here is between Natera and Molecular Loop, not Invitae (or Labcorp). Natera’s damages expert argues that the price at which Molecular Loop sold the Asserted Patent family in 2021 bears on the reasonable royalty. Labcorp’s expert counters that the price was “significant[ly] discount[ed]” relative to the price of a hypothetical negotiation. Ex. 4 at 61. But the evidence shows that the reason Invitae bought the Asserted Patents at an allegedly “discounted” price was to sue Natera. The jury should be permitted to take this into account when determining whether the 2021 agreement is comparable.

Secondary Considerations: Labcorp argues that the commercial success of products embodying the Asserted Claims, as well as industry recognition and long-felt, unmet need, support the nonobviousness of the claimed invention. See, e.g., Ex. 5 at 21–25; Ex. 6 ¶¶ 1330–1335. In response, Natera should be able to put on evidence about the circumstances by which Invitae

acquired the Asserted Patents and whether and how those transactions reflect or bear on this supposed industry recognition, long-felt, unmet need, and commercial success. *See, e.g., Personalized User Model, L.L.P. v. Google Inc.*, No. 09-525, 2014 WL 807736, at *3 (D. Del. Feb. 27, 2014) (“[C]ircumstances surrounding the sale of the patents is relevant to rebutting [Patent Owner’s] contentions that the patents are commercially successful.”). That is, the history of how and why Invitae came to own the Asserted Patents, sell them, and buy them back is relevant to its claims that the patents are non-obvious. *Id.* It would be prejudicial to Natera for Labcorp to present arguments regarding secondary considerations without permitting Natera to respond with evidence of how Invitae viewed the Asserted Patents.

Labcorp’s cases are inapposite. Natera does not seek to use evidence from the *ArcherDX* Case for an improper purpose, i.e., as substantive evidence, *see Johns Hopkins Univ. v. Alcon Lab’ys. Inc.*, No. 15-525, 2018 WL 4178159, at *21 (D. Del. Aug 30, 2018), or to attack Invitae’s character, *see Willis Elec. Co., Ltd. v. Polygroup Ltd. et al.*, No. 15-3443, D.I. 930, at 15–16 (D. Minn Jan. 5, 2024); *see also 10X Genomics, Inc. v. Nanostring Techs., Inc.*, No. 21-653, D.I. 277, at 3 (D. Del. Nov. 2, 2023) (precluding evidence of willful infringement in prior litigation); *AVM Techs. LLC v. Intel Corp.*, No. 15-33, D.I. 637, at 1–2 (D. Del. Apr. 19, 2017) (precluding evidence of summary judgment of no damages in prior litigation); *CellTrust Corp. v. Ionlake, LLC*, No. 1-2855, 2023 WL 3052733, at *4–6 (D. Minn. Apr. 23, 2023) (precluding evidence of other lawsuits); *Cosmos Granite (W.), LLC v. Minagrex Corp.*, No. 19-1697, 2021 WL 5140226, at *2 (W.D. Wash. Nov. 4, 2021) (same).

To be sure, there may be aspects of the *ArcherDX* Case that are inadmissible, as Natera explains in its second motion *in limine*. But a blanket ban on any mention it, or of how and why Invitae acquired the Asserted Patents would prejudice Natera. Labcorp’s motion should be denied.

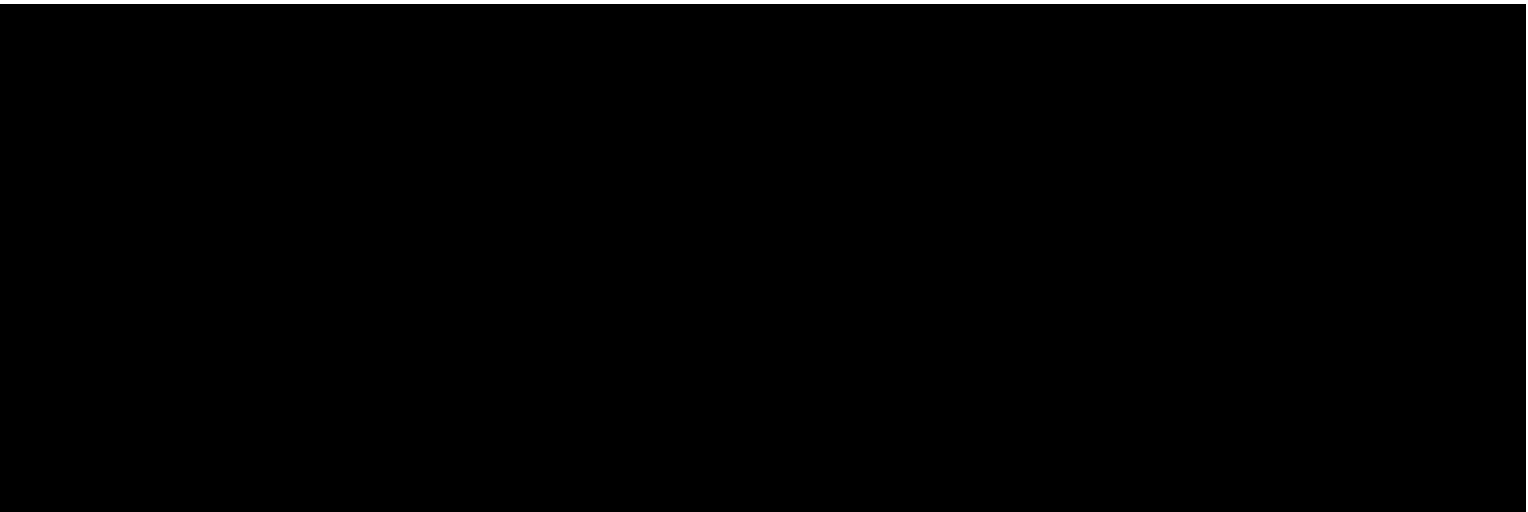
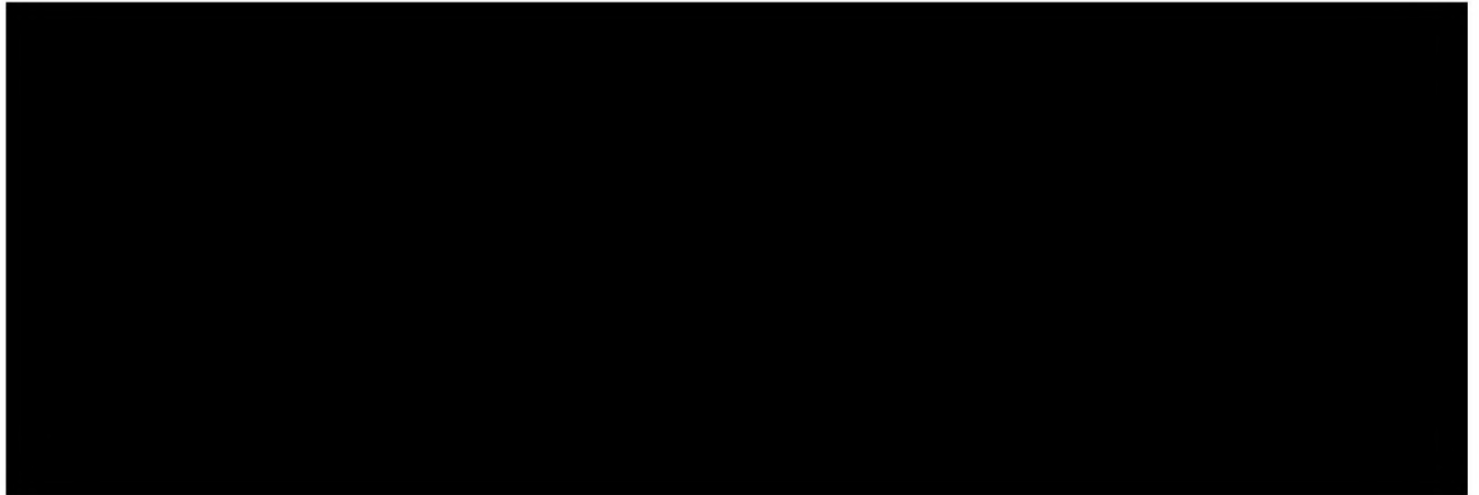
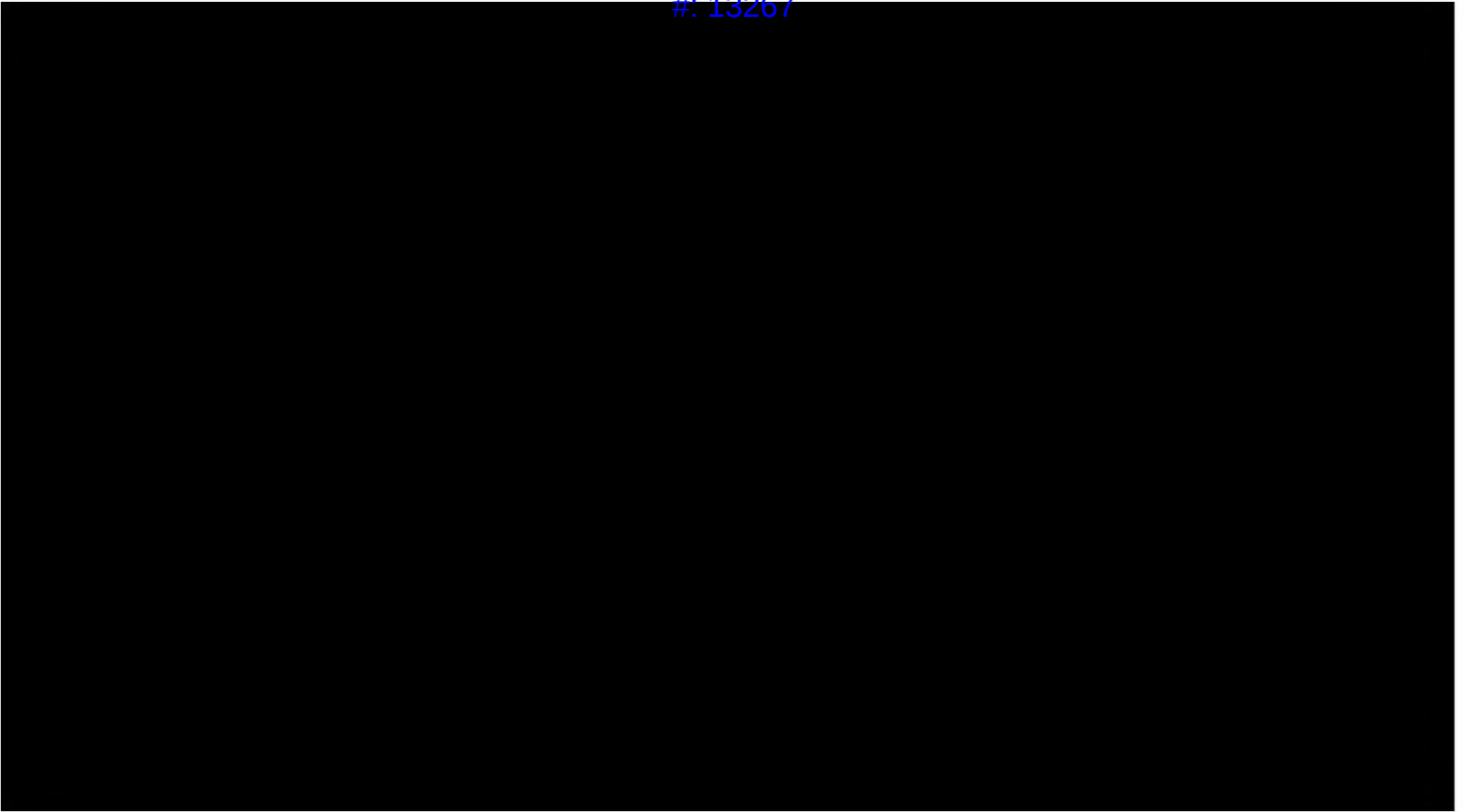
EXHIBIT 1

REDACTED

EXHIBIT 2

REDACTED

EXHIBIT 3



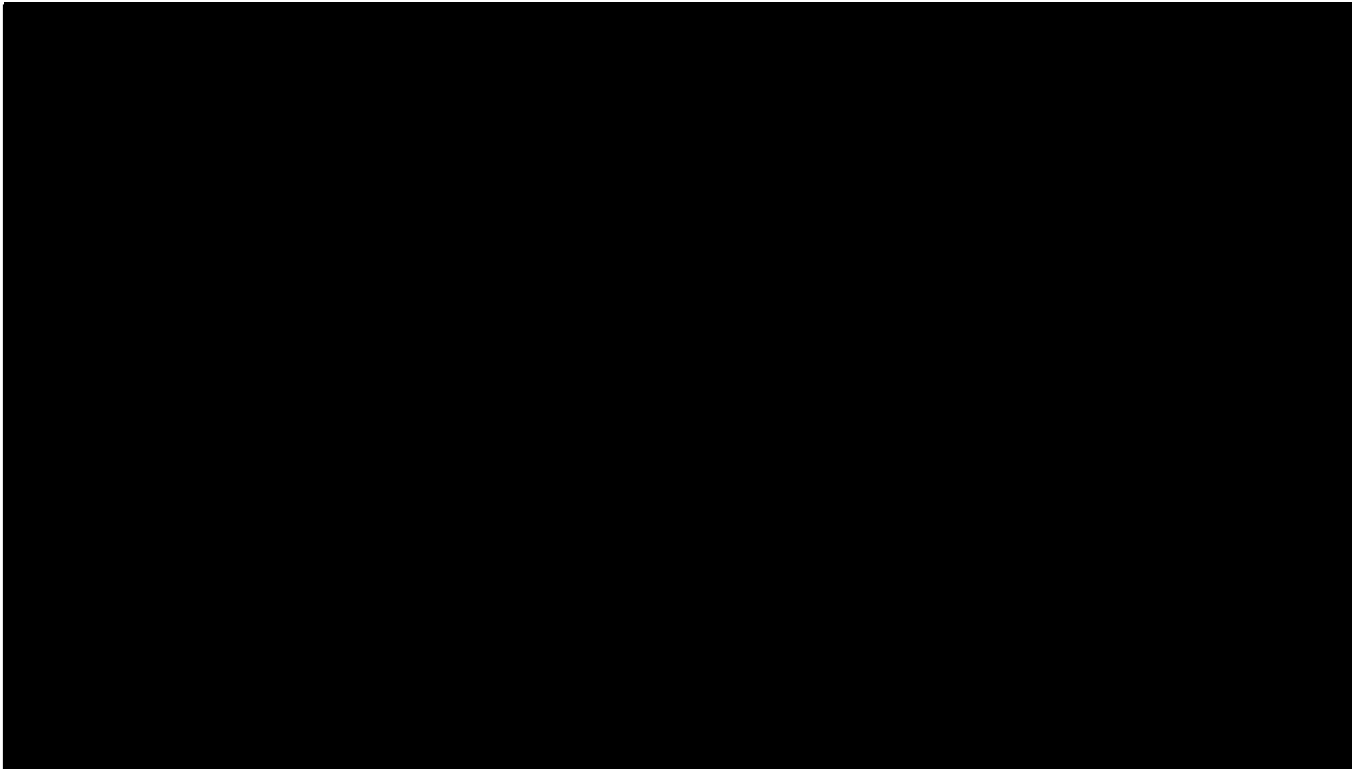
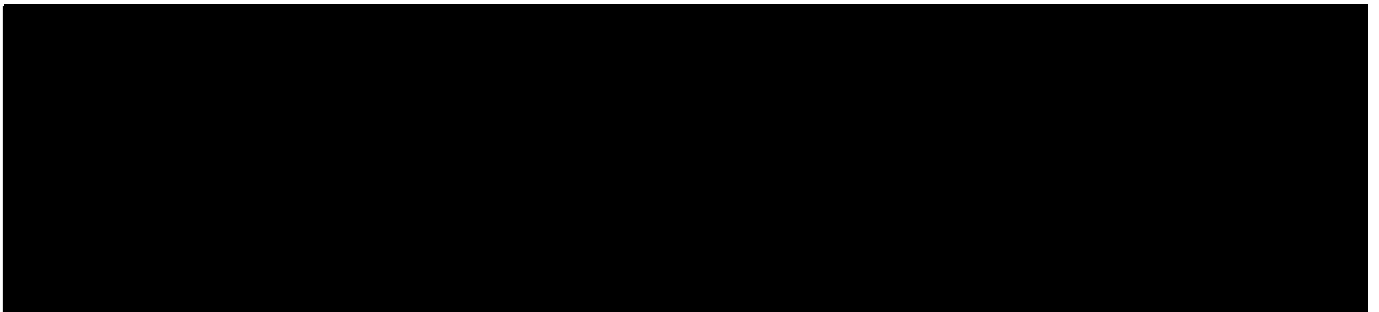
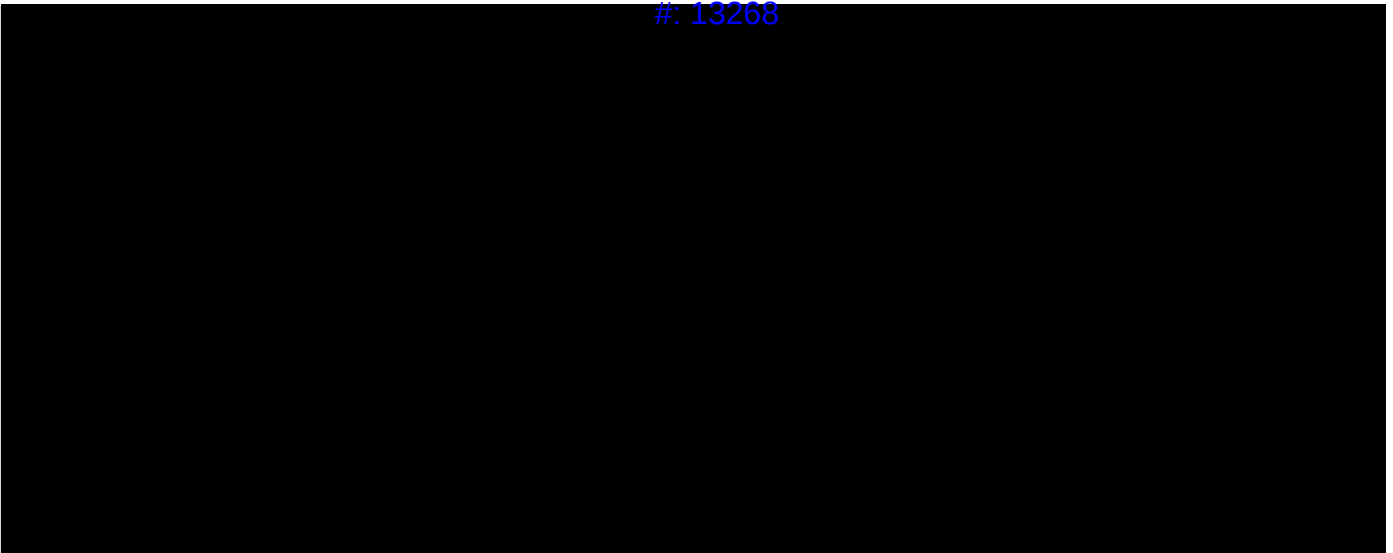


EXHIBIT 4



OCEAN TOMO®

A PART OF  **JS|HELD**

INVITAE CORPORATION

V.

NATERA, INC.

Civil Action Nos. 1:21-cv-00669 & 1:21-cv-01635

United States District Court for the District of Delaware

EXPERT REPORT OF ALEXANDER L. CLEMONS

June 16, 2023



established the marketplace.”³¹² Similarly, even in June 2021, DeciBio explained that, “[o]verall, the MRD / monitoring space is still in the relatively early stages of research, development, and clinical adoption today.”³¹³ As of October 2018, Signatera had launched for research use only, but would not launch commercially for clinical use for almost another year.³¹⁴ Additionally, Signatera’s rapid revenue growth from 2019 through 2022 would not be known in 2018.³¹⁵ The lump sum purchase price for the MIP Assets, originally set in the July 2017 Merger Agreement, does not account for these and other developments in the MRD market. However, a running royalty, such as the 10% royalty rate contained in the BD / ArcherDX License, by its very nature, results in increased or decreased royalty payments as licensed sales increase or decrease.

Fourth, even if the financial terms of the Good Start / Molecular Loop Asset Purchase and Royalty Agreements could be argued to include value relating to the use of the Patents-in-Suit by third parties, such as Natera, any such value would include a significant discount to account for the costs and risks associated with attempting to license or litigate with such third party, such as the cost of a licensing program, the cost of patent litigation, the risk of patents being found invalid, and the risk of patents being found non-infringed. In the context of the hypothetical negotiation, however, the Patents-in-Suit are assumed to be valid and infringed.

Based on the above, the Good Start / Molecular Loop Asset Purchase and Royalty Agreements are not economically comparable to a license that would result from the hypothetical negotiation in this case and are not indicative of the value of the Patents-in-Suit or a reasonable royalty for the Patents-in-Suit.

11.1.2.2 Molecular Loop / Invitae Asset Purchase and Cross License Agreements

Effective March 13, 2021, Invitae and Molecular Loop entered into an “Asset Purchase Agreement.”³¹⁶ Effective the same day, Invitae and Molecular Loop entered into a “Cross License Agreement” (the Asset Purchase Agreement and the Cross License Agreement referred to as the “Molecular Loop / Invitae Asset

³¹² Deposition of Kevin Masukawa, February 28, 2023, pp. 63, 84.

³¹³ Zhou, Susan, “Industry Snapshot: The nascent ctDNA MRD space continues to see rapid growth,” *DeciBio*, June 29, 2021, <https://www.decibio.com/insights/industry-snapshot-the-nascent-ctdna-mrd-space-continues-to-see-rapid-growth>.

³¹⁴ “Natera Launches Signatera™ Personalized Circulating Tumor DNA Technology for Cancer Research,” *Natera*, August 21, 2017, <https://www.prnewswire.com/news-releases/natera-launches-signatera-personalized-circulating-tumor-dna-technology-for-cancer-research-300506771.html>; Natera, Inc., SEC Form 10-K for the fiscal year ended December 31, 2019, p. 15, <https://d18rn0p25nwr6d.cloudfront.net/CIK-0001604821/fb612ec5-278c-4e4c-bfba-fa516dd7f4d8.pdf>.

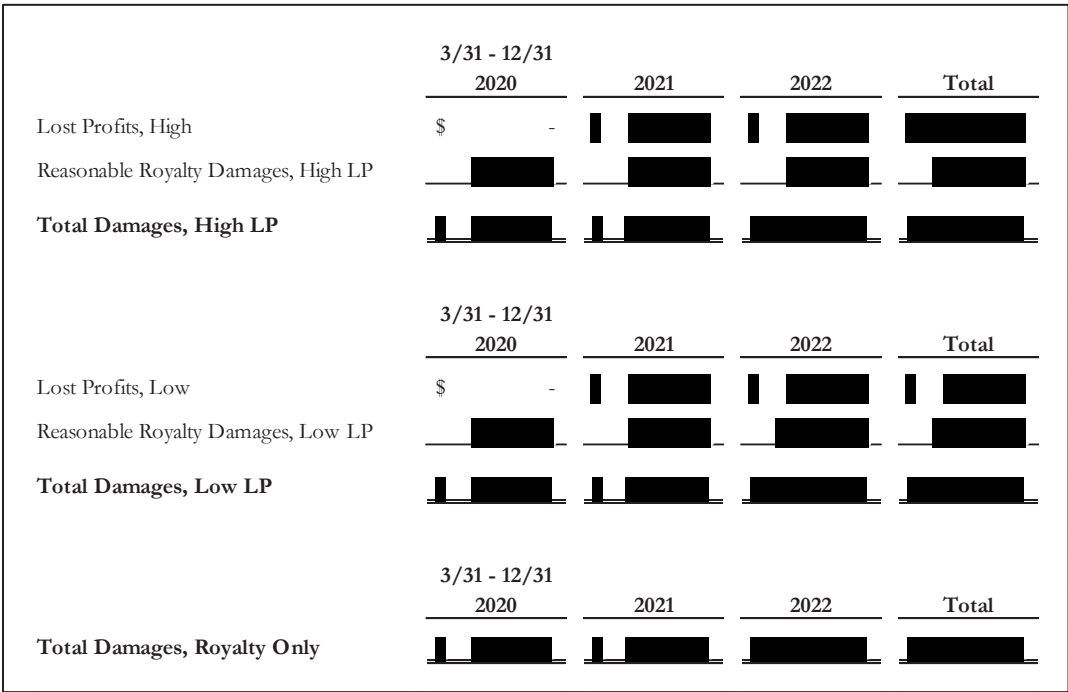
³¹⁵ Appendix 7.1; INVT-00419829, tab “Signatera Gross Profit”.

³¹⁶ Invitae0000003173-188 at 173-174.



royalties, in addition to or as an alternative to lost profits, I have analyzed quantitative and qualitative valuation metrics, including the *Georgia-Pacific* factors, and have reached a conclusion regarding the appropriate reasonable royalties due to Invitae for Natera’s use of the Patents-in-Suit in connection with the Accused Product. As summarized in the figure below, I have calculated total damages, both including and excluding lost profits.

Figure 26: Summary of Damages through 2022⁵¹¹



I reserve the right to update my damages calculations if updated sales information is provided.

16 SIGNATURE

Respectfully submitted,

Alexander L. Clemons

June 16, 2023

Alexander L. Clemons

Date

⁵¹¹ Appendix 3.1.

EXHIBIT 5

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

INVITAE CORPORATION,

Plaintiff,

Case No. 21-cv-669-GBW

V.

JURY TRIAL DEMANDED

NATERA, INC.

Defendant.

INVITAE CORPORATION,

Case No. 21-cv-01635-GBW

Plaintiff,

JURY TRIAL DEMANDED

V.

NATERA, INC.

Defendant.

**INVITAE CORPORATION'S SUPPLEMENTAL RESPONSES AND OBJECTIONS TO
NATERA, INC.'S FIRST SET OF INTERROGATORIES (NOS. 1-8)**

Pursuant to Rules 26 and 33 of the Federal Rules of Civil Procedure, the Local Rules of the United States District Court for the District of Delaware (“Local Rules”), the District of Delaware Default Standard for Discovery, including Discovery of Electronically Stored Information (“Default Standard”), and any other applicable Orders or rules, Plaintiff Invitae Corporation (“Invitae”) hereby makes the following supplemental responses and objections to Defendant Natera, Inc.’s (“Natera”) First Set Of Interrogatories (Nos. 1-8).

assembly that allows accurate identification of certain cancer-causing mutations that are otherwise difficult to identify.

The nonobviousness of the Asserted Patents is further shown by industry praise for the Genome Analysis Toolkit (GATK) tools identified as used in the Accused Products upon information and belief. *See generally* D.I. 1. For example, the Mutect2 tool in GATK is described as “stable and relatively accurate” and “one of the most widely used mutation-calling tools”. *See* Chen, Z., Yuan, Y., Chen, X. et al., *Systematic comparison of somatic variant calling performance among different sequencing depth and mutation frequency*. Sci Rep 10, 3501 (2020).

As required under the scheduling order and the local rules, Invitae will provide expert testimony regarding the nonobviousness of the Asserted Patents.

FIRST SUPPLEMENTAL RESPONSE TO INTERROGATORY NO. 2 (2023-02-15):

Subject to its general and specific objections, and based on its investigation to date, Invitae supplements its response to further respond as follows:

Facts further supporting objective indicia of non-obviousness of Invitae’s Asserted Patents include the commercial success attributable to the claimed inventions in the products that embody and/or infringe the Asserted Patents. Such facts include without limitation: the high level of commercial success of Invitae’s embodying products and Natera’s accused Signatera products attributable to the claimed inventions; the speed with which Invitae’s embodying products and Natera’s accused Signatera products achieved commercial success; the significant sales and revenues of Invitae’s embodying products and Natera’s accused Signatera products attributable to the claimed inventions; the large number of clinicians, patients, pharma partners, academia partners, and other collaborators adopting Invitae’s embodying products and Natera’s accused Signatera products attributable to the claimed inventions; the large number and wide extent of

Natera's collaboration and partnerships with pharmaceutical companies, academia, federal health care system members, BGI, FMI, [REDACTED] and others involving the accused Signatera products attributable to the claimed inventions; the number of publications utilizing and/or discussing Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions; the market shares of Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions; the regulatory status of the accused Signatera products (e.g., FDA approval and CE marking) attributable to the claimed inventions; the coverage of the accused Signatera products from private or public insurance companies/agencies (e.g., Medicare and Medicare Advantage) attributable to the claimed inventions; and third-party reports discussing the above. Such commercial success also supports that there existed a long-felt, unmet need in the industry and that prior attempts to meet that need failed.

Facts further supporting objective indicia of non-obviousness of Invitae's Asserted Patents also include the industry praise and recognition for the inventions of the Asserted Patents, for software and bioinformatics tools that perform key steps of Invitae's Asserted Patents, and for the products that embody or infringe Invitae's Asserted Patents attributable to the claimed inventions. Such facts include without limitation: awards won by Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions; awards won by Sentieon's software attributable to the implementation of GATK HaplotypeCaller and Mutect 2 (e.g., <https://www.sentieon.com/products/>, <https://precision.fda.gov/challenges/truth/results>, <https://precision.fda.gov/challenges/10/results>); awards won by, industry recognition of, and wide adoption of Broad Institute GATK attributable to the claimed inventions (e.g., <https://www.nature.com/articles/srep17875>, <https://www.sciencedirect.com/science/article/pii/S2001037019301473>,

https://csc.fi/ja/web/blog/post?p_p_id=com_liferay_blogs_web_portlet_BlogsPortlet&p_p_lifecycle=0&p_p_state=normal&p_p_mode=view&p_r_p_categoryId=394145); professional acclaim for Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions (e.g., research papers discussing or utilizing and clinical studies utilizing Invitae's embodying products and Natera's accused Signatera products); industry reports discussing and praising the success or advantages of Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions; competitors discussing, comparing and praising the success or advantages of Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions; the large number of clinicians, patients, pharma partners, academia partners, and other collaborators adopting Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions; the large number and wide extent of Natera's collaboration and partnerships with pharmaceutical companies, academia, federal health care system members, BGI, FMI, SRL, and others involving the accused Signatera products attributable to the claimed inventions; the number of publications utilizing and/or discussing Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions; the regulatory status of the accused Signatera products (e.g., FDA approval and CE marking) attributable to the claimed inventions; the coverage of the accused Signatera products from private or public insurance companies/agencies (e.g., Medicare and Medicare Advantage) attributable to the claimed inventions; and third party reports discussing and praising Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions. The industry praise and recognition attributable to the claimed inventions also support that the industry recognized the

significance and unexpected results of the inventions of Invitae's Asserted Patents and products that embody or infringe Invitae's Asserted Patents.

Facts further supporting objective indicia of non-obviousness of Invitae's Asserted Patents also include the existence of long-felt, persistent need in the industry recognized by skilled artisans that had not been satisfied before the inventions of the Asserted Patents but was satisfied by the inventions of the Asserted Patents. Such facts include without limitation: the Asserted Patents and the prosecution histories discussing the drawbacks, failings, and needs not met by prior art; the Asserted Patents and the prosecution histories discussing the benefits of the inventions of the Asserted Patents and how the inventions meet needs not met by prior art; publications discussing the drawbacks, failings, and needs not met by prior art; publications discussing the benefits of the inventions of the Asserted Patents and how the inventions meet needs not met by prior art; discussion of differences between the inventions in the Asserted Patents and prior art; discussions of the benefits of Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions, discussions of the differences between Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions and prior art products and techniques, and of how Invitae's embodying products and Natera's accused Signatera products meet needs not met by prior art products and techniques attributable to the claimed inventions; industry reports discussing the drawbacks, failings, and needs not met by prior art products and techniques, the benefits of Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions, the differences between Invitae's embodying products and Natera's accused Signatera products attributable to the claimed inventions and prior art products and techniques, and how Invitae's embodying products and Natera's accused Signatera products meet needs not met by prior art products and techniques

attributable to the claimed inventions; documents produced by the parties discussing the aforementioned exemplary facts.

Facts further supporting objective indicia of non-obviousness of Invitae's Asserted Patents also include the presumption of the existence of and/or the existence of a nexus between the objective considerations described above and the claimed inventions in Invitae's Asserted Patents. Such facts include without limitation: Natera's accused Signatera products infringe claims of Invitae's Asserted Patents; Invitae's embodying products embody claims of Invitae's Asserted Patents; the secondary considerations described above attributable to the fact that Invitae's embodying products and/or Natera's accused Signatera products practice Invitae's Asserted Patents; the secondary considerations described above did not solely result from factors other than the claimed inventions; and documents from the parties and from third parties recognizing, discussing, or otherwise confirming the above. For example, Invitae's embodying products and Natera's accused Signatera products use modified versions of GATK HaplotypeCaller and/or Mutect 2 to perform sequence assembly and alignment and variant calling using genetic sequence data. The sequencing, sequence analysis, and variant calling processes are integral to the functionality of these products. These products are personalized cancer recurrence monitoring products that require identification of somatic mutations unique to each patient. Without establishing the patient-unique variant profile, which is obtained using the claimed invention, Invitae's embodying products and Natera's accused Signatera products do not function as claimed. Thus, the claimed inventions are key to the functionality of both genetic testing products. While Invitae's embodying product uses an in-house modification of GATK and Natera's Signatera uses Sentieon's implementation of GATK, the underlying operation is not changed and practices the claimed invention of the Asserted Patents. Further, the claimed inventions, including the two-

EXHIBIT 6

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

INVITAE CORPORATION,

Plaintiff,

v.

NATERA, INC.

Defendant.

Case No. 21-cv-669-GBW

JURY TRIAL DEMANDED

**HIGHLY CONFIDENTIAL –
OUTSIDE ATTORNEYS’ EYES
ONLY**

INVITAE CORPORATION,

Plaintiff,

v.

NATERA, INC.

Defendant.

Case No. 21-cv-1635-GBW

JURY TRIAL DEMANDED

**HIGHLY CONFIDENTIAL –
OUTSIDE ATTORNEYS’ EYES
ONLY**

**REBUTTAL EXPERT REPORT OF DAN E. KRANE TO THE OPENING EXPERT
REPORT OF MICHAEL METZKER, PHD**

Dated: July 21, 2023

By: 

Dr. Dan E. Krane

x. Claim 27: “the sequence reads comprise at least one million sequence reads”

1328. Dr. Metzker opines that Li (2009) anticipates and/or renders obvious '308 Claim 27 for the reasons described for '308 Claim 19. Metzker Opening Report ¶ 1730. I disagree and incorporate my analysis of '308 Claim 19 by reference. *See supra* analysis for '308 Claim 19.

1329. Li (2009) does not anticipate or render obvious this claim also because it does not anticipate or render obvious Claim 20. *See supra* analysis for '308 Claim 20.

L. Objective Indica of Non-Obviousness

1330. In addition to my analyses *supra*, I also provide an analysis in this section regarding objective indicia of nonobviousness. In addition to other documents I cite below, I reference the Asserted Patents and their file histories throughout. *See* Invitae0000000001, Invitae0000002509, Invitae0000002795.

1331. First, the commercial success of the products that embody and/or infringe the Assertd Patents that is attributable to the claimed inventions supports objective indicia of non-obviousness. For example, Invitae's embodying products and Natera's accused Signatera products are both commercially successful, became commercially successful quickly, and made significant sales and revenues, with a substantial market share. For example, Natera's Form 10-K submitted on February 25, 2022, on page 37, describes the high level of competition in the market space. Additionally, a large number of clinicians, patients, pharma partners, academia partners, and other collaborators adopted these same products, such as but not limited to Natera's collaborations and partnerships with BGI, FMI, [REDACTED] and others, or the scientific publications which utilize and/or discuss the aforementioned products. *See, e.g.*, Invitae0010003276 (describing among other things the quality and capability of Invitae's embodying products for use in academic studies); NTRA-INVT-00016144 at 16159, 16163 (Natera's BD Pharma Core Deck). Additionally, the regulatory

status (such as FDA approval and CE marking) and coverage from public and private insurance (such as Medicare and Medicare Advantage) of the accused Signatera products also supports this. All of these commercial successes as described also support the long-felt and unmet need in the industry for the claimed inventions described *infra*.

1332. Second, there was also a long-felt and unmet need in the industry for the claimed inventions, and prior attempts to meet that need failed. Specifically, the long-felt but unresolved needs in the industry for a sequence assembly tool capable of overcoming the limitations of then-current software, which required researchers to compromise between sensitivity to different types of mutations. Even more so, prior software required tradeoffs between positional accuracy, being able to include detailed information from each read, and difficulty interpreting certain types of mutations altogether, as are all documented in the prior art Dr. Metzker has provided. The long-felt need for a solution to these problems that could be implemented in connection with existing platforms, which the claimed methods provide, shows nonobviousness. As explained *supra* the facts demonstrating commercial success also support the existence of a long-felt and unmet need in the industry for the claimed inventions.

1333. Third, the nonobviousness of the Asserted Patents is further shown by industry praise and recognition attributable to the claimed inventions for the inventions of the Asserted Patents, for software and bioinformatics tools that perform key steps of Invitae's Asserted Patents, and for the products that embody or infringe Invitae's Asserted Patents. For example, Sentieon's software has won a number of awards attributable to their implementation of GATK HaplotypeCaller and Mutect2. Exs. 3, 4, and 5. As another example, the variant calling tool in GATK is described as "stable and relatively accurate" and "one of the most widely used mutation-

calling tools.” Ex. 6; *see also, e.g.* ILLUMINA-0008343 (explaining that GATK is industry standard); Invitae0010017712 (explaining that GATK is the default);

1334. A nexus exists between all of these facts and the invention claimed in the Asserted Patents. For a variant caller, factors for its success include the speed and accuracy of the sequence analysis and variant calling processes. My understanding is substantiated by my experience as I describe *supra* as well as, at least, testimony from Eric Banks regarding his experience developing HaplotypeCaller. *See* Banks Depo. at 166:1-168:9. Additionally, GATK is the industry standard, and is the most widely adopted caller in bioinformatics. *See* NTRA-INVNT-00234865 at 234867 (“Put together the pipeline using Sentieon Haplopyter, an improved version of the **industry standard GATK Haplotype Caller** for short variant SNV/INDEL calling and post processing steps of decomposing multiple allelic calling...”). Additionally, Dr. Raheleh Salari testified that [REDACTED]

[REDACTED] The Cancer Genome Atlas (TCGA) had already validated GATK. *See* Salari Depo at 68:9-69:4; 69:23-70:14. This is in accord with my understanding of the field. The embodying and accused products are personalized cancer recurrence monitoring products that require the precise identification of mutations unique to each patient. Without identifying such mutations, Invitae’s embodying products and Natera’s accused Signatera products do not function as described. Thus, the claimed invention is necessary for the proper function of both products. *See* Krane Opening Report Part XI; NTRA-INVNT-00016144 at 16162. I incorporate by reference my opinions regarding the variant calling process in Signatera in my opening report. As Invitae’s embodying products use an in-house modification of GATK and Natera’s Signatera uses a licensed Sentieon implementation of GATK, it can be seen that the underlying sequence assembly and analysis functions, which practice the claimed invention of the Asserted Patents, are the key features of

from the Asserted Patents that are both desireable and unchanged between the products. Additionally, the claimed invention, including the novel and inventive two-step alignment enable variant callers such as GATK HaplotypeCaller and Mutect2 to call variants (including SNVs and indels) with greater accuracy and less computational resources than other variant callers which do not practice the claimed invention, such as GATK UnifiedGenotyper.

1335. For at least these reasons, it is my understanding that the objective indicia of non-obviousness show that the Asserted Claims are not obvious.

XI. SECTION 112 ANALYSIS

1336. I disagree with Dr. Metzker's Section 112 analysis.

A. Validity Based Upon Enablement and Written Description

1337. I have been informed that Section 112 of the Patent Code requires the specification of a patent to enable one of ordinary skill in the art to practice the full scope of the claimed invention without undue experimentation as of the filing date of the patent. I have also been informed that the specification, drawings, and claims in a patent must allow a person of ordinary skill in the art to recognize that the invention was invented by the patentee and was in the patentee's possession at the time of filing. I understand these requirements.

1338. I have been asked to analyze whether the Asserted Patents satisfy the written description and enablement requirements and to thusly respond to Dr. Metzker's opinions. It is my opinion that Dr. Metzker is incorrect in his analyses and that the Asserted Patents are adequately described and sufficiently enabled for one of ordinary skill in the art at the time of Asserted Patents' filings.

1339. Dr. Metzker's opinion is premised on the wrong understanding of the term "mutations"—"the claimed 'mutations' detectable by methods of the invention, is interpreted to

IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	C.A. No. 21-669 (GBW)
)	
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	
<hr/>		
LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	C.A. No. 21-1635 (GBW)
)	
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	

**PLAINTIFF'S REPLY IN SUPPORT OF ITS MOTION *IN LIMINE* NO. 2: TO
EXCLUDE EVIDENCE AND ARGUMENT REGARDING THE PRIOR LITIGATION
BETWEEN INVITAE AND NATERA**

OF COUNSEL:

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Dated: August 13, 2025

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*Attorneys for Plaintiff Laboratory
Corporation of America Holdings*

Natera confirms that it intends to discuss *ArcherDX* to argue before the jury that “Invitae bought the Asserted Patents...to sue Natera.” Opp. at 2. Natera thus intends to improperly pursue a narrative that Invitae purchased the Asserted Patents as revenge for first being sued by Natera.

Whether Invitae purchased the Asserted Patents solely to assert against Natera is disputed.¹ Even if true, however, there is nothing nefarious about this. Moreover, this has no relevance to whether Natera infringed the Asserted Patents, the Asserted Patents’ validity, or the related damages. The only purpose Natera’s argument serves is to paint Labcorp in a bad light. Yet, as Natera itself argued in the prior *ArcherDX* case, “[a]llowing Defendant[] to present nonsensical arguments irrelevant to the issues before the jury would not only waste time but also divert the jury’s attention to extraneous matters.” No. 20-cv-125, D.I. 580-1, Ex. 17-3 at 2.

As to damages, Natera contends that the jury needs to know Invitae’s motivation to purchase the Asserted Patents—purportedly retaliation for Natera’s prior lawsuit—to evaluate the purchase agreement for the hypothetical negotiation. Neither party’s damages experts, however, presents valuations dependent on Invitae’s motivation for filing suit. As to secondary considerations, Natera contends that “the history of how and why Invitae came to own the Asserted Patents, sell them, and buy them back is relevant to its claims that the patents are non-obvious.” Opp. at 3. As the *Google* case cited by Natera explains, however, what is relevant to commercial success is “[e]vidence of [*the patentee*]’s financial state prior to selling the patents-in-suit.” 2014 WL 807736, at *3. The relevant circumstances are those of Molecular Loop, who sold the patent, not of Invitae. Natera cites no case allowing the inflammatory contention that a party purchased a patent for retaliatory litigation to be used for damages or secondary considerations.

¹ Ex. 1 at 311:4-8

August 13, 2025

Respectfully submitted,

FARNAN LLP

/s/ Brian E. Farnan

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*Attorneys for Plaintiff Laboratory
Corporation of America Holdings*

CERTIFICATE OF SERVICE

I, Brian E. Farnan, hereby certify that on August 13, 2025, a copy of PLAINTIFF'S REPLY IN SUPPORT OF ITS MOTION IN LIMINE NO. 2: TO EXCLUDE EVIDENCE AND ARGUMENT REGARDING THE PRIOR LITIGATION BETWEEN INVITAE AND NATERA was served on the following as indicated:

Via E-Mail

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/s/ Brian E. Farnan

Brian E. Farnan (Bar No. 4089)

EXHIBIT 1

REDACTED

EXHIBIT 19C

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-669 (GBW)
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	
<hr/>		
LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	C.A. No. 21-1635 (GBW)
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	

**PLAINTIFF'S MOTION IN LIMINE NO. 3: TO EXCLUDE EVIDENCE AND
ARGUMENT REGARDING INVITAE'S OVERALL FINANCIAL CONDITIONS**

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Dated: February 9, 2024

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Pursuant to Federal Rules of Evidence 402 and 403, Plaintiff Invitae Corporation (“Invitae”) moves to preclude Defendant Natera, Inc. (“Natera”) from offering evidence, testimony, argument, or otherwise referencing Invitae’s overall financial condition, including potential bankruptcy, delisting from NYSE, stock price, and employee layoffs, etc. Invitae’s overall financial condition now, or in the past, is wholly irrelevant to Invitae’s claim for patent infringement. But even if it has some marginal relevance here, its probative value is substantially outweighed by that it would unfairly prejudice Invitae and confuse or mislead the jury.

I. INVITAE’S OVERALL FINANCIAL CONDITION IS IRRELEVANT TO ANY ISSUE IN THIS CASE.

A party’s overall financial condition has no relevance to any issue relating to infringement or patent validity. *See, e.g., Collier v. Airtex, Inc.*, No. 87 C 4097, 1990 WL 119551, at *1 (N.D. Ill. Aug. 14, 1990) (“Evidence of plaintiffs’ financial condition does not appear to be relevant to any issue relating to infringement or patent validity.”); *Liqwd, Inc. v. L’Oreal USA, Inc.*, C.A. No. 17-14-JFB-SRF, 2019 WL 2775515, at *1 (D. Del. July 2, 2019) (“The Court agrees that any evidence as to defendants’ overall financial status is irrelevant and is potentially prejudicial.”). There is no reason this case should be an exception to this commonsense principle.

At the parties’ meet and confer, Natera contended that evidence regarding Invitae’s overall financial condition is relevant to lost profits, reasonable royalty, and future damages. Natera’s position lacks merit. Indeed, neither sides’ experts discussed Invitae’s overall financial condition in forming their opinions on damages.

Lost profits. Invitae’s overall financial condition is not relevant to lost profits analysis, including the third *Panduit* factor—“manufacturing and marketing capability.” *Panduit Corp. v. Stahl Bros. Fibre Works*, 575 F.2d 1152, 1156 (6th Cir. 1978). Invitae’s overall financial condition is distinct from its manufacturing and marketing capacity of its PCM product (the lost

sales of which caused Invitae's lost profits). Invitae as a company has numerous product lines. And its financial performance is determined by many factors beyond its product sales. Either Invitae has the capacity to fill the market relevant for lost profits, or it does not. There is no need for Natera to raise allegations about employee layoffs or bankruptcy status.

Reasonable royalty. Invitae's overall financial condition is not relevant to reasonable royalty either. To determine a reasonable royalty, a hypothetical negotiation would have taken place at the time of first infringement between the patent owner and the infringer. *See Lucent Techs., Inc. v. Gateway, Inc.*, 580 F.3d 1301, 1324 (Fed. Cir. 2009). In this case, the hypothetical negotiation would have taken place on March 31, 2020 (issuance date of the '799 Patent) between third-party Molecular Loop (then patent owner) and Natera. Hence, the reasonable royalty analysis requires no inquiry into Invitae's overall financial condition, especially its recent condition.

Future damages. Future damages is typically resolved by post-trial briefing. Thus, to the extent Invitae's financial condition is relevant to future damages, it should be addressed *after* the jury returns a verdict.

II. EVIDENCE OF INVITAE'S OVERALL FINANCIAL CONDITION IS HIGHLY PREJUDICIAL TO INVITAE AND WILL CONFUSE OR MISLEAD THE JURY

Allowing Natera to present evidence regarding Invitae's overall financial condition to the jury would be highly prejudicial to Invitae because such evidence has no purpose except to paint Invitae in a bad light. Such evidence is intended only to confuse or mislead the jury from the key issues in the case, which are whether Natera infringes Invitae's patents. *See, e.g., In re Homestore.com, Inc. Sec. Litig.*, No. CV 01-11115 RSWL (CWx), 2011 WL 291176, at *1 (C.D. Cal. Jan. 25, 2011) ("Evidence of a party's financial condition is generally not relevant and can be unduly prejudicial, as it can distract the jury from the real issues in the case.").

Evidence regarding bankruptcy is particularly likely to taint the jury's opinion of a party, thereby resulting in unfair prejudice and confusion. *See, e.g., HTC Corp. v. Tech. Properties Ltd.*, No. 5:08-CV-00882-PSG, 2013 WL 4782598, at *2 (N.D. Cal. Sept. 6, 2013) (“A reference to bankruptcy may trigger visceral reactions among jurors and the court believes such a reaction carries a risk of substantial unfair prejudice. Moreover, there is a substantial risk that evidence of TPL’s bankruptcy will confuse the issues.”); *HSM Portfolio LLC v. Elpida Memory Inc.*, C.A. No. 11-770-RGA, D.I. 1220 at 2 (D. Del. Feb. 17, 2016) (“TPL’s bankruptcy is excluded, since being bankrupt does not make a company more avaricious than if it is not bankrupt. It is also unfairly prejudicial, and thus even were there some slight probative value, it would be greatly outweighed by the prejudice.”); *Magelky v. BNSF Ry. Co.*, No. 1:06-CV-025, 2008 WL 238451, at *2 (D.N.D. Jan. 28, 2008) (“[Evidence of bankruptcy], even if relevant, would be unfairly prejudicial, confuse the issues, mislead the jury, and result in undue delay and a waste of time. Therefore, such evidence shall be excluded pursuant to Rule 403 of the Federal Rules of Evidence”).

Given its lack of probative value and the high likelihood of jury confusion and unfair prejudice to Invitae, Defendant should be precluded from introducing evidence or argument concerning Invitae’s overall financial condition.

Dated: February 9, 2024

Respectfully submitted,

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CERTIFICATE OF SERVICE

I, Brian E. Farnan, hereby certify that on February 9, 2024, a copy of PLAINTIFF INVITAE CORPORATION'S MOTION IN LIMINE NO. 3: TO EXCLUDE EVIDENCE AND ARGUMENT REGARDING INVITAE'S OVERALL FINANCIAL CONDITIONS was served on the following as indicated:

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**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

NATERA’S OPPOSITION TO LABCORP’S MOTION *IN LIMINE* NO. 3

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Invitae's business began collapsing in mid-2022, and Invitae filed for Chapter 11 bankruptcy on February 13, 2024.¹ Plaintiff Labcorp then bought substantially all of Invitae's assets in that bankruptcy, including these Asserted Patents and the part of Invitae's business that competed with Natera's accused product, Signatera. Labcorp now seeks to preclude Natera from referencing or offering evidence or argument regarding what the moving brief described as "Invitae's overall financial condition, including potential bankruptcy, delisting from NYSE, stock price, and employee layoffs, etc.," which Natera treats as including the subsequent bankruptcy itself. Invitae's Motion *in Limine* No. 3 ("MIL 3") at 1.

Invitae's financial condition is directly relevant to the parties' claims and defenses in this litigation, including Labcorp's claim for lost profits and its argument that secondary considerations, like commercial success, demonstrate the non-obviousness of the Asserted Patents. There are aspects of this request with which Natera agrees, but those should be taken up individually, not with a blanket ban on any mention of Invitae's financial condition.

I. ARGUMENT

Labcorp seeks Invitae's lost profits through November 2023 (i.e., before the Court's injunction of Invitae's PCM in the *ArcherDX* case), and its damages expert has opined that if Natera had not sold its accused Signatera product, "Invitae would have likely captured all (but no less than 50%) of those sales in the pharmaceutical market with sales of its PCM product." Ex. 1 at 38; *see also id.* at 4–5, 37–43, Fig. 13, 102. To recover for Invitae's lost profits, Labcorp must prove that Invitae had the manufacturing and marketing capability to make the allegedly infringing sales that were actually made by Natera. *Wechsler v. Macke Int'l Trade, Inc.*, 486 F.3d 1286, 1294

¹ *In re Invitae Corp.*, No. 24-11362-MBK, Debtors' Motion for Entry of Interim Final Orders, D.I. 18 (D.N.J. Bankr. Feb. 14, 2024); *In re Invitae Corp.*, No. 24-11362-MBK, Declaration of Ana Schrank, Chief Financial Officer of Invitae Corporation, in Support of Chapter 11 Filing, First Day Motions, and Access to Cash Collateral, D.I. 21 (D.N.J. Bankr. Feb. 14, 2024).

(Fed. Cir. 2007). Invitae’s business failures are directly relevant to whether it could have in fact exploited the alleged demand for the patented product during the relevant time. *Id.* (holding lost profits not available where patentee “was unable to produce a product during the period of infringement.”); *Gargoyles, Inc. v. United States*, 113 F.3d 1572, 1578 (Fed. Cir. 1997) (holding lost profits not available where patentee “has not proven capacity to produce the [additional products] sufficient to receive lost profits.”); *cf.*, *APEX Fin. Options, LLC v. Gilbertson*, No. CV 19-0046-WCB-SRF, 2022 WL 622130, at *1 (D. Del. Mar. 3, 2022) (declining to preclude evidence regarding plaintiffs’ “financial condition” under Rules 402 & 403).

Evidence regarding Invitae’s financial state is also relevant to the parties’ arguments regarding commercial success for purposes of obviousness under 35 U.S.C. § 103. For example, Natera should be permitted to “attempt to rebut [Invitae]’s effort to show commercial success of the patents-in-suit by presenting evidence that the patents were not commercial successes for [Invitae] or [Molecular Loop Biosciences, LLC (‘Molecular Loop’)],” the entity from whom Invitae acquired the Asserted Patents, because “lack of commercial success may be probative evidence to rebut a showing of commercial success.” *Personalized User Model, L.L.P. v. Google Inc.*, C.A. 09-525-LPS, 2014 WL 807736, at *3 (D. Del. Feb. 27, 2014). Invitae’s bankruptcy, despite it having multiple products allegedly incorporating the patented technology, is directly relevant to whether the Asserted Patents in fact led to any commercial success. Likewise, evidence showing that Invitae was “not successful at the times [it] owned the patents-in-suit is probative of [Natera]’s contention that its own commercial success is in no way due to its alleged practice of the patented technology.” *Id.* at *3. Natera should be permitted to introduce evidence tending to show that the Asserted Patents were not a commercial success for Invitae or Molecular Loop, and that Signatera’s commercial success is unrelated to the claimed invention.

There are also practical reasons why Labcorp's motion sweeps too broadly. Labcorp has been substituted for Invitae as plaintiff in this case. But nearly all the evidence given by the plaintiff party in this case is about Invitae—Invitae's sale and marketing of an allegedly competing product, Invitae's documents, Invitae's witnesses, Invitae's interactions with the inventors. And Labcorp has given no evidence about itself in this case, nor could it—discovery had long been closed by the time that Labcorp substituted in as the plaintiff. Thus, the jury will need some context for why all the evidence about the plaintiff is referring to Invitae when the named plaintiff is Labcorp, and to obscure the reason for that would be impractical for the attorneys and for the witnesses, and it would surely create juror confusion.

The cases Invitae cites in support of its broad motion *in limine* are inapposite. *See HTC Corp. v. Tech. Properties Ltd.*, No. 5:08-CV-00882-PSG, 2013 WL 4782598, at *2 (N.D. Cal. Sept. 6, 2013) (precluding mention of bankruptcy to rebut evidence on the success of plaintiff's IP licensing program); *Magelky v. BNSF Ry. Co.*, No. 1:06-CV-025, 2008 WL 238451, at *2 (D.N.D. Jan. 28, 2008) (precluding mention of plaintiff's bankruptcy in personal injury lawsuit); *HSM Portfolio LLC v. Elpida Memory Inc.*, C.A. No. 11-770-RGA, D.I. 1220 at 2–3 (D. Del. Feb. 17, 2016) (precluding use of evidence of bankruptcy as improper character evidence under Rule 404(b)). Natera does not intend to introduce evidence of Invitae's financial condition for any of these improper purposes. But Invitae has put at issue its capacity to have historically exploited the additional sales opportunities that would have existed had Natera not sold Signatera, as well as the alleged commercial success of the patented technology. That puts Invitae's financial situation at issue in this case.

EXHIBIT 1



OCEAN TOMO®

A PART OF  **JS|HELD**

INVITAE CORPORATION

V.

NATERA, INC.

Civil Action Nos. 1:21-cv-00669 & 1:21-cv-01635

United States District Court for the District of Delaware

EXPERT REPORT OF ALEXANDER L. CLEMONS

June 16, 2023



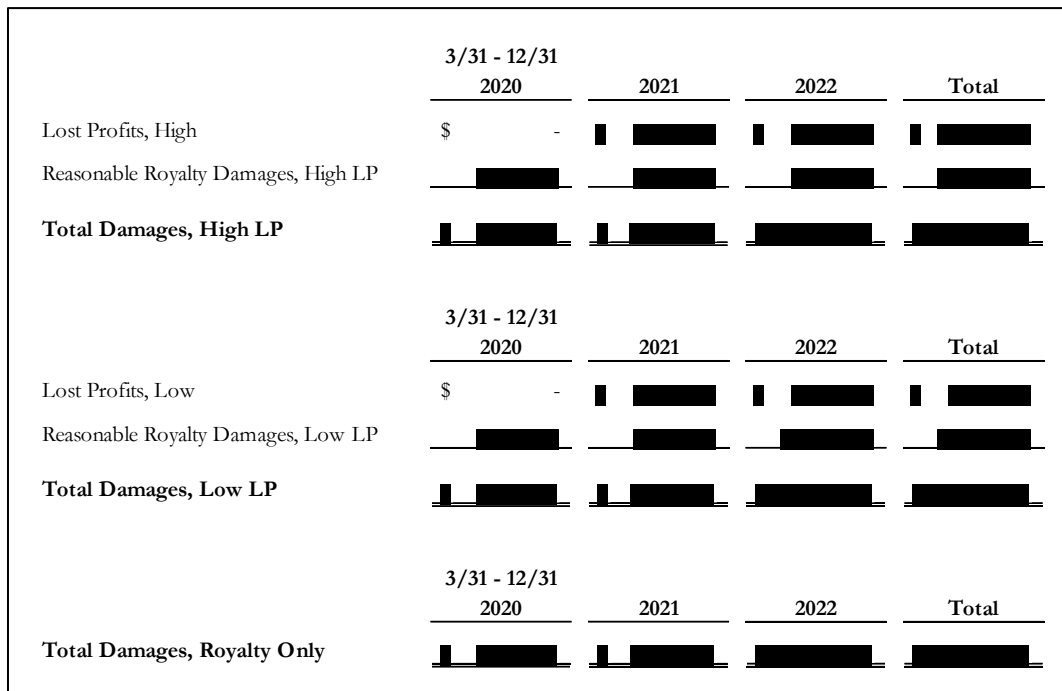
understanding of the facts and circumstances surrounding this matter, my review of the produced documentation, testimony, third party information available to date, and any underlying assumptions upon which I have relied. The information in this report is based on discovery to date and information that is currently available to me. Accordingly, my opinions described herein should be considered preliminary and subject to change based on future discovery, the testimony of other experts, and other case developments. I reserve the right to submit a supplemental report if both necessary and allowed by the Court. In addition to this report, I may rely on excerpts taken from videotaped depositions and/or demonstrative exhibits that illustrate the concepts and conclusions contained in this report.

3 SUMMARY OF OPINIONS

Based on the totality of the circumstances in this case and the information available to me at this time, I have concluded that the appropriate form of compensation in this case is an award of lost profits damages, with reasonable royalties on any residual sales; however, I have also performed an analysis of reasonable royalty damages on all sales as an alternative.¹⁴

Regarding lost profits, I have analyzed each of the *Panduit* factors and have reached a conclusion regarding the lost profits that Invitae would have realized, but for Natera's infringement of the Patents-in-Suit. I have calculated both a high and low lost profits amount as further described below. Regarding reasonable royalties, in addition to or as an alternative to lost profits, I have analyzed quantitative and qualitative valuation metrics, including the *Georgia-Pacific* factors, and have reached a conclusion regarding the appropriate reasonable royalties due to Invitae for Natera's use of the Patents-in-Suit in connection with the Accused Product. As summarized in the figure below, I have calculated total damages, both including and excluding lost profits.

¹⁴ I note that my damages calculations assume that all of the Patents-in-Suit will be found to be valid and infringed. However, in the event that any Patents-in-Suit are found to be either invalid or not infringed, it would be straightforward to recalculate damages starting at the earliest issuance date of any remaining patents.

**Figure 1: Summary of Damages through 2022¹⁵**

I reserve the right to update my damages calculations if updated sales information is provided.

4 RELEVANT PARTIES

4.1 Invitae



Founded in 2010 and headquartered in San Francisco, California, Invitae Corporation, is “a medical genetics company[] that provides genetic information to improve healthcare of people in the United States, Canada, and internationally.”¹⁶ Invitae “offers genetic tests in various clinical areas, including hereditary cancer, precision oncology, women’s health, rare diseases, and pharmacogenomics; digital health solutions; and health data

¹⁵ Appendix 3.1.

¹⁶ “Invitae Corporation – Public Company Profile,” *S&P Capital IQ*, capitaliq.com/CIQDotNet/company.aspx?companyId=222707176. I understand that the company was formerly known as Locus Development, Inc., and changed its name to Invitae Corporation in 2012.



naïve assay “liked the convenience of needing no tissue biopsy (which can be hard to obtain for some patients).”¹⁷³ However, pharmaceutical companies that purchased Signatera have already revealed their preference for the higher sensitivity and specificity of a tumor-informed test, rather than the convenience of a tumor-naïve test, through their selection of Signatera rather than Reveal in the real world. This indicates that such customers are likely to purchase PCM, another tumor-informed test, rather than Reveal, a tumor-naïve test, in the but for world.

Taken together, the above analysis indicates that, in the absence of Natera’s Signatera product, Invitae would have likely captured all of Signatera sales in the pharmaceutical market for MRD products; however, at a very minimum, Invitae would have split the sales roughly evenly with Guardant.

Based on the above, it is my understanding that there are no commercially acceptable non-infringing alternatives to the Patents-in-Suit for the Accused Products, it is my opinion that Invitae’s PCM product would have captured all (but no less than 50%) of Signatera sales in the pharmaceutical market in the but for world, and the second *Panduit* factor is met.

9.3 Sufficient Capacity

The third prong of the *Panduit* test requires that a patentee demonstrate that it possessed sufficient manufacturing, marketing, and financial capacity to make the additional sales that it claims to have lost to the infringer.

Regarding manufacturing and marketing capacity, I understand that, because of its robust testing and marketing capabilities, Invitae could have sold its PCM product in place of all of the infringing sales of Signatera in the pharmaceutical market during the relevant lost profits damages period.¹⁷⁴ [REDACTED]

[REDACTED]
[REDACTED]
[REDACTED]
[REDACTED]
[REDACTED]
[REDACTED]
[REDACTED]

[REDACTED] Additionally, as discussed above in Section 9.2, Mr. Moshkevich testified that [REDACTED]

¹⁷³ Alpert, Bill, “How Natera Is Defending Its Lead in a \$15B Cancer-Testing Market,” *Barron’s*, June 22, 2021, <https://www.barrons.com/articles/natera-stock-cancer-testing-market-51624372368>.

¹⁷⁴ Discussion with Richard Lusk; Discussion with Jim Stuart. I understand that Invitae’s lost profits damages do not start until the date of Invitae’s acquisition of the Patents-in-Suit on March 13, 2021.

¹⁷⁵ Deposition of Jim Stuart, April 6, 2023, pp. 6-7, 129.

¹⁷⁶ Deposition of Jim Stuart, April 6, 2023, p. 130.

¹⁷⁷ Deposition of Richard Lusk, June 9, 2023, pp. 8, 116.

¹⁷⁸ Deposition of Solomon Moshkevich, May 23, 2023, pp. 13, 155-156.



[REDACTED]”¹⁷⁹ [REDACTED]
 [REDACTED] 180 [REDACTED]
 [REDACTED]
 [REDACTED]
 [REDACTED]
 [REDACTED] [REDACTED]
 [REDACTED]¹⁸² As a result, it
 is clear that Invitae has sufficient manufacturing and marketing capacity to capture all of its lost PCM sales to
 Signatera in the pharmaceutical market during the relevant lost profits damages period.¹⁸³

Regarding financial capacity, it is my understanding that Invitae would not need to make any significant capital expenditures to increase its manufacturing or marketing capacity in order to capture its lost sales, due to its existing sufficient capacity.¹⁸⁴

Based on the above, it is my opinion that Invitae had sufficient capacity to satisfy 100% of the demand for Signatera in the pharmaceutical market during the relevant lost profits damages period, and the third *Panduit* factor is met.

9.4 Quantification

The final prong of the *Panduit* test requires the patent holder to properly quantify the amount of lost profits it suffered due to the infringement.

I understand that Invitae's lost profits damages do not start until the date of Invitae's acquisition of the Patents-in-Suit on March 13, 2021.¹⁸⁵ As a result, I have not considered lost profits to Invitae before March 13, 2021.

As discussed above, but for Natera's sales of Signatera, Invitae would have likely captured all (but no less than 50%) of those sales in the pharmaceutical market with sales of its PCM product. To calculate Invitae's lost

¹⁷⁹ Deposition of Solomon Moshkevich, May 23, 2023, p. 148.

¹⁸⁰ Discussion with Richard Lusk.

¹⁸¹ Discussion with Jim Stuart.

¹⁸² Discussion with Jim Stuart.

¹⁸³ See, Appendix 5.3; Appendix 5.4.

¹⁸⁴ Discussion with Richard Lusk; Discussion with Jim Stuart.

¹⁸⁵ Invitae 0000003173-188 at 173; “14/250,891 | 3851.0380003: SEQUENCE ASSEMBLY – Assignments,” *USPTO*, <https://patentcenter.uspto.gov/applications/14250891/assignments?application=>; “17/322,610 | 3851.0380006: SEQUENCE ASSEMBLY – Assignments,” *USPTO*, <https://patentcenter.uspto.gov/applications/17322610/assignments?application=>; “17/322,587 | 3851.0380005: SEQUENCE ASSEMBLY – Assignments,” *USPTO*, <https://patentcenter.uspto.gov/applications/17322587/assignments?application=>.



profits from these sales, I first considered the revenue generated by Natera from sales of Signatera in the pharmaceutical market starting on March 13, 2021.¹⁸⁶

Regarding Natera's Signatera revenue categorization, I understand that Signatera CLIA is the commercial product used for direct patient care,¹⁸⁷ Signatera RUO is used by pharmaceutical companies and academic partners and is distinct from CLIA,¹⁸⁸ Signatera Prospective is a prospective trial that is a clinical trial that will track a patient sample forward looking,¹⁸⁹ and Signatera CDx (companion diagnostics) is used by a pharmaceutical company to do testing related to a specific pharmaceutical that they are developing.¹⁹⁰ Revenues from Signatera RUO, Prospective, and CDx are categorized under Signatera Pharma,¹⁹¹ which is the pharmaceutical and clinical trials related to the Signatera product and also includes sales to academia and federal programs.¹⁹²

In order to calculate Invitae's lost revenue, I first calculated Natera's Signatera revenue for the pharmaceutical market (i.e., sales categorized as Signatera Pharma), from March 13, 2021, through 2022.¹⁹³ I then applied Invitae's but-for market share of 100% (but no less than 50%) of Signatera sales in the pharmaceutical market, discussed above, to determine the amount of PCM revenue that was lost by Invitae as a result of Natera's infringing sales of Signatera.¹⁹⁴ My calculation of Invitae's lost revenue is shown in the following figure.¹⁹⁵

¹⁸⁶ Appendix 5.5.

¹⁸⁷ Deposition of David Bessette, February 9, 2023, p. 60.

¹⁸⁸ Deposition of David Bessette, February 9, 2023, pp. 61-62.

¹⁸⁹ Deposition of David Bessette, February 9, 2023, p. 93.

¹⁹⁰ Deposition of David Bessette, February 9, 2023, p. 62.

¹⁹¹ NTRA-INVT-00419829, tab "Signatera Gross Profit", rows 31-33.

¹⁹² Deposition of David Bessette, February 9, 2023, pp. 128, 138.

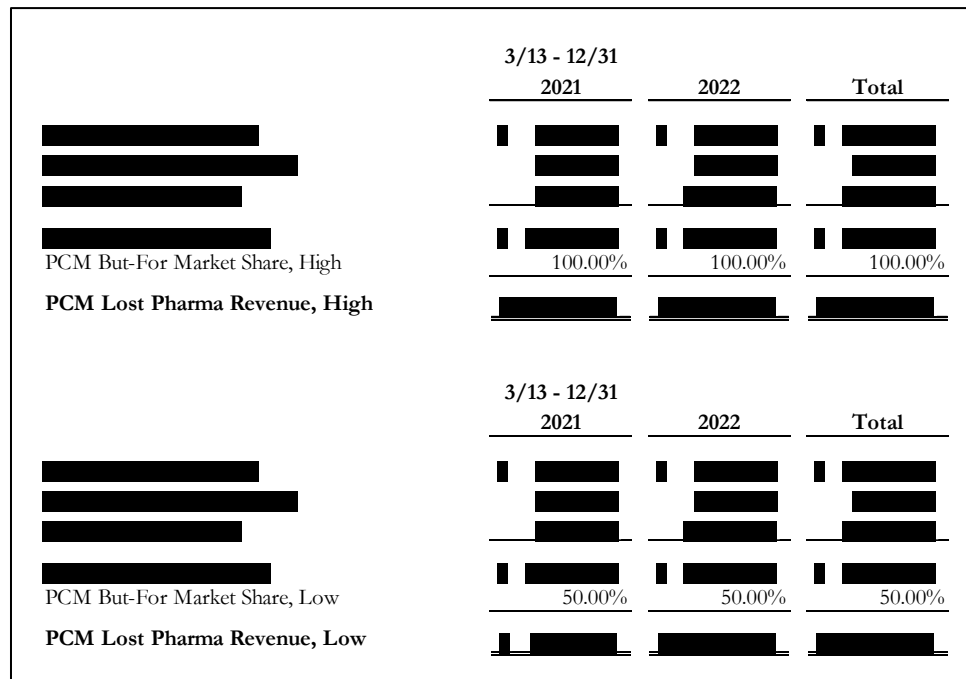
¹⁹³ Appendix 5.5.

¹⁹⁴ Appendix 5.5.

¹⁹⁵ Appendix 5.5.



Figure 11: Invitae's Lost Revenues in the Pharmaceutical Market through 2022¹⁹⁶



I note that it is conservative to assume that Invitae would only generate as much revenue from its lost sales as Natera generated from its infringing sales in the pharmaceutical market, as Invitae's PCM product has historically had a higher ASP than Natera's Signatera product, in the pharmaceutical market.¹⁹⁷

Next, I considered the incremental profits that would have been generated by Invitae from its lost revenue. Based on Invitae's produced financial documents,

However, as noted above, I have conservatively assumed that Invitae would capture its lost sales at . Additionally, due to the increased volume of PCM tests being run by Invitae, I understand that Invitae's incremental costs of goods sold ("COGS") per unit would also decrease.²⁰⁰

¹⁹⁶ Appendix 5.5.

¹⁹⁷ Appendix 6.1; Appendix 6.2. *See also*, Deposition of Richard Lusk, June 9, 2023, Exhibit 5, tab "Segment Summary".

¹⁹⁸ Appendix 6.2; Invitae0000003349, and tab "2021-2022".

¹⁹⁹ Deposition of Richard Lusk, June 9, 2023, Exhibit 5, tab "Gross Margin Assumption".

²⁰⁰ Discussion with Richard Lusk.

²⁰¹ Deposition of Jim Stuart, April 6, 2023, pp. 6-7, 130-131.



Similarly, Solomon Moshkevich, General Manager for Oncology at Natera, testified that for Natera “costs have gone down as [they] scaled and implemented efficiencies.”²⁰² Mr. Moshkevich testified that [REDACTED]

203

I understand that if Invitae were to increase its PCM volume by capturing its lost sales, its COGS would decrease.²⁰⁴ [REDACTED]

06

Based on Signatera's ASP in the pharmaceutical market and PCM's projected COGS at high volume reflected in the LRP, I have calculated Invitae's incremental profit margin on lost sales, as shown in the figure below.²⁰⁸

²⁰² Deposition of Solomon Moshkevich, May 23, 2023, pp. 13, 109.

²⁰³ Deposition of Solomon Moshkevich, May 23, 2023, p. 111.

²⁰⁴ Discussion with Richard Lusk.

²⁰⁵ Deposition of Richard Lusk, June 9, 2023, pp. 84, 87-88, 108

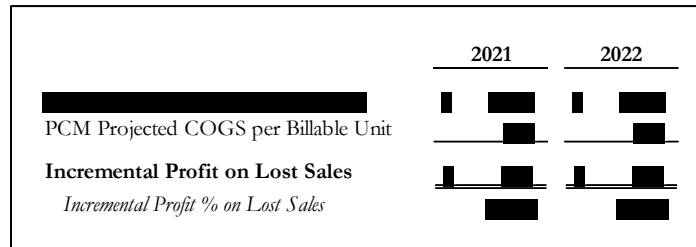
²⁰⁶ Deposition of Richard Lusk, June 9, 2023, Exhibit 5, tab “Gross Margin Assumption”, row 18.

Deposition of Richard Lusk, June 9, 2023, pp. 24-26.

²⁰⁷ Appendix 5.4; Appendix 5.9; Deposition of Richard Lusk, June 9, 2023, Exhibit 5, tab “Growth Assumptions”, row 25. [REDACTED]

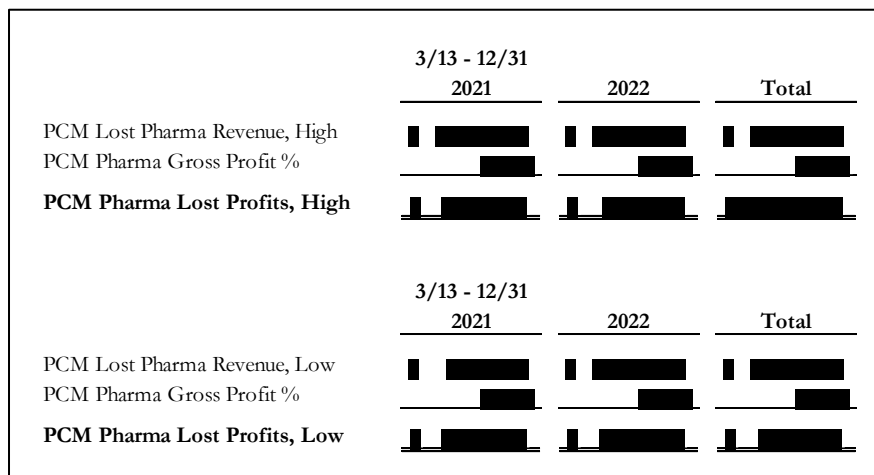
Appendix 6.1.

²⁰⁸ Appendix 5.2.

**Figure 12: Invitae's Incremental Profit on Lost Sales²⁰⁹**

Based on discussion with Richard Lusk, Vice President of Financial Planning and Analysis at Invitae, I understand that Invitae would not need to incur any additional incremental costs, apart from COGS to capture its lost sales.²¹⁰

Finally, I applied the gross profit margins calculated above to Invitae's lost revenue, in order to calculate Invitae's lost profits on their lost revenue, as shown in the following figure.²¹¹

Figure 13: Invitae's Lost Profits from Pharmaceutical Companies through 2022²¹²

²⁰⁹ Appendix 5.2. I note that the gross profit %s calculated above are [Redacted]. Appendix 6.1.

²¹⁰ Discussion with Richard Lusk. [Redacted]

Deposition of Richard Lusk, June 9, 2023, pp. 98-99.

²¹¹ Appendix 5.1.

²¹² Appendix 5.1.



Based on the above analysis of the *Panduit* factors, it is my opinion that, but for Natera's infringement of the Patents-in-Suit, Invitae would have realized lost profits, as calculated in the figure above.

For those sales of the Accused Product not accounted for in my calculation of Invitae's lost profits, I have calculated the reasonable royalty due on the residual sales in Section 13 below.

10 REASONABLE ROYALTY COMPENSATION

10.1 Overview

It is my understanding that in accordance with applicable statutory law, upon a finding of liability in a patent infringement action, the patentee is entitled to no less than "a reasonable royalty for the use made of the invention by the infringer[.]"²¹³

My determination of a reasonable royalty begins with the conclusion that there is no established royalty rate for the Patents-in-Suit. In general, a determination of whether there is an established royalty is based on a review of any relevant agreements produced and transactions relative to the following criteria defined in the *Sun Studs Inc. v. ATA Inc.* case:²¹⁴

- The agreements must have been entered into prior to when infringement began.
- The rate must not have been paid under threat of suit or in settlement of litigation.
- The rate must be paid for comparable rights.
- The rate must be paid by enough parties to indicate it is reasonable.

It is my opinion that there is no established royalty rate for the patented technology. Therefore, in the absence of an established royalty, I have based my determination of a reasonable royalty on a hypothetical negotiation between a willing licensee and a willing licensor around the time the alleged infringement began (the hypothetical negotiation date). The parties to the negotiation would have assumed that the Patents-in-Suit were valid and would be infringed by the prospective licensee unless he/she obtained a license. The reasonable royalty analysis focuses on the economic and bargaining positions of the plaintiff and defendant at the time of the hypothetical negotiation and the likely outcome of such negotiation given their positions.

This is consistent with the definition in the *Georgia-Pacific* case, specifically, "[t]he amount that a licensor (such as the patentee) and a licensee (such as the infringer) would have agreed upon (at the time the infringement began) if both had been reasonably and voluntarily trying to reach an agreement; that is, the amount which a prudent licensee—who desired, as a business proposition, to obtain a license to manufacture and sell a particular article embodying the patented invention—would have been willing to pay as a royalty and yet be

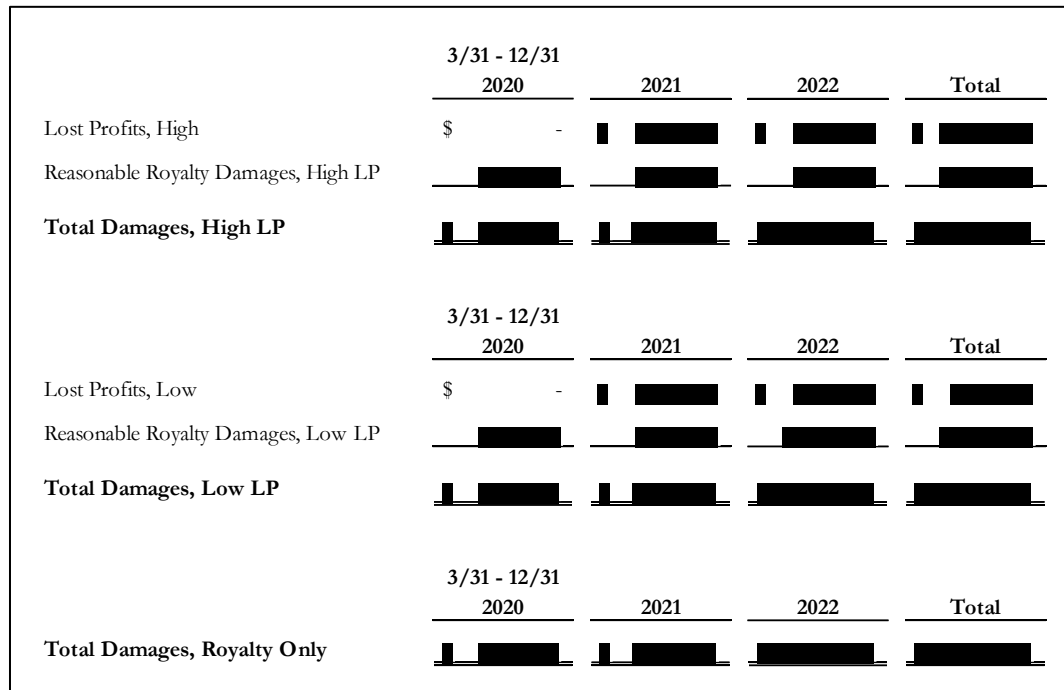
²¹³ 35 U.S.C. § 284.

²¹⁴ *Sun Studs, Inc. v. ATA Equip. Leasing, Inc.*, 872 F.2d. 978, 993 (Fed. Cir. 1989).



royalties, in addition to or as an alternative to lost profits, I have analyzed quantitative and qualitative valuation metrics, including the *Georgia-Pacific* factors, and have reached a conclusion regarding the appropriate reasonable royalties due to Invitae for Natera's use of the Patents-in-Suit in connection with the Accused Product. As summarized in the figure below, I have calculated total damages, both including and excluding lost profits.

Figure 26: Summary of Damages through 2022⁵¹¹



I reserve the right to update my damages calculations if updated sales information is provided.

16 SIGNATURE

Respectfully submitted,

Alexander L. Clemons

Alexander L. Clemons

June 16, 2023

Date

⁵¹¹ Appendix 3.1.

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	
v.)	C.A. No. 21-669 (GBW)
)	
)	
NATERA, INC.)	
)	
Defendant.)	
)	
<hr style="border: 0.5px solid black;"/>		
LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	
)	
v.)	C.A. No. 21-1635 (GBW)
)	
)	
NATERA, INC.)	
)	
Defendant.)	

**PLAINTIFF’S REPLY IN SUPPORT OF ITS MOTION *IN LIMINE* NO. 3: TO
EXCLUDE EVIDENCE AND ARGUMENT REGARDING INVITAE’S OVERALL
FINANCIAL CONDITION**

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*Attorneys for Plaintiff Laboratory
Corporation of America Holdings*

Dated: August 13, 2025

Natera argues that Invitae’s overall financial condition is relevant to rebut Labcorp’s arguments on lost profits and commercial success. Opp. at 1.

As to lost profits, however, neither party’s expert discussed Invitae’s financial state in their damages opinions, whether for lost profits (including manufacturing capacity for “additional sales opportunities”) or otherwise. Br. at 1; Opp. at 3. This makes sense, because Invitae’s overall financial condition and bankruptcy do not bear on its ability to manufacture or market its product, Br. at 2, a point that renders Natera’s case law irrelevant, Opp. at 1–2. Certainly, Natera has no evidence to suggest otherwise; if it did, its expert surely would have said so.

Second, and similarly, no party’s expert has asserted that Invitae’s overall financial condition shows commercial success of the Asserted Patents. In *Google*, the court explained that evidence of a party’s “lack of commercial success *may be* probative evidence to *rebut* a showing of commercial success.” *Personalized User Model, L.L.P. v. Google Inc.*, No. 09-cv-525-LPS, 2014 WL 807736, at *3 (D. Del. Feb. 27, 2014) (emphasis added). But because neither party’s experts used Invitae’s overall financial condition to argue commercial success, there is nothing to rebut. And *Apex*—a securities fraud case—is wholly inapposite. *APEX Fin. Options, LLC v. Gilbertson*, No. 19-cv-46-WCB-SRF, 2022 WL 622130, at *1 (D. Del. Mar. 3, 2022).

Natera further argues that the jury would be confused if it cannot discuss Invitae’s financial condition, because “all the evidence about the plaintiff is referring to Invitae.” Opp. at 3. But Invitae’s overall financial condition is unnecessary to explain to the jury that the identity of the plaintiff changed from Invitae to Labcorp because Labcorp bought Invitae. Natera’s insistence on referring to Invitae’s bankruptcy is just an attempt to prejudicially paint Invitae in a bad light.

Invitae’s financial condition remains irrelevant to any claim in this case and introducing it would be highly prejudicial. Br. at 2–3. Labcorp’s motion should be granted.

August 13, 2025

Respectfully submitted,

FARNAN LLP

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CERTIFICATE OF SERVICE

I, Brian E. Farnan, hereby certify that on August 13, 2025, a copy of PLAINTIFF'S REPLY IN SUPPORT OF ITS MOTION IN LIMINE NO. 3: TO EXCLUDE EVIDENCE AND ARGUMENT REGARDING INVITAE'S OVERALL FINANCIAL CONDITION was served on the following as indicated:

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EXHIBIT 20A

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

**DEFENDANT'S MOTION *IN LIMINE* NO. 1:
PRECLUDE EVIDENCE OR ARGUMENT THAT ANTICIPATION BY A
PRIOR ART SYSTEM CANNOT BE ESTABLISHED USING
MULTIPLE DOCUMENTS THAT DESCRIBE THE SYSTEM**

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I. INTRODUCTION

Natera respectfully moves to preclude Invitae from offering evidence or argument suggesting that anticipation by a prior-art system cannot be established through multiple documents describing that system. Such evidence and argument by Invitae would misstate the law and would thus be irrelevant, prejudicial, and likely to confuse and mislead the jury. *See* Fed. R. Evid. 402 & 403.

II. BACKGROUND

The Asserted Patents cover a computerized algorithm, *see, e.g.*, Ex. A at 61:3–14, for assembling and comparing genetic data. Some of the prior art on which Natera relies are software programs that pre-date the Asserted Patents. One such prior-art software is “NextGENe,” which was the subject of Natera’s motion for summary judgment of anticipation. *See* D.I. 224, 225. In opposing that motion, Invitae made the surprising (and previously undisclosed) argument that Natera’s reliance on multiple documents to demonstrate NextGENe’s functionality and features precludes a finding of anticipation because, Invitae argued, “[a]ll authorities on anticipation require a *single* prior art reference.” D.I. 246 at 26 (emphasis in original). Invitae’s argument seems to be that, even where the asserted prior art is a product or system (here, software) and not a printed publication, and the defendant relies on multiple documents to establish the functionality of that prior art—here, to prove what the software did and how it worked—the challenge is one of obviousness rather than anticipation. During a meet and confer, Invitae’s counsel indicated that Invitae believes it is entitled to argue this position before the jury. But it would be a misstatement of the law to do so and should therefore be prohibited.¹

¹ Invitae also has never properly challenged whether the evidence proffered by Natera concerns the same prior art system, and it is too late now for that argument. Invitae’s experts never opined that the documents Natera’s experts use to demonstrate the functionality of a particular prior-art system do not, in fact, describe that system, and in the

III. ARGUMENT

Printed publications—patents, scientific papers, articles—are the most common form of prior art. Where anticipation rests on a printed publication, it is hornbook law that all elements of the claim must be found in one such printed document. But a patent claim can also be anticipated by something tangible that existed in the past—an air conditioner or blender, for example—or, as relevant here, a software program or system. In such circumstances, the pre-existing article is itself the single prior art reference. For example, under 35 U.S.C. § 102(a), the prior use or knowledge of an invention can anticipate an asserted patent claim. Likewise, under 35 U.S.C. § 102(g)(2), someone else’s invention may anticipate a patent claim, whether or not it is made public, provided that it was not abandoned, suppressed, or concealed. *See Tyco Healthcare Grp. LP v. Ethicon Endo-Surgery, Inc.*, 774 F.3d 968, 976–77 (Fed. Cir. 2014).

It is well settled that, where the prior art is a product or system, “it is permissible for a defendant to establish anticipation by using several documents that reveal how a single prior art system works.” *IOENGINE, LLC v. PayPal Holdings, Inc.*, 607 F. Supp. 3d 464, 518–19 (D. Del. 2022); *see also Altera Corp. v. PACT XPP Techs., AG*, No. 14-02868-JD, 2015 WL 3830982, at *3 (N.D. Cal. June 19, 2015) (“Multiple documents that describe a single prior art device count as a single prior art reference.”). That is because the system itself is the single piece of prior art that establishes a lack of novelty; the documents used to prove the system’s functionality are simply evidence. *See, e.g., Sonoscan, Inc. v. Sonotek, Inc.*, 936 F.2d 1261, 1263 (Fed. Cir. 1991) (“That the offered product is in fact the claimed invention may be established by any relevant evidence, such as memoranda, drawings, correspondence, and testimony of witnesses.” (citation omitted));

case of NextGENe, Invitae’s expert admitted that they do. *See* Ex. B at 261:13–22. Nor has Invitae raised this argument in any of its interrogatory responses, including its validity-contention response. *See* Ex. C at 7–69. Invitae should not now be permitted to attempt to overcome this defect by presenting arguments to the jury that contradict the law.

see also British Telecomm. PLC v. IAC/InteractiveCorp., No. 18-366-WCB, 2020 WL 3047989, at *6 (D. Del. June 8, 2020) (“It was permissible for [the defendant] to use several documents as evidence about how a single prior art system worked.”); *Daedalus Blue, LLC v. MicroStrategy Inc.*, No. 20-551-RCY, 2023 WL 5941736, at *9 (E.D. Va. Sept. 12, 2023) (“For product-based anticipation . . . secondary materials about a product may be relied upon as evidence of how the prior art product works for anticipation purposes.”).

Indeed, this Court has held that it is appropriate to rely on “executable software, [a] user manual, **and** source code” to show how a single prior-art system operated for purposes of proving anticipation. *See Finjan, Inc. v. Symantec Corp.*, No. 10-593-GMS, 2013 WL 5302560, at *12 (D. Del. Sept. 19, 2013) (emphasis added), *aff’d*, 577 F. App’x 999 (Fed. Cir. 2014).

In light of this overwhelming authority, Invitae should not be permitted to mislead or confuse the jury by suggesting that a prior art software system is *per se* not anticipatory because Natera relies on multiple sources to demonstrate the functionality and elements of the prior art software. Such argument is not only irrelevant as a matter of law but also misleading and confusing, as it would put before the jury a theory based on an erroneous legal standard. *See, e.g., Honeywell Int., Inc. v. Hamilton Sundstrand Corp.*, 378 F. Supp. 2d 459, 481–82 (D. Del. 2005) (excluding validity theory that applies the wrong legal standard under Rules 402 and 403). Natera respectfully moves the Court to preclude such evidence or argument from Invitae.

EXHIBIT A

Page 1

VOLUME: I
PAGES: 1-326
EXHIBITS: 1-33

UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE
NO. 1:21-cv-01635-LPS

INVITAE CORPORATION,)
Plaintiff,)
vs.)
NATERA, INC.,)
Defendant.)

VIDEOTAPED DEPOSITION OF INVITAE
CORPORATION BY GREGORY J. PORRECA, PhD, called as a
witness by and on behalf of the Defendant, pursuant
to the applicable provisions of the Federal Rules
of Civil Procedure, Rule 30(b)(6), before P. Jodi
Ohnemus (remotely), RPR, RMR, CRR, CA-CSR #13192,
NH-LSR #91, MA-CSR #123193, and Notary Public,
within and for the Commonwealth of Massachusetts,
at Cambridge, Massachusetts, on Friday, April 28,
2023, commencing at 9:47 a.m.

CONFIDENTIAL

Page 2	Page 4
<p>1 APPEARANCES:</p> <p>2</p> <p>3 (Via Videoconference)</p> <p>4 WEIL, GOTSHAL & MANGES, LLP</p> <p>5 BY: Christopher M. Pepe, Esq.</p> <p>6 2001 M Street NW, Suite 600</p> <p>7 Washington, DC 20036</p> <p>8 202 682-7153</p> <p>9 Christopher.pepe@weil.com</p> <p>10 For the Plaintiff, Deponent and</p> <p>11 Molecular Loop Biosolutions</p> <p>12</p> <p>13</p> <p>14 (Via Videoconference)</p> <p>15 MATORIN LAW OFFICE, LLC</p> <p>16 BY: Mitchell J. Matorin, Esq.</p> <p>17 18 Grove Street, Suite 2</p> <p>18 Wellesley, MA 02482</p> <p>19 781 453-0100</p> <p>20 Mmatorin@matorinlawoffice.com</p> <p>21 For the Deponent and Molecular</p> <p>22 Loop Biosolutions</p> <p>23</p> <p>24</p> <p>25</p>	<p>1 I N D E X</p> <p>2</p> <p>3 TESTIMONY OF: PAGE</p> <p>4</p> <p>5 GREGORY J. PORRECA</p> <p>6 (By Mr. Stone) 10</p> <p>7</p> <p>8</p> <p>9</p> <p>10</p> <p>11</p> <p>12</p> <p>13</p> <p>14</p> <p>15</p> <p>16</p> <p>17</p> <p>18</p> <p>19</p> <p>20</p> <p>21</p> <p>22</p> <p>23</p> <p>24</p> <p>25</p>
Page 3	Page 5
<p>1 APPEARANCES: (CONT'D)</p> <p>2</p> <p>3 (Via Videoconference)</p> <p>4 GROOMBRIDGE WU BAUGHMAN</p> <p>5 & STONE, LLP</p> <p>6 BY: Eric Stone, Esq.</p> <p>7 Ariella Barel, Esq.</p> <p>8 Daniel Klein, Esq.</p> <p>9 565 Fifth Avenue, Suite 2900</p> <p>10 New York, NY 10017</p> <p>11 332 269-0030</p> <p>12 Eric.stone@groombridgewu.com</p> <p>13 Ariella.barel@groombridgewu.com</p> <p>14 Dan.klein@groombridgewu.com</p> <p>15 For the Defendants</p> <p>16</p> <p>17 ALSO PRESENT:</p> <p>18 (Via Videoconference)</p> <p>19 Kevin Gallagher, Video Operator</p> <p>20</p> <p>21 (Via Videoconference)</p> <p>22 Carissa Narciso,</p> <p>23 Veritext Concierge</p> <p>24</p> <p>25</p>	<p>1 E X H I B I T S</p> <p>2 EXHIBIT DESCRIPTION PAGE</p> <p>3</p> <p>4 Exhibit 1 Greg Porreca Linked-In 16</p> <p>5 profile</p> <p>6 Exhibit 2 US Patent 10,604,799 27</p> <p>7 Exhibit 3 email, 9/27/2011, 30</p> <p>8 ML-PORRECA0000000076-78</p> <p>9 Exhibit 4 email, 9/28/2011, 46</p> <p>10 ML-PORRECA0000000080-81</p> <p>11 Exhibit 5 Invention Disclosure Form, 58</p> <p>12 ML-PORRECA0000000068-74</p> <p>13 Exhibit 6 US Patent, 11,149,308 153</p> <p>14 Exhibit 7 US Patent 11,155,863 153</p> <p>15 Exhibit 8 US Patent 8,209,130 156</p> <p>16 Exhibit 9 US Patent 8,738,300 156</p> <p>17 Exhibit 10 Bio IT World 2011, Boston, 160</p> <p>18 MA, ML-PORRECA0000001649,</p> <p>19 multipage document</p> <p>20 Exhibit 11 email, 2/13/2011, 168</p> <p>21 Invitae0010119047</p> <p>22 Exhibit 12 DePristo, et al., 168</p> <p>23 manuscript, 20-page document</p> <p>24 Exhibit 13 email, 1/13/2011, 175</p> <p>25 Invitae0010118439</p>


2 (Pages 2 - 5)

Page 6				Page 8			
1	Exhibit 14	NextGENe, Manion, et al.,	175	1	VIDEO OPERATOR: We are now going on the		
2		February 2009,		2	record at approximately 9:47 a.m. Today's date is		
3		Invitae0010118440-442		3	April 28th, 2023. This is media unit No. 1 in the		
4	Exhibit 15	NextGENe, Levan, et al.,	175	4	video-recorded deposition of Gregory Porreca, taken		
5		September 2008		5	in the matter of Invitae Corporation versus Natera,		
6	Exhibit 16	email, 8/19/2009,	187	6	Inc. It is filed in the US District Court for the		
7		Invitae0010122472-474		7	District of Delaware. I have two case numbers: CA		
8	Exhibit 17	email, 2/12/2013,	196	8	No. 21-669 and CA No. 21-1634 -- 35, rather.		
9		Invitae0010111931-932		9	My name is Kevin Gallagher. I am the		
10	Exhibit 18	email, 3/18/2014,	199	10	court -- I am the videographer. The court reporter		
11		Invitae0010091296		11	is Jodi Ohnemus, and the concierge is Carissa		
12	Exhibit 19	abstract, Kennedy, et al.,	201	12	Narcisco. We're all from the firm of Veritext		
13		Invitae0010091297-298		13	Legal Solutions.		
14	Exhibit 20	article, Umbarger, et al.,	206	14	At this time the attorneys present in the		
15		ML-PORRECA00000001584-592		15	deposition will identify themselves and their		
16	Exhibit 21	email, 2/8/2013,	220	16	affiliations for the record.		
17		Invitae0010135520-521		17	MR. STONE: Sure. My name is Eric Stone.		
18	Exhibit 22	Overview of MIP Technology,	224	18	I'm with the firm of Groombridge Wu Baughman &		
19		1/27/2017,		19	Stone. I'm joined today by my colleagues Ariella		
20		Invitae0010126923-939		20	Barel and Dan Klein and together we represent		
21	Exhibit 23	letter, Jeffrey Luber,	230	21	Natera.		
22		3/16/2017, five-page		22	MR. PEPE: Chris Pepe from Weil Gotshal,		
23		document		23	representing Invitae and the witness.		
24	Exhibit 24	Description of Technology,	242	24	MR. MATORIN: Mitchell Matorin, Matorin		
25		Invitae0010126595-597		25	Law Office in Wellesley, Massachusetts,		
Page 7				Page 9			
1	Exhibit 25	email, 3/5/2017,	243	1	representing both the witness and Molecular Loop.		
2		Invitae0010126590-594		2	VIDEO OPERATOR: And now our court		
3	Exhibit 26	Good Start Genetics	267	3	reporter will swear or affirm the witness and we		
4		Intellectual Property		4	can proceed.		
5		Overview		5	GREGORY J. PORRECA, PhD, having		
6		Invitae0010126201-215		6	satisfactorily been identified by		
7	Exhibit 27	Agreement and Plan of	271	7	the production of a driver's license,		
8		Merger, 118-page document		8	and being first duly sworn by the Notary		
9	Exhibit 28	email, 12/18/2017,	276	9	Public, was examined and testified as		
10		Invitae0000003686-689		10	follows to interrogatories.		
11	Exhibit 29	Sale of MIP Assets to	281	11	COURT REPORTER: Thank you. Go right		
12		Molecular Loop Biosolutions,		12	ahead.		
13		LLC, Invitae0000003121-169		13	MR. STONE: I will. I actually have a		
14	Exhibit 30	First Amendment to Asset	293	14	preliminary question for counsel which I was going		
15		Purchase Agreement,		15	to jump in and do before the witness was sworn;		
16		Invitae0000003101-102		16	but, you know, I didn't want to talk over you.		
17	Exhibit 31	Third Amendment to Asset	293	17	I don't care which of you defends the		
18		Purchase Agreement,		18	deposition, but I don't want to play Canadian		
19		Invitae00000003105-106		19	doubles. Which of you is going to be playing the		
20	Exhibit 32	email, 8/7/2020,	304	20	primary role in defending?		
21		Invitae0000003205-206		21	MR. PEPE: I will.		
22	Exhibit 33	Asset Purchase Agreement,	317	22	MR. STONE: That's fine. Totally okay.		
23		3/13/2021,		23	MR. PEPE: Just note there may be times		
24		Invitae0000003946-979		24	where -- where Mitch may speak.		
25				25	MR. STONE: And that's -- absolutely.		

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<p style="text-align: right;">Page 58</p> <p>1 A. Yes. This would be the first diagram of 2 the algorithm. 3 Q. Let's look at Exhibit 5 to your 4 deposition, and then I'm going to want a break in a 5 minute 'cause I can hear my voice going. But let's 6 look at Exhibit 5 for a moment. 7 (Exhibit 5, Invention Disclosure Form, 8 ML-PORRECA000000068-74.) 9 A. Okay. 10 Q. Doctor Porreca, I've placed before you 11 what I've marked as Exhibit 5 to your deposition, 12 which bears the Bates numbers ML-PORRECA 68 through 13 74. It's a document entitled "Invention Disclosure 14 Form." 15 Do you see that there? 16 A. I do. 17 Q. It lists as the -- people who conceived of 18 and/or reduced to practice the invention, yourself 19 and Doctor Kennedy; correct? 20 A. That is correct. 21 Q. And then there is a section entitled 22 "Description of the Invention"? 23 A. Yes. 24 Q. And that continues on for a couple of 25 pages; and on page 4 of this document actually has</p>	<p style="text-align: right;">Page 60</p> <p>1 A. Tom Meyers was our IP attorney at the time 2 for the company. 3 Q. In house or outside counsel? 4 A. Outside counsel. 5 Q. And it says (as read): 6 "On what date did you make such a 7 disclosure?" 8 Answer: "September 28, 2011." 9 You see that? 10 A. I do see that. 11 Q. Fair to say, then, that you had the idea 12 on September 27, 2011, and were in a position to 13 disclose the idea to your lawyer the next day? 14 A. That's what this document indicates. 15 Q. Is it right? 16 A. As far as I can remember, I believe it is 17 correct. 18 Q. On the top of the next page it says (as 19 read): 20 "When did you first do any experimental 21 work towards carrying out the invention?" 22 You see that there? 23 A. I do. 24 Q. And the answer is "N/A." 25 A. Yes.</p>
<p style="text-align: right;">Page 59</p> <p>1 the photograph of the whiteboard; correct? 2 A. That is correct. 3 Q. Then it says (as read): 4 "When did you first think of this 5 invention?" 6 Answer: "September 27, 2011." 7 Is that right? 8 A. That's correct. 9 Q. And I guess I should ask two questions: 10 That's what it says. And it's accurate; correct? 11 A. That is what it says. And that is 12 accurate. 13 Q. Thank you. And it says (as read): 14 "What record do you have to substantiate 15 this date?" 16 Then it says (as read): 17 "This disclosure, email from Greg to Caleb 18 with photo of whiteboard outlining method." 19 You see that? 20 A. I do see that. 21 Q. And it says (as read): 22 "To whom did you first disclose this 23 invention?" 24 And the answer is "Tom Meyers." 25 Who's that?</p>	<p style="text-align: right;">Page 61</p> <p>1 Q. Is that meaning not applicable? 2 A. Correct. 3 Q. And the reason that that's your answer is 4 that you didn't do any experimental work towards 5 carrying out the invention; correct? 6 A. That's correct, because it was a 7 computational algorithm. 8 Q. Right. The -- the invention is a 9 computational algorithm. It's not something that 10 you do physically; correct? 11 A. It's not something that -- I -- I think 12 the way I answered that question was it's not some 13 kind of a wet lab technique. It's a computational 14 algorithm. 15 Q. And then you say, (as read): 16 "When did you first make written 17 description of the invention?" 18 Answer: "September 27, 2011." 19 You see that there? 20 A. I do. 21 Q. Now, on every page of this document you 22 and Doctor Kennedy have signed it and dated it 23 November 7, 2011, other than the last page; is that 24 correct? 25 A. So there's a signature -- there are two</p>

16 (Pages 58 - 61)

<p style="text-align: right;">Page 322</p> <p>1 Q. Fair enough.</p> <p>2 Were you surprised that Invitae had sued</p> <p>3 Natera?</p> <p>4 MR. PEPE: Object to form.</p> <p>5 A. Not -- probably not totally surprised, no.</p> <p>6 Q. One second. Almost done.</p> <p>7 Do you know a person at Natera named</p> <p>8 Bernard Zimmerman?</p> <p>9 A. I don't know him personally, no.</p> <p>10 [REDACTED]</p> <p>11 [REDACTED]</p> <p>12 [REDACTED]</p> <p>13 [REDACTED]</p> <p>14 [REDACTED]</p> <p>15 [REDACTED]</p> <p>16 [REDACTED]</p> <p>17 [REDACTED]</p> <p>18 [REDACTED]</p> <p>19 [REDACTED]</p> <p>20 [REDACTED]</p> <p>21 [REDACTED]</p> <p>22 [REDACTED]</p> <p>23 [REDACTED]</p> <p>24 [REDACTED]</p> <p>25 [REDACTED]</p>	<p style="text-align: right;">Page 324</p> <p>1 DEPONENT'S ERRATA SHEET</p> <p>2 AND SIGNATURE INSTRUCTIONS</p> <p>3</p> <p>4</p> <p>5 The original of the Errata Sheet has</p> <p>6 been delivered to Mitchell Matorin, Esq.</p> <p>7 When the Errata Sheet has been</p> <p>8 completed by the deponent and signed, a copy</p> <p>9 thereof should be delivered to each party of record</p> <p>10 and the ORIGINAL delivered to Eric Stone, Esq., to</p> <p>11 whom the original deposition transcript was</p> <p>12 delivered.</p> <p>13</p> <p>14</p> <p>15 INSTRUCTIONS TO DEPONENT</p> <p>16</p> <p>17 After reading this volume of your</p> <p>18 deposition, indicate any corrections or changes to</p> <p>19 your testimony and the reasons therefor on the</p> <p>20 Errata Sheet supplied to you and sign it. DO NOT</p> <p>21 make marks or notations on the transcript volume</p> <p>22 itself.</p> <p>23</p> <p>24 REPLACE THIS PAGE OF THE TRANSCRIPT WITH THE</p> <p>25 COMPLETED AND SIGNED ERRATA SHEET WHEN RECEIVED.</p>
<p style="text-align: right;">Page 323</p> <p>1 MR. STONE: All right. We are out of</p> <p>2 time, and I think we're in a great place.</p> <p>3 Doctor Porreca, you've told us that you</p> <p>4 don't expect to come to trial. So it has been a</p> <p>5 pleasure meeting you, and I really appreciate your</p> <p>6 time.</p> <p>7 THE WITNESS: Likewise. Pleasure meeting</p> <p>8 you as well.</p> <p>9 VIDEO OPERATOR: We're now going off the</p> <p>10 record at approximately 6:23 p.m.</p> <p>11 (Whereupon the deposition ended at</p> <p>12 6:23 p.m.)</p> <p>13</p> <p>14</p> <p>15</p> <p>16</p> <p>17</p> <p>18</p> <p>19</p> <p>20</p> <p>21</p> <p>22</p> <p>23</p> <p>24</p> <p>25</p>	<p style="text-align: right;">Page 325</p> <p>1 Commonwealth of Massachusetts</p> <p>2 Middlesex, ss.</p> <p>3</p> <p>4</p> <p>5 I, P. Jodi Ohnemus, Notary Public</p> <p>6 in and for the Commonwealth of Massachusetts,</p> <p>7 do hereby certify that there came before me</p> <p>8 (remotely) on the 28th day of April, 2023, the</p> <p>9 deponent herein, who was duly sworn by me; that the</p> <p>10 ensuing examination upon oath of the said deponent</p> <p>11 was reported stenographically by me and transcribed</p> <p>12 into typewriting under my direction and control;</p> <p>13 and that the within transcript is a true record of</p> <p>14 the questions asked and answers given at said</p> <p>15 deposition.</p> <p>16</p> <p>17 I FURTHER CERTIFY that I am neither</p> <p>18 attorney nor counsel for, nor related to or</p> <p>19 employed by any of the parties to the action</p> <p>20 in which this deposition is taken; and, further,</p> <p>21 that I am not a relative or employee of any</p> <p>22 attorney or financially interested in the outcome</p> <p>23 of the action.</p> <p>24</p> <p>25 IN WITNESS WHEREOF I have hereunto set my</p> <p>26 hand and affixed my seal of office this</p> <p>27 30th day of April, 2023, at Waltham.</p> <p>28</p> <p>29 </p> <p>30</p> <p>31 P. Jodi Ohnemus, RPR, RMR, CRR,</p> <p>32 CSR, Notary Public,</p> <p>33 Commonwealth of Massachusetts</p> <p>34 My Commission Expires:</p> <p>35 3/3/2028</p>

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1 ATTACH TO DEPOSITION OF: GREGORY J. PORRECA, PhD
CASE: INVITAE VS. NATERA

2

ERRATA SHEET

3

INSTRUCTIONS: After reading the transcript of your
deposition, note any change or correction to your
testimony and the reason therefor on this sheet.

5 DO NOT make any marks or notations on the
transcript volume itself. Sign and date this
errata sheet (before a Notary Public, if required).

Refer to page 324 of the transcript for errata
sheet distribution instructions.

8 PAGE LINE

CHANGE: _____

9 REASON: _____

CHANGE: _____

10 REASON: _____

CHANGE: _____

11 REASON: _____

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12 REASON: _____

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13 REASON: _____

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14 REASON: _____

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15 REASON: _____

CHANGE: _____

16 REASON: _____

CHANGE: _____

17 REASON: _____

18 I have read the foregoing transcript of
my deposition and except for any corrections or
changes noted above, I hereby subscribe to the
transcript as an accurate record of the statements
made by me.

21 _____
GREGORY J. PORRECA, PhD

22

Subscribed and sworn to before me
23 this _____ day of _____, 2023.

24 _____
Notary Public

25 My Commission Expires:

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EXHIBIT B

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Page 1

1 UNITED STATES DISTRICT COURT
2 FOR THE DISTRICT OF DELAWARE

3 *****

4 INVITAE CORPORATION,
5 Plaintiff,

6 vs. Case No. 1:21-cv-01635-GBW
Case No. 1:21-cv-00669-GBW

7 NATERA, INC.,
8 Defendant.

9 *****

10 **HIGHLY CONFIDENTIAL - ATTORNEYS EYES ONLY**

11 REMOTE VIDEOTAPED DEPOSITION OF
12 DAN EDWARD KRANE, PH.D.
13 New York, New York
14 August 31, 2023
15
16
17
18
19
20
21

22 Reported by:
23 KATHY S. KLEPFER, RMR, RPR, CRR, CLR
24 JOB NO. 6062706
25

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<p style="text-align: right;">Page 2</p> <p>1 August 31, 2023</p> <p>2 8:30 a.m.</p> <p>3 REMOTE VIDEOTAPED deposition of DAN</p> <p>4 EDWARD KRANE, PH.D., before Kathy S.</p> <p>5 Klepfer, a Registered Professional Reporter,</p> <p>6 Registered Merit Reporter, Certified</p> <p>7 Realtime Reporter, Certified Livenote</p> <p>8 Reporter, and Notary Public of the State of</p> <p>9 New York.</p> <p>10</p> <p>11</p> <p>12</p> <p>13</p> <p>14</p> <p>15</p> <p>16</p> <p>17</p> <p>18</p> <p>19</p> <p>20</p> <p>21</p> <p>22</p> <p>23</p> <p>24</p> <p>25</p>	<p style="text-align: right;">Page 4</p> <p>1 INDEX</p> <p>2 EXAMINATION OF DAN E. KRANE, PH.D.: PAGE</p> <p>3 By Mr. Klein 8</p> <p>4</p> <p>5</p> <p>6 KRANE EXHIBITS: PAGE</p> <p>7 Exhibit 1, Expert Report of Dan E. Krane 5</p> <p>8 Exhibit 2, Rebuttal Expert Report of Dan E. 5</p> <p>Krane to the Opening Expert Report of Michael</p> <p>9 Metzker, Ph.D.</p> <p>10 Exhibit 3, Corrected Rebuttal Expert Report of 5</p> <p>Dan E. Krane to the Opening Expert Report of</p> <p>11 Istavan Albert, Ph.D.</p> <p>12 Exhibit 4, Reply Expert Report of Dan E. Krane, 5</p> <p>Ph.D. to Rebuttal Expert Report of Istavan</p> <p>13 Albert, Ph.D.</p> <p>14 Exhibit 5, Reply Expert Report of Dan E. Krane, 5</p> <p>Ph.D. to Rebuttal Expert Report of Michael</p> <p>15 Metzker, Ph.D.</p> <p>16 Exhibit 6, U.S. Patent 10,604,799 56</p> <p>17 Exhibit 7, CigarUtils.java file 173</p> <p>18 Exhibit 8, U.S. Patent No. 11,155,863 223</p> <p>19</p> <p>20</p> <p>21</p> <p>22</p> <p>23</p> <p>24</p> <p>25</p>
<p style="text-align: right;">Page 3</p> <p>1 APPEARANCES:</p> <p>2</p> <p>3 BLUE PEAK PARTNERS</p> <p>4 Attorneys for Plaintiff</p> <p>5 3139 W. Holcombe Blvd.</p> <p>6 PMB 8160</p> <p>7 Houston, TX 77025</p> <p>8 BY: JUSTIN CONSTANT, ESQ.</p> <p>9</p> <p>10 GROOMBRIDGE WU BAUGHMAN & STONE, LLP</p> <p>11 Attorneys for Defendant</p> <p>12 565 Fifth Avenue</p> <p>13 New York, NY 10017</p> <p>14 BY: DANIEL KLEIN, ESQ.</p> <p>15 daniel.klein@groombridgewu.com</p> <p>16 ARIELLA BAREL, ESQ.</p> <p>17 ariella.barrel@groombridgewu.com</p> <p>18</p> <p>19</p> <p>20</p> <p>21 ALSO PRESENT:</p> <p>22 JEFF MENTON, Videographer</p> <p>23 CARISSA NARCISCO, Exhibit Tech.</p> <p>24</p> <p>25</p>	<p style="text-align: right;">Page 5</p> <p>1 (Krane Exhibit 1, Expert Report of Dan</p> <p>2 E. Krane, marked for identification as of</p> <p>3 this date.)</p> <p>4 (Krane Exhibit 2, Rebuttal Expert</p> <p>5 Report of Dan E. Krane to the Opening Expert</p> <p>6 Report of Michael Metzker, Ph.D., marked for</p> <p>7 identification as of this date.)</p> <p>8 (Krane Exhibit 3, Corrected Rebuttal</p> <p>9 Expert Report of Dan E. Krane to the Opening</p> <p>10 Expert Report of Istavan Albert, Ph.D.,</p> <p>11 marked for identification as of this date.)</p> <p>12 (Krane Exhibit 4, Reply Expert Report</p> <p>13 of Dan E. Krane, Ph.D. to Rebuttal Expert</p> <p>14 Report of Istavan Albert, Ph.D., marked for</p> <p>15 identification as of this date.)</p> <p>16 (Krane Exhibit 5, Reply Expert Report</p> <p>17 of Dan E. Krane, Ph.D. to Rebuttal Expert</p> <p>18 Report of Michael Metzker, Ph.D., marked for</p> <p>19 identification as of this date.)</p> <p>20 THE VIDEOGRAPHER: Good morning.</p> <p>21 We're going on the video record at</p> <p>22 approximately 8:35 a.m. on August 31, 2023.</p> <p>23 Please note that this deposition is</p> <p>24 being conducted virtually. Quality of</p> <p>25 recording depends on the quality of camera</p>

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<p style="text-align: right;">Page 6</p> <p>1 and internet connections of participants. 2 What is seen from witness and heard 3 on-screen is what will be recorded. 4 Audio and video recording will 5 continue to take place unless all parties 6 agree to go off the record. 7 This is video media disk 1 of the 8 video-recorded deposition of Daniel Krane, 9 taken by counsel for the defendant, in the 10 matter of Invitae Corporation versus Natera, 11 Inc. This case is filed in the United 12 States District Court, District of Delaware. 13 There are two case numbers: 21-669-GDW and 14 21-1635-GDW. 15 This deposition is being conducted 16 remotely using virtual technology. My name 17 is Jeff Menton. I am the certified legal 18 videographer. The court reporter is Kathy 19 Klepfer, and we are both from Veritext New 20 York. 21 All counsel consent to this remote 22 video arrangement and waive any objections 23 to this manner of reporting. 24 If there are any objections to the 25 court reporter swearing in the witness</p>	<p style="text-align: right;">Page 8</p> <p>1 DAN EDWARD KRANE, called as a 2 witness, having been duly sworn by a Notary 3 Public, was examined and testified as 4 follows: 5 EXAMINATION BY 6 MR. KLEIN: 7 Q. Well, Good morning. 8 Could you state and spell your name 9 and provide your home address, please? 10 A. Yes. My name is Dan Edward Krane. 11 And let me just note that that's -- I've been 12 seeing "Daniel" show up on a few of the things 13 here. It's actually my legal name is Dan, and 14 that is spelled D-A-N, and the last name is 15 spelled K-R-A-N-E. 16 My home address is 1102 Mead, M-E-A-D, 17 Road, in Xenia, X-E-N-I-A, Ohio. The Zip Code 18 is 45385. 19 Q. Thank you. And I think I'll be able 20 to get your name right. And also, you have 21 great initials. We share in both. 22 So have you been deposed before? 23 A. I have not been deposed in a patent 24 litigation situation before, but I have been 25 deposed in the context of criminal trials and,</p>
<p style="text-align: right;">Page 7</p> <p>1 remotely on this remote video arrangement, 2 please state them now. 3 Not hearing any objections, counsel 4 will now state their appearances and 5 affiliations for the record, beginning with 6 the noticing attorney, and then the court 7 reporter will swear the witness in. 8 MR. KLEIN: Daniel Klein from 9 Groombridge Wu Baughman & Stone here on 10 behalf of defendant Natera, Inc., and with 11 me is my colleague Ariella Barel. 12 MR. CONSTANT: Justin Constant with 13 Blue Peak Law Group, representing Invitae. 14 * * * 15 16 17 18 19 20 21 22 23 24 25</p>	<p style="text-align: right;">Page 9</p> <p>1 on occasion, in some civil trials involving DNA 2 testing. 3 Q. Were those federal or state court 4 proceedings in which you were deposed? 5 A. I believe both. I'm certain of 6 federal. I'm pretty confident of state as well. 7 Q. How recently were you last deposed in 8 a case? 9 A. You know, to some extent, they all 10 blend together, but the one that comes most 11 clearly to mind would have been about two and a 12 half years ago. 13 Q. Okay. So I'll just go over some 14 basics which you probably know, but because the 15 official record of these proceedings is going to 16 be the transcript, I'll need verbal answers from 17 you as opposed to head nods or physical 18 gestures. 19 I will do my best not to speak over 20 you. I would appreciate you doing the same. 21 There may on occasion be an instance where I 22 accidentally cut you off. I will do my best not 23 to do that and give you time to finish your 24 answer. 25 If I ask you a question and you</p>

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<p>Page 258</p> <p>1 your rebuttal to Dr. Metzker.</p> <p>2 A. I see from my Table of Contents that</p> <p>3 there's some discussion about the description of</p> <p>4 CASAVA on page 22, but the specific response to</p> <p>5 Dr. Metzker does begin later.</p> <p>6 Would you like me to look first at</p> <p>7 page 170?</p> <p>8 Q. Yes, please.</p> <p>9 A. All right. I am at page 170.</p> <p>10 Q. Now, you understand that what the --</p> <p>11 Dr. Metzker refers to that, in his opinion,</p> <p>12 shows a read-to-contig description is the Q</p> <p>13 score, correct?</p> <p>14 A. I understand that he characterizes the</p> <p>15 Q score as a read-to-contig description.</p> <p>16 Q. And why don't you take a look at page</p> <p>17 173 of your report.</p> <p>18 A. I'm at page 173.</p> <p>19 Q. Uh-huh. And you see you've got a</p> <p>20 call-out from the CASAVA manual there?</p> <p>21 A. I see that.</p> <p>22 Q. Right above paragraph 714?</p> <p>23 A. Yes.</p> <p>24 Q. And it says, "The relative</p> <p>25 probabilities of these alignments for each read</p>	<p>Page 260</p> <p>1 Court, would you also agree that this Q score is</p> <p>2 likewise a description of one reference -- of</p> <p>3 one sequence with reference to another sequence</p> <p>4 in a, albeit, literal and narrow form?</p> <p>5 MR. CONSTANT: Objection. Form.</p> <p>6 THE WITNESS: Counsel, just to -- in</p> <p>7 an effort to save us time and to give you a</p> <p>8 thorough answer and very efficiently, let me</p> <p>9 just point you to what I say in paragraph</p> <p>10 715 and, you know, it begins "when Q scores</p> <p>11 merely indicate probability."</p> <p>12 And if you want, we can look further</p> <p>13 at what's there, but I think the answer to</p> <p>14 your question is what's in my report in 715.</p> <p>15 So, in some very narrow literal sense, a Q</p> <p>16 score is a descriptor, but it's not the kind</p> <p>17 of descriptor that will be useful for the</p> <p>18 application that's described in these</p> <p>19 patents, that combination step.</p> <p>20 BY MR. KLEIN:</p> <p>21 Q. I understand.</p> <p>22 But so, too, is a CIGAR string on its</p> <p>23 own, in your opinion, equally useful or not</p> <p>24 useful, correct?</p> <p>25 MR. CONSTANT: Objection. Form.</p>
<p>Page 259</p> <p>1 are used to call the indel's genotype and</p> <p>2 calculate the associated quality score."</p> <p>3 Correct?</p> <p>4 A. It does say that.</p> <p>5 Q. And then on page 174, at the top, it</p> <p>6 says, "For the second stage of indel calling,</p> <p>7 the variant caller realigns all intersecting</p> <p>8 reads to each candidate indel, in addition to</p> <p>9 aligning the read to the reference and any</p> <p>10 alternate indel candidates at the same site."</p> <p>11 Do you see that as well?</p> <p>12 A. That's at the top of the call-out,</p> <p>13 yes.</p> <p>14 Q. And then this next paragraph within</p> <p>15 that call-out says, "The relative likelihoods of</p> <p>16 all alignments for each read are used to assign</p> <p>17 probabilities to each of the three possible</p> <p>18 indel genotypes," correct?</p> <p>19 A. The three genotypes being homozygous,</p> <p>20 heterozygous, or not present, yes.</p> <p>21 Q. Correct. And so my question is, in</p> <p>22 the same way that you had described a CIGAR</p> <p>23 string on its own as, in a very literal and</p> <p>24 narrow sense, being a description within the</p> <p>25 meaning of the patent claims as construed by the</p>	<p>Page 261</p> <p>1 THE WITNESS: A CIGAR string is so</p> <p>2 much more useful than the Q score, and yet,</p> <p>3 the CIGAR string, taken entirely by itself,</p> <p>4 is not all the information that's necessary.</p> <p>5 BY MR. KLEIN:</p> <p>6 Q. Thank you.</p> <p>7 I now want to turn your attention to</p> <p>8 your discussion of NextGENe, which I'll refer</p> <p>9 you to page 149 in your rebuttal to Dr. Metzker.</p> <p>10 A. I'm on page 149.</p> <p>11 Q. Page 149.</p> <p>12 A. I'm at that page.</p> <p>13 Q. Now, in paragraph 604, you list out</p> <p>14 LeVan (2008), Liu, L-I-U, (2009), Manion, (April</p> <p>15 2009), and Manion (March 2009).</p> <p>16 You see that?</p> <p>17 A. Yes, that's in paragraph 604.</p> <p>18 Q. And you don't dispute that those</p> <p>19 references describe the NextGENe system,</p> <p>20 correct?</p> <p>21 A. Those are all descriptive of the</p> <p>22 NextGENe system, in whole or in part.</p> <p>23 Q. Thank you.</p> <p>24 Now, I want to turn to you paragraph</p> <p>25 615.</p>

66 (Pages 258 - 261)

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<p style="text-align: right;">Page 290</p> <p>1 Q. And that -- if I could direct you to 2 page 141 of your opening report. 3 A. Very helpful. Thank you. 4 Q. You're welcome. 5 A. Yes, that is on point. 6 Q. And the license that you were 7 referring to is what's called the Archer-BD 8 license agreement, correct? 9 A. That is correct. 10 Q. And that license agreement involves 11 patents covering technology related to 12 stochastic labeling, correct? 13 A. Stochastic labeling is involved, yes. 14 MR. KLEIN: Can we just go off the 15 record for like two minutes? 16 I'm sorry. 17 THE VIDEOGRAPHER: Going off the video 18 record at 4:44 p.m. 19 (Recess.) 20 THE VIDEOGRAPHER: We're back on the 21 video record at 4:47 p.m. 22 Please proceed. 23 MR. CONSTANT: Sorry. Dan, how 24 much -- do you know how much time we have 25 left?</p>	<p style="text-align: right;">Page 292</p> <p>1 THE VIDEOGRAPHER: We're on the 2 record. 3 MR. KLEIN: We are on the record. 4 MR. CONSTANT: Oh, we are? I 5 apologize. 6 Yes, so we reserve the right under 7 Federal Rules of Civil Procedure 30(e) to 8 give an errata, and that's it. No further 9 questions. 10 THE VIDEOGRAPHER: Would you like to 11 give the court reporter any transcripts 12 orders? 13 MR. CONSTANT: No, I -- I don't need a 14 transcript, and just the Weil default. 15 THE VIDEOGRAPHER: All right. Ready 16 to go off? 17 MR. KLEIN: Yeah, we can go off the 18 record. I want to say something about the 19 transcript order, but we don't need to be on 20 the record for that. 21 THE VIDEOGRAPHER: Okay. This 22 concludes today's testimony given by Dan 23 Krane, Ph.D. The total number of media 24 disks was 7 and will be retained by Veritext 25 New York. The time is 4:49 p.m., and we're</p>
<p style="text-align: right;">Page 291</p> <p>1 MR. KLEIN: 14. 2 MR. CONSTANT: Sorry. I just realized 3 I had my speaker off. There we go. 4 Can you say that one more time? 5 MR. KLEIN: 14 minutes. 6 MR. CONSTANT: 14 minutes. All right. 7 I got it. Sorry. I thought I was losing my 8 mind. 9 MR. KLEIN: No worries. 10 MR. CONSTANT: I appreciate it. 11 MR. KLEIN: Of course. 12 Dr. Krane, I have no further 13 questions. I really appreciate your time 14 today. 15 THE WITNESS: Well, Dan, it's been a 16 long day, but I appreciate your good nature, 17 and I'm glad that we've had a chance to 18 talk. I hope that I've been able to be of 19 some help to you. 20 MR. KLEIN: Yeah. Thank you. 21 MR. CONSTANT: Okay. Yeah, and if you 22 don't mind, could we go back on the record 23 for just one minute just so I can reserve 24 the right to give an errata under 30(e)? 25 And that's it.</p>	<p style="text-align: right;">Page 293</p> <p>1 going off the video record. 2 (Whereupon, the deposition concluded 3 at 4:49 p.m.) 4 oOo 5 6 7 8 9 10 11 12 DAN E. KRANE, PH.D. 13 14 Subscribed and sworn to 15 before me this day 16 of 2023. 17 18 19 20 21 22 23 24 25</p>

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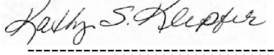
<p>1 CERTIFICATE</p> <p>2 STATE OF NEW YORK)</p> <p>3 : ss</p> <p>4 COUNTY OF NEW YORK)</p> <p>5 I, Kathy S. Klepfer, a Registered</p> <p>6 Merit Reporter and Notary Public within and</p> <p>7 for the State of New York, do hereby</p> <p>8 certify:</p> <p>9 That DAN E. KRANE, PH.D., the witness</p> <p>10 whose deposition is herein before set forth,</p> <p>11 was duly sworn by me and that such</p> <p>12 deposition is a true record of the testimony</p> <p>13 given by such witness.</p> <p>14 I further certify that I am not</p> <p>15 related to any of the parties to this action</p> <p>16 by blood or marriage and that I am in no way</p> <p>17 interested in the outcome of this matter.</p> <p>18 In witness whereof, I have hereunto</p> <p>19 set my hand this 5th day of September 2023.</p> <p>20 </p> <p>21 KATHY S. KLEPFER, RPR, RMR, CRR, CLR</p> <p>22</p> <p>23</p> <p>24</p> <p>25</p>	<p>Page 294</p>
<p>1 NAME OF CASE: Invitae v. Natera</p> <p>2 DATE OF DEPOSITION: August 31, 2023</p> <p>3 NAME OF WITNESS: Dan E. Krane, Ph.D.</p> <p>4 Reason Codes:</p> <p>5 1. To clarify the record.</p> <p>6 2. To conform to the facts.</p> <p>7 3. To correct transcription errors.</p> <p>8 Page _____ Line _____ Reason _____</p> <p>9 From _____ to _____</p> <p>10 Page _____ Line _____ Reason _____</p> <p>11 From _____ to _____</p> <p>12 Page _____ Line _____ Reason _____</p> <p>13 From _____ to _____</p> <p>14 Page _____ Line _____ Reason _____</p> <p>15 From _____ to _____</p> <p>16 Page _____ Line _____ Reason _____</p> <p>17 From _____ to _____</p> <p>18 Page _____ Line _____ Reason _____</p> <p>19 From _____ to _____</p> <p>20 Page _____ Line _____ Reason _____</p> <p>21 From _____ to _____</p> <p>22 Page _____ Line _____ Reason _____</p> <p>23 From _____ to _____</p> <p>24 _____</p> <p>25 DAN E. KRANE, PH.D.</p>	<p>Page 296</p>

EXHIBIT C

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

INVITAE CORPORATION,

Plaintiff,

Case No. 21-cv-669-GBW

V.

JURY TRIAL DEMANDED

NATERA, INC.

**HIGHLY CONFIDENTIAL –
ATTORNEYS EYES ONLY**

Defendant.

ATTORNEYS EYES ONLY

INVITAE CORPORATION,

Plaintiff,

Case No. 21-cv-01635-GBW

V.

JURY TRIAL DEMANDED

NATERA, INC.

**HIGHLY CONFIDENTIAL –
ATTORNEYS EYES ONLY**

Defendant.

HIGHLY CONFIDENTIAL
ATTORNEYS EYES ONLY

**INVITAE CORPORATION'S SUPPLEMENTAL RESPONSES AND OBJECTIONS TO
NATERA, INC.'S SECOND SET OF INTERROGATORIES (NO. 9)¹**

Pursuant to Rules 26 and 33 of the Federal Rules of Civil Procedure, the Local Rules of the United States District Court for the District of Delaware (“Local Rules”), the District of Delaware Default Standard for Discovery, including Discovery of Electronically Stored Information (“Default Standard”), and any other applicable Orders or rules, Plaintiff Invitae

¹ Invitae notes that Natera identified this Interrogatory as being Interrogatory No. 8. Prior to serving this Interrogatory, however, Natera had already served eight interrogatories. Accordingly, Invitae identifies this Interrogatory as Interrogatory No. 9.

Corporation (“Invitae”) hereby makes the following supplemental responses and objections to Defendant Natera, Inc.’s (“Natera”) Second Set Of Interrogatories (No. 9).

The failure of Invitae to make a specific objection to any particular aspect of Natera’s Interrogatories is not, and should not be construed as, an admission that responsive documents or information exist. Any statement that Invitae will produce documents or information does not mean that any such documents or information exist.

GENERAL OBJECTIONS

1. The following responses, while based on a diligent investigation by Invitae and its counsel, are necessarily supported only by those facts and writings presently and specifically known and readily available. Discovery in this matter is ongoing. As this Action proceeds, further information and/or documents may be considered, or their significance better understood, and Invitae reserves the right to change, amend or supplement these responses. Invitae therefore makes these responses without prejudice to its right to produce at any stage of these proceedings, including at trial, evidence of any facts or information that Invitae may later recall or discover. Invitae further reserves the right to change, amend or supplement any or all of the matters contained in these responses with facts or information that it learns were omitted, including by inadvertence, mistake, or excusable neglect, and as additional facts are ascertained and contentions are made in this litigation. A partial response to any interrogatory that has been objected to in whole or in part is not a waiver of the objection. By asserting various objections, Invitae does not waive other objections that may become applicable.

2. These responses are made solely for the purposes of this Action, and are subject to all objections as to competence, authenticity, relevance, materiality, privilege, and admissibility. All such objections and grounds are expressly reserved and may be interposed at the time of trial

3. Each and all of Invitae's general objections are hereby expressly incorporated into each and all of Invitae's specific responses. For particular emphasis, one or more of these general objections may be reiterated in a specific response. The absence or inclusion or any reiteration in a specific response is neither intended as, nor shall be construed as, a limitation or waiver of any general objection or any other specific objection made herein.

4. No incidental or implied admissions are intended by the responses below. The fact that Invitae has answered or objected to all or part of an interrogatory should not be construed or taken as an admission that Invitae accepts or admits the existence of any purported facts set forth or assumed by such interrogatory or that Invitae has waived or intended to waive any part of any objection to the interrogatory.

5. Invitae objects to the interrogatories, including the definitions and instructions contained therein, to the extent that they call for information and/or documents protected by the attorney-client privilege, attorney work-product doctrine, or other applicable privileges or immunities. Invitae further objects to the interrogatories to the extent that they purport to seek or call for the information constituting, recording, or reflecting the work product of Invitae's attorneys, including their thoughts, opinions, or mental impressions in connection with the preparation, prosecution, avoidance or defense of any claim by or against Invitae. Invitae also objects to the interrogatories to the extent that they seek information protected by the right of privacy contained in the United States Constitution, or other applicable statute or case law. Nothing contained in these responses is intended as, nor shall in any way be deemed, a waiver of the attorney-client privilege, attorney work product doctrine, right of privacy or other applicable privilege or immunity. Invitae objects to logging privileged documents created on or after the date of the filing of the Complaint in this Action. Invitae does not waive, intentionally or

otherwise, any attorney-client privilege, work-product immunity, or any other privilege, immunity, or other protection that may be asserted to protect any information from disclosure.

6. Invitae objects to the interrogatories, including the definitions and instructions contained therein, to the extent that they prematurely seek expert discovery.

7. Invitae objects to the interrogatories, including the definitions and instructions contained therein, to the extent that they seek discovery of confidential and/or competitive information, including, for example, trade secrets or other confidential research, development or commercial information. Invitae will only produce such information in accordance with the protective order to be entered in this Action, including special safeguards regarding the handling of and access to highly confidential or competitive information.

8. Invitae objects to the interrogatories, including the definitions and instructions contained therein, to the extent that they call for information and/or documents that Invitae may not produce without the consent of third parties. To the extent the consent of any third party is necessary to produce any such information and/or documents, Invitae will not produce such information and/or documents until it has received such consent.

9. Invitae objects to the interrogatories, including the definitions and instructions contained therein, to the extent that they call for information and/or documents that are not relevant to any claim or defense in this Action and/or that are not proportional to the needs of the case.

10. Invitae objects to the interrogatories, including the definitions and instructions contained therein, to the extent that they purport to require Invitae to search for or produce information and/or documents that are not within its possession, custody or control. Invitae will use reasonable diligence to locate information and/or documents within its possession, custody, or control.

11. Invitae objects to the interrogatories, including the definitions and instructions contained therein, to the extent that (i) the discovery sought by any such interrogatory is unreasonably cumulative, duplicative, obtainable from other sources that are more convenient, less burdensome or less expensive, the information is as easily ascertainable to the Natera as it is to Invitae, or is readily available from public sources, and/or (ii) compliance with any such interrogatory would be unduly burdensome, expensive, harassing and/or oppressive.

12. Invitae objects to the interrogatories, including the definitions and instructions contained therein, as overly broad and unduly burdensome to the extent that they fail to specify an appropriate time period, thereby seeking information and/or documents that are not relevant to any claim or defense in this Action and/or that are not proportional to the needs of the case.

13. Invitae objects to the interrogatories, including the definitions and instructions contained therein, to the extent that they call for legal conclusions.

14. Invitae objects to the interrogatories, including the definitions and instructions contained therein, to the extent that they are vague and ambiguous.

15. Invitae objects to the definition of “Invitae,” “you”, and “your” as being overbroad, unduly burdensome, and oppressive, to the extent that it purports to impose duties beyond those imposed by the Federal Rules of Civil Procedure, the Local Rules, or any order or ruling by the Court in this action, including by seeking information and/or documents that are not relevant to any claim or defense to the needs of the case. Invitae also objects to this definition to the extent it renders any part of any interrogatory unduly burdensome, harassing, oppressive, or overbroad to the extent it purports to include entities other than Invitae. For purposes of its responses, Invitae will construe these terms to mean only Invitae, and will produce documents and/or information only to the extent they are in possession, custody, or control of Invitae.

16. Invitae objects to Natera's definitions of "document," "communication," "regarding," "identify or identifying," and "identify all facts" as being overly broad, unduly burdensome and oppressive, calling for information protected by the attorney-client privilege or work product doctrine, outside the scope of discovery, and as seeking information and documents beyond Invitae's possession, custody, or control.

17. Invitae objects to each Interrogatory to the extent it seeks production of "all," and "each," document that refers or relates to a particular subject on the grounds of overbreadth, undue burden and expense, and that it calls for information outside the scope of discovery.

18. Invitae objects to each Interrogatory to the extent a response is sought with respect to a question of law or to the extent a response calls for an expert opinion.

19. Invitae also objects to each Instruction as unduly burdensome, harassing, oppressive and overbroad to the extent it is inconsistent with or calls for discovery beyond the scope of the Federal Rules of Civil Procedure, the Local Rules for the District of Delaware, or any order or ruling of this or any other Court, including by seeking information and/or documents that are not relevant to any claim or defense in this Action and/or that are not proportional to the needs of the case. Invitae will comply with the requirements of the Federal Rules of Civil procedure, the Local Rules, and any order or ruling by the Court in this Action in responding to the interrogatories.

20. Invitae objects to each Interrogatory to the extent it seeks information already in Natera's possession or is available to Natera from public sources for which the burden of obtaining such information is the same or less for Natera as it is for Invitae. Invitae provides these responses with the understanding that Invitae is in possession of or has access to such sources, including, without limitation, Invitae's website.

21. Invitae's agreement to produce any category of information or documents is not a representation that any such information or documents in that category actually exist in Invitae's possession, custody, or control, or can be located through a reasonable search, or that such documents are relevant.

22. Subject to and without waiving these general Objections, Invitae responds and specifically objects to Natera's interrogatories as follows:

INTERROGATORY NO. 9:

Describe in full and informative detail all facts, evidence, and arguments that Plaintiff contends rebut the arguments in Natera's Initial Invalidity Contentions that the Asserted Claims are invalid, including the level of education, training, specialty, and experience that Plaintiff contends a person having ordinary skill in the art for the subject matter described and claimed in the Asserted Patents would have had as of the date of the claimed invention(s). Your response should identify each of the alleged differences between the inventions claimed in the Asserted Patents and the prior art, any alleged lack of motivation to combine, and any alleged lack of reasonable expectation of success. It should also identify all documents and information supporting or contradicting such contentions, and the natural persons most knowledgeable of such contentions and documents.

RESPONSE TO INTERROGATORY NO. 9 (2022-06-21):

Invitae incorporates each and all of its General Statements and Objections as if set forth fully herein. Invitae further objects to this interrogatory as a contention interrogatory that prematurely seeks expert discovery. Invitae will provide its validity positions in one or more expert reports served in accordance with the schedule set by the Court and incorporates those reports by reference into this response. Invitae further objects to this interrogatory as vague, ambiguous, unduly burdensome, overbroad, harassing, and oppressive. Invitae further objects to this interrogatory to the extent it calls for a legal conclusion. Invitae further objects to this interrogatory to the extent it is compound and contains subparts in violation of Rule 33 of the Federal Rules of Civil Procedure. Invitae further objects to this interrogatory to the extent it calls for information protected from discovery under the attorney-client privilege, the attorney work-product doctrine,

or any other applicable privilege or immunity. Invitae further objects to this interrogatory to the extent it seeks information concerning patent claims and claim terms. Invitae further objects to this interrogatory to the extent it improperly attempts to shift the burden of proof to Invitae with respect to validity.

Subject to its general and specific objections, and based on its investigation to date, Invitae responds as follows:

On March 31, 2020, the United States Patent and Trademark Office duly and legally issued U.S. Patent No. 10,604,799 (“799 Patent”). On October 19, 2021, the United States Patent and Trademark Office duly and legally reissued U.S. Patent No. 11,149,308 (“308 Patent”). On October 26, 2021, the United States Patent and Trademark Office duly and legally issued U.S. Patent No. 11,155,863 (“863 Patent”). Under 35 U.S.C. § 282(a), a “patent shall be presumed valid. Each claim of a patent (whether in independent, dependent, or multiple dependent form) shall be presumed valid independently of the validity of other claims; dependent or multiple dependent claims shall be presumed valid even though dependent upon an invalid claim.”

Regarding Natera’s allegations of anticipation as stated in its Claim Charts, Appendices 1-12, Invitae responds as follows:

- Appendix 1: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents’ sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing technology. For example, Natera is unable to cite a single passage referring to “contigs”

in support of its allegations that claim elements 1[e] and [g] of the '799 Patent were disclosed and/or rendered obvious in the prior art. Nor does Natera's cited prior art disclose the similar claim elements in the '308 and '863 Patents.

- Appendix 2: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents' sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing technology. For example, Natera's citations in support of its allegations that claim element 1[g] of the '799 Patent was disclosed and/or rendered obvious in the prior art merely recite experimental results, failing to mention any form of combination of descriptions even once. The prior art cited in Appendix 2, to the extent it generates contigs at all, does not align reads to the contigs, but realigns reads to the reference. Nor does Natera's cited prior art disclose the similar claim elements in the '308 and '863 Patents.
- Appendix 3: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents' sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing technology. For example, Natera's citations in support of its allegations that claim

element 1[g] of the '799 Patent was disclosed and/or rendered obvious in the prior art in fact describe an entirely different process, one that only functions once indels have been identified. Nor does Natera's cited prior art disclose the similar claim elements in the '308 and '863 Patents.

- Appendix 4: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents' sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing technology. For example, Natera's citations in support of its allegations that claim element 1[g] of the '799 Patent was disclosed and/or rendered obvious in the prior art in actuality merely recites an ordinary contig-based assembly process. The cited prior art merely teaches an improved technique for generating contigs. Nor does Natera's cited prior art disclose the similar claim elements in the '308 and '863 Patents.
- Appendix 5: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents' sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing technology. For example, Natera fails to provide a single citation that even mentions contigs in support of its allegations that claim element 1[d] of the '799 Patent was

disclosed and/or rendered obvious in the prior art. Nor does Natera's cited prior art disclose the similar claim element in the '308 and '863 Patents. The cited prior art in Appendix 6 fails to disclose alignment of reads to contigs followed by combining reference alignments and sequence read alignments.

- Appendix 6: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents' sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing technology. For example, Natera's citations in support of its allegations that claim element 1[g] of the '799 Patent was disclosed and/or rendered obvious in the prior art in actuality merely recites an ordinary contig-based assembly process. Nor does Natera's cited prior art disclose the similar claim elements in the '308 and '863 Patents.
- Appendix 7: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents' sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing technology. For example, Natera's citations in support of its allegations that claim element 1[g] of the '799 Patent was disclosed and/or rendered obvious in the prior art in actuality merely recites an ordinary contig-based assembly process. Even to the

- extent Natera contends the cited prior art discloses alignment reads to contigs and alignment of contigs to a reference, those processes are not used as part of an integrated process. Nor does Natera's cited prior art disclose the similar claim elements in the '308 and '863 Patents.
- Appendix 8: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents' sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing technology. For example, Natera's citations in support of its allegations that claim element 1[g] of the '799 Patent was disclosed and/or rendered obvious in the prior art in actuality merely recites an ordinary contig-based assembly process. Even to the extent Natera contends the cited prior art discloses alignment reads to contigs and alignment of contigs to a reference, those processes are not used as part of an integrated process. Nor does Natera's cited prior art disclose the similar claim elements in the '308 and '863 Patents.
 - Appendix 9: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents' sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing

- technology. For example, Natera's citations in support of its allegations that claim element 1[g] of the '799 Patent was disclosed and/or rendered obvious in the prior art in actuality merely recites an ordinary contig-based assembly process. The cited prior art does not disclose alignment of contigs to a reference. Nor does Natera's cited prior art disclose the similar claim elements in the '308 and '863 Patents.
- Appendix 10: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents' sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing technology. For example, Natera's citations in support of its allegations that claim element 1[g] of the '799 Patent was disclosed and/or rendered obvious in the prior art in actuality merely recites an ordinary contig-based assembly process. The cited prior art does not disclose alignment of reads to contigs. Nor does Natera's cited prior art disclose the similar claim elements in the '308 and '863 Patents.
 - Appendix 11: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents' sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing technology. For example, Natera's very first citation in support of its allegations that

the '799 Patent was disclosed and/or rendered obvious in the prior art in fact describes an entirely different assembly process, one that does not use a reference sequence. Nor does Natera's cited prior art disclose the similar claim elements in the '308 and '863 Patents.

- Appendix 12: The cited prior art in this Claim Chart does not anticipate any of the Asserted Claims because it fails to specifically disclose, teach, or embody the unique combination of steps involved in the Asserted Patents' sequence assembly approach, specifically the assembly approach in which sequencing reads are grouped into contigs and aligned to a reference genome, the original individual reads are re-aligned to the contigs, and then the two are combined, improving upon then-current DNA sequencing technology. For example, Natera's citations in support of its allegations that claim element 1[g] of the '799 Patent was disclosed and/or rendered obvious in the prior art in actuality merely recites an ordinary contig-based assembly process. Nor does Natera's cited prior art disclose the similar claim elements in the '308 and '863 Patents.

Regarding Natera's allegations of obviousness, Natera has cited an excessive and unreasonable number of references as support, claiming that they render the Asserted Claims obvious "alone and/or in combination." This gives rise to an excessive and unreasonable number of potential combinations, rendering Natera's claims of obviousness entirely lacking in specificity. Should Natera narrow its allegations of obviousness to a more specific degree, Invitae will respond accordingly.

Regarding Natera's allegation that references from the time of the invention of the patent in similar and related fields disclosed relevant teachings reflecting motivations to combine, Natera has failed entirely to demonstrate this. At no point in any of Natera's Claim Charts, which it

describes as citing and presenting teachings reflecting motivations to combine, is a teaching reflecting motivation to combine actually found. In fact, at least some of Natera's cited prior art actually teaches away, such as in Appendix 11, where a method of sequence assembly without the use of a reference genome is described as a great achievement. Moreover, Natera's argument that there was a motivation to combine prior art is stated generically, without taking into account the individual features of the individual prior art references. To the extent Natera states its prior art and proposed motivations to combine more with more specificity, Invitae will respond accordingly.

Regarding Natera's allegation that skilled artisans were supposedly motivated and had a reasonable expectation of success to use the claimed method of sequence assembly, Natera has also failed to demonstrate this. Again, if skilled artisans truly had a reasonable expectation of success, Natera would not have been limited to prior art such as that which it cites in Appendix 11, which plainly teaches a method of sequence assembly entirely divorced from that which is claimed in the Asserted Patents. Moreover, Natera's argument that there was a reasonable expectation of successfully combining the prior art to achieve the claimed invention is stated generically, without taking into account the individual features of the individual prior art references. To the extent Natera states its prior art and bases for reasonable expectation of success with more specificity, Invitae will respond accordingly.

FIRST SUPPLEMENTAL RESPONSE TO INTERROGATORY NO. 9 (2023-04-28):

Invitae incorporates by reference its prior responses to this Interrogatory. Subject to its general and specific objections, and based on its investigation to date, Invitae further responds as follows:

Natera's Contentions Based on 35 U.S.C. §§ 102 and/or 103

The Asserted Patents are presumed valid pursuant to Pursuant to 35 U.S.C. § 282. Natera has not met its burden in showing with clear and convincing evidence that any prior art, alone or in combination, invalidates pursuant to 35 U.S.C. §§ 102 and/or 103, any Asserted Claim of the Asserted Patents. To the extent the alleged prior art is mentioned, described, or discussed by the Asserted Patents and/or known and considered by the PTO, the Asserted Patents were granted and are presumed valid over the prior art.

Regarding Natera's allegations of obviousness, Natera has cited an excessive and unreasonable number of references as support, claiming that they render the Asserted Claims obvious alone and/or in combination. This gives rise to an excessive and unreasonable number of potential combinations, rendering Natera's claims of obviousness entirely lacking in specificity. Further, Natera has not provided contentions explaining how the quoted text from the prior art references discloses a claim limitation. Natera also relies on the same disclosure of the same reference for different limitations in the same claim without explanation. Natera has also failed to provide contentions explaining why disclosures from one prior art reference would be combinable with different embodiments from the same reference or with disclosures from any other prior art reference(s) on a limitation-by-limitation basis.

To the extent that Natera demonstrates each of the claim elements was independently known in the prior art, Natera has failed to demonstrate obviousness because it has not identified any specific and sufficient basis to modify or combine known elements in each reference with a different element in another reference, with a reasonable expectation of success, to achieve the claimed invention. Natera's contentions rely upon after-the-fact reasoning and read the teachings of the invention at issue into the prior art and thus fail to overcome hindsight biases.

Natera's attempt to place prior art references in various categories and to combine one category with another fails to show a motivation to modify or combine individual references. Most of these references are not explained or relied upon in Natera's invalidity contentions. Natera fails to show that one of ordinary skill in the art would consider modifying such references or would have any expectation of success in doing so. For example, Natera has also failed to identify motivations to modify references or whether the references themselves function in a manner sufficient to accomplish their objectives and thus do not require modification. As another example, Natera has failed to show that references within each category are in the same or analogous field such that one of ordinary skill in the art would be motivated to look to the teachings of a given reference when considering another reference.

Appendix 1 – NextGENe

Natera has not met its burden in showing that the NextGENe software and associated references invalidate any Asserted Claims of the Asserted Patents. NextGENe, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample
- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps

- assembling a contig from at least some of the plurality of sequence reads; or assembling a contig using the at least some of the sequence reads, the contig including information about positions of the at least some of the sequence reads relative to each other or to a reference
- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome
- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- creating the contig by overlapping consensus assembly; or assembling the contig comprises overlap consensus assembly
- creating the contig by searching a prefix tree for overlap between the reads; or assembling the contig by searching a prefix tree for overlap between the contig and the sequence of the reference genome

- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell
- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome

- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory
- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings in the computer-readable memory
- the reference genome is a human genome
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 2 – GATK

Natera has not met its burden in showing that the GATK toolkit and associated references invalidate any Asserted Claims of the Asserted Patents. GATK, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the

references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for assembling sequence reads
- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample
- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps
- assembling a contig from at least some of the plurality of sequence reads; or assembling a contig using the at least some of the sequence reads, the contig including information about positions of the at least some of the sequence reads relative to each other or to a reference
- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome
- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome

- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid
- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- creating the contig by overlapping consensus assembly; or assembling the contig comprises overlap consensus assembly
- creating the contig by searching a prefix tree for overlap between the reads; or assembling the contig by searching a prefix tree for overlap between the contig and the sequence of the reference genome
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell
- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another

- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory

- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the reference genome is a human genome
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 3 – CASAVA

Natera has not met its burden in showing that the CASAVA software and associated references invalidate any Asserted Claims of the Asserted Patents. CASAVA, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for assembling sequence reads
- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample
- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps
- assembling a contig from at least some of the plurality of sequence reads; or assembling a contig using the at least some of the sequence reads, the contig including information about positions of the at least some of the sequence reads relative to each other or to a reference

- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome
- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid
- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- creating the contig by overlapping consensus assembly; or assembling the contig comprises overlap consensus assembly
- creating the contig by searching a prefix tree for overlap between the reads; or assembling the contig by searching a prefix tree for overlap between the contig and the sequence of the reference genome
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments

to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell

- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig

- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory
- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the reference genome is a human genome
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 4 – Trans-ABySS

Natera has not met its burden in showing that the Trans-ABySS analysis pipeline and associated references invalidate any Asserted Claims of the Asserted Patents. Trans-ABySS, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid

because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample
- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps
- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome
- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference

genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome

- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell
- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters

- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory
- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 5 – Dindel

Natera has not met its burden in showing that the Dindel program and associated references invalidate any Asserted Claims of the Asserted Patents. Dindel, as disclosed in Natera's

contentions, does not render any claim of the Asserted Patents invalid because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for assembling sequence reads
- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample
- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps
- assembling a contig from at least some of the plurality of sequence reads; or assembling a contig using the at least some of the sequence reads, the contig including information about positions of the at least some of the sequence reads relative to each other or to a reference
- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome
- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the

mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome

- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid
- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- creating the contig by overlapping consensus assembly; or assembling the contig comprises overlap consensus assembly
- creating the contig by searching a prefix tree for overlap between the reads; or assembling the contig by searching a prefix tree for overlap between the contig and the sequence of the reference genome
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell
- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another

- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory

- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the reference genome is a human genome
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 6 – Etter

Natera has not met its burden in showing that Etter invalidates any Asserted Claims of the Asserted Patents. Etter, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample
- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps
- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome

- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid
- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell
- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read

- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length

- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory
- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the reference genome is a human genome
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 7 – Illumina GA

Natera has not met its burden in showing that Illumina GA and associated references invalidate any Asserted Claims of the Asserted Patents. Illumina GA, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample
- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a

reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps

- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome
- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid
- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell

- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second

gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty

- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory
- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 8 – George

Natera has not met its burden in showing that George invalidates any Asserted Claims of the Asserted Patents. George, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample

- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- obtaining nucleic acid from the biological sample obtained from the human subject
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps
- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome
- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid

- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- creating the contig by overlapping consensus assembly; or assembling the contig comprises overlap consensus assembly
- creating the contig by searching a prefix tree for overlap between the reads; or assembling the contig by searching a prefix tree for overlap between the contig and the sequence of the reference genome
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell
- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads

- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory
- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string

- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 9 – Li

Natera has not met its burden in showing that Li invalidates any Asserted Claims of the Asserted Patents. Li, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample
- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps
- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome
- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference

- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid
- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell
- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another

- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory

- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 10 – Schwartz

Natera has not met its burden in showing that Schwartz invalidates any Asserted Claims of the Asserted Patents. Schwartz, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample
- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- obtaining nucleic acid from the biological sample obtained from the human subject
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps
- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome

- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid
- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell
- creating the contig by overlapping consensus assembly; or assembling the contig comprises overlap consensus assembly
- creating the contig by searching a prefix tree for overlap between the reads; or assembling the contig by searching a prefix tree for overlap between the contig and the sequence of the reference genome
- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation

- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- sequencing the template nucleic acid by sequencing-by-synthesis
- sequencing the template nucleic acid by next generation sequencing
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty

- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory
- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings in the computer-readable memory
- the reference genome is a human genome
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 11 – Reinhardt

Natera has not met its burden in showing that Reinhardt invalidates any Asserted Claims of the Asserted Patents. Reinhardt, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample

- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- obtaining nucleic acid from the biological sample obtained from the human subject
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps
- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome
- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid

- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell
- creating the contig by overlapping consensus assembly; or assembling the contig comprises overlap consensus assembly
- creating the contig by searching a prefix tree for overlap between the reads; or assembling the contig by searching a prefix tree for overlap between the contig and the sequence of the reference genome
- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads

- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory
- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the reference genome is a human genome
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string

- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 12 – WO '206

Natera has not met its burden in showing that WO '206 and other related references invalidate any Asserted Claims of the Asserted Patents. WO '206, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample
- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps
- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome
- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig

- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid
- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell
- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another

- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory

- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory
- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 13 – Schneeberger

Natera has not met its burden in showing that Schneeberger invalidates any Asserted Claims of the Asserted Patents. Schneeberger, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following:

- a method for accurately identifying differences between a reference human genome and sequence reads obtained from a biological sample
- a method for assembling and aligning a plurality of sequence reads having mutations of different types
- obtaining nucleic acid from the biological sample obtained from the human subject
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps
- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the

reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome

- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid
- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell
- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion

- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty

- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory
- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the reference genome is a human genome
- the instructions further cause the processor to create a file or variable containing a description of the mutations
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the description of the mutations comprises variant and positional information

Appendix 14 – HC 2011

Natera has not met its burden in showing that HaplotypeCaller (2011) (HC 2011) or HaplotypeCaller (2012) (HC 2012) invalidates any Asserted Claims of the Asserted Patents. HC 2011 or HC 2012, as disclosed in Natera's contentions, does not render any claim of the Asserted Patents invalid because, for example, the the references do not disclose, teach, or render obvious alone or in combination with other prior art at least the following.

- obtaining a sample comprising template nucleic acid; or obtaining nucleic acid from the biological sample obtained from the human subject
- sequencing the template nucleic acid to generate a plurality of sequence reads; or sequencing the sample to generate the plurality of sequence reads
- inputting a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory; or performing genotyping by one or more computer software programs executing on at least one computer processor

coupled to a computer-readable memory to perform a number of steps; or inputting a reference genome and the plurality of sequence reads into a computer system comprising a non-transitory memory and a processor coupled to the non-transitory memory, wherein the non-transitory memory has instructions stored thereon that, when executed by the processor, cause the processor to perform a number of steps

- identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome; or aligning the contig to the reference human genome to obtain a reference alignment and storing the reference alignment in the computer-readable memory, the reference alignment indicative of first differences between the contig and the reference human genome; or identifying a plurality of contig-to-reference descriptions of the mutations by aligning the contig to a sequence of the reference genome
- identifying a plurality of read:contig descriptions by aligning each of the plurality of sequence reads to the contig; or aligning the at least some of the sequence reads to the contig to obtain sequence read alignments and storing the sequence read alignments in the computer-readable memory, the sequence read alignments indicative of second differences between the at least some of the sequence reads and the contig; or identifying a plurality of read-to-contig descriptions by aligning each of the at least some of the plurality of sequence reads to the contig
- combining the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference
- generating a read-to-reference description by aligning at least one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome
- genotyping at least some of the sequence reads using a multi-stage alignment
- genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences, the genotyping comprising mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome
- attaching barcode sequences to the template nucleic acid
- assigning the reads to subsets based on the barcode sequences
- assigning the reads to subsets based on the barcode sequences and creating a unique contig for that subset
- sequencing the template nucleic acid by fragmenting the template nucleic acid, attaching the fragments to a surface of channels in a flow cell, and amplifying the attached fragments to create clusters, each cluster comprising a plurality of copies of the same template in one of the channels of the flow cell

- identifying a mutation based on the alignments to the contig and the reference sequence
- identifying a plurality of mutations
- identifying a plurality of mutations, wherein a first mutation is within about 100 nucleotides of a second mutation
- identifying a plurality of mutations, wherein the first mutation is a substitution and the second mutation is a deletion
- identifying a plurality of mutations, wherein the mutation is a deletion at the end of a sequence read
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 100 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 10 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel occur within 5 bases of one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first substitution and the first indel are proximal to one another
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel occurs at an end of a sequence read among the at least some of the sequence reads
- identifying a plurality of mutations, wherein the multiple mutations including mutations of different types including a first substitution and a first indel and the first indel has a length exceeding a length of one or more of the sequence reads
- sequencing the template nucleic acid by sequencing-by-synthesis
- sequencing the template nucleic acid by next generation sequencing
- aligning the contig to a reference sequence by using a first set of alignment parameters
- aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters
- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome
- aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig

- aligning, using a first substitution probability and a first gap penalty, the contig to the reference human genome and aligning, using a second substitution probability and a second gap penalty, the at least some of the sequence reads to the contig, wherein the first gap penalty is greater than the second gap penalty
- aligning the contig to a reference sequence by using a first set of alignment parameters and aligning each of the plurality of sequence reads to the contig by using a second set of alignment parameters, wherein the first set of alignment parameters includes a first gap penalty and a first substitution penalty; the second set of alignment parameters includes a second gap penalty and a second substitution penalty; and the first gap penalty > the second gap penalty
- the sequence reads include sequence reads less than 150 bases in length
- the sequence reads comprise at least one million sequence reads
- storing the reference alignment in the computer readable memory by generating a first compact idiosyncratic gaped element report (CIGAR) string representing the reference alignment and storing the first CIGAR string in a Binary Alignment Map (BAM) format or a sequence alignment map (SAM) format in the computer readable memory
- storing the sequence read alignments in the computer-readable memory by generating second CIGAR strings representing the sequence read alignments and storing the second CIGAR strings in the BAM format or the SAM format in the computer readable memory
- storing results of genotyping the at least some of the sequence reads by generating a plurality of CIGAR strings and storing the plurality of CIGAR strings the computer-readable memory
- the template nucleic acid is DNA or RNA
- the reference genome is a human genome
- the instructions further cause the processor to create a file or variable containing a description of the mutations, wherein the file or variable is a binary alignment map (BAM) file comprising a Compact Idiosyncratic Gapped Alignment Report (CIGAR) string

Further, the accused functionality is Sentieon's DNaseq and TNseq which are based on the methodology of recent versions of GATK HaplotypeCaller and Mutect 2, respectively, not the old versions of HaplotypeCaller. Natera alleges that HC 2011 and HC 2012 work in the same way as current HaplotypeCaller. However, HaplotypeCaller has undergone changes and improvements that have changed key functionalities. An examination of the GATK source code since version 2.0 and the repository history, which are publicly available, reveal that HC 2011 and HC 2012 miss key functionalities of the patented methods. For example, a new bubble concept

was introduced to HaplotypeCaller in GATK 2.4. The bubble concept is similar to the intermediary “contig” in the patented methods. This concept is absent from HC 2011 or HC 2012. As another example, key functions that generate read:reference alignment by mapping read:haplotype alignment to haplotype:reference alignment were introduced to HaplotypeCaller in GATK 2.5. These functions are absent from HC 2011 or HC 2012.

102(g)

Conception is defined as when the inventor formed in his or her mind “a definite and permanent idea of the complete operative invention, as it is hereafter to be applied in practice,” which idea is “so clearly defined in the inventor’s mind that only ordinary skill would be necessary to reduce the invention to practice, without extensive research or experimentation.” *Burroughs Wellcome Co. v. Barr Laboratories, Inc.*, 40 F.3d 1223, 1228, 32 U.S.P.Q.2d 1915 (Fed. Cir. 1994). Natera relies on two whiteboard images (NTRA-INVT-00411179, NTRA-INVT-00411182) taken by Ryan Poplin to show conception. However, these images do not show Ryan Poplin and others at the Broad Institute formed in their mind a definite and permanent idea of the complete operative invention. To the extent Natera alleges that these images correspond to HC 2011 and HC 2012, they still do not support conception at least because (1) HC 2011 and HC 2012 do not disclose the claimed invention as shown by the discussion above regarding Appendix 14; and (2) these images do not show the functionalities of HC 2011 or HC 2012 in sufficient details.

In general, to constitute an actual reduction to practice of the invention the party seeking to prove the reduction must show (1) that it constructed an invention meeting all of the limitations of the claim at issue, or if in an interference all of the limitations of the interference count; and (2) that the invention would work for its intended purpose. Natera relies on HC 2011 and HC 2012 as alternative reduction to practice. As discussed above regarding Appendix 14, HC 2011 and

HC 2012 do not meet all of the limitations of the claims at issue. Further, Natera also has not shown that the invention worked for its intended purpose.

Natera relies on a number of Broad documents to show diligence. Natera has not provided any explanations about how the cited Broad documents support that Broad Institute did not abandon, suppress, or conceal the alleged early versions of HaplotypeCaller.

Natera's Contentions Based on 35 U.S.C. § 112

The Asserted Patents are presumed valid pursuant to 35 U.S.C. § 282. Natera has not met its burden in showing with clear and convincing evidence that the Asserted Claims of the Asserted Patents are invalid for lack of written description, lack of enablement, or indefiniteness.

Natera's contentions did no more than listing a number of terms and alleging they do not satisfy the § 112 requirements with no explanations. "The patent specification is written for a person of skill in the art, and such a person comes to the patent with the knowledge of what has come before. Placed in that context, it is unnecessary to spell out every detail of the invention in the specification; only enough must be included to convince a person of skill in the art that the inventor possessed the invention and to enable such a person to make and use the invention without undue experimentation." *Falkner v. Inglis*, 448 F.3d 1357, 1366 (Fed. Cir. 2006). For example, Natera's contentions fail to explain why a person of ordinary skill in the art would not recognize from reading the specification that the inventors possessed the full scope of the claimed invention. Also for example, Natera's contentions fail to conduct any analysis using the *Wands* factors to show a person of ordinary skill in the art would not make and use the full scope of the claimed invention without undue experimentation. Also for example, Natera's contentions likewise fail to explain why the claim terms do not "inform those skilled in the art about the scope of the invention

with reasonable certainty.” *Nautilus, Inc. v. Biosig Instruments, Inc.*, 572 U.S. 898, 901, 910 (2014).

The Asserted Patents provide sufficient § 112 support to the claim terms. The following charts identify exemplary disclosures from the specification that provides § 112 support to the claim terms identified in Natera’s contentions Part V.C. The burden of proof is on Natera. Invitae reserves right to rely on additional disclosure from the specification and file history of the patents, state of art or understanding of a skilled artisan at the relevant time, other facts and factors considered by law, and expert discovery.

Claim Terms	Asserted Patents	Exemplary Disclosure in the '799 Patent
Contig assembly and alignment elements, generally	799, 308, 863	Fig. 1, Fig. 2, 2:30-5:39, 12:34-21:63
Template nucleic acid	799, 308, 863	2:30-5:39, 5:60-9:35
Plurality of sequence reads	799, 308, 863	2:30-5:39, 13:25-16:43
Description, descriptions, descriptions of mutations	799, 863	2:30-5:39, 20:32-48, 21:5-27
Mutation(s)	799, 308, 863	2:30-5:39, 20:32-23:5
identifying a plurality of contig:reference descriptions of mutations by aligning the contig to said reference genome	799	2:30-5:39, 16:44-20:48
combining the contig:reference descriptions with the read:contig descriptions of mutations to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference	799	2:30-5:39, 21:12-22:44
identifying a mutation based on the alignments to the contig and the reference sequence	799	2:30-5:39, 21:12-23:5
mutations are identified, identifying a mutation	799	2:30-5:39, 21:12-23:5
a plurality of mutations are identified	799	2:30-5:39, 22:45-23:5

a first mutation is within about 100 nucleotides of a second mutation	799	2:30-5:39, 22:45-23:5
reference sequence	799	2:30-5:39
within about 100	799	2:30-5:39, 22:45-23:5
an end of a sequence read	799, 308	2:30-5:39, 22:45-23:5
first substitution penalty	799	2:30-5:39, 16:44-21:11
the first set of alignment parameters includes a first gap penalty . . . ; the second set of alignment parameters includes a second gap penalty . . . ; and the first gap penalty>the second gap penalty	799	2:30-5:39, 16:44-21:11
Nucleic acid	308	2:30-5:39, 5:60-9:35
Multi-stage alignment	308	2:30-5:39, 16:44-21:11
Alignment(s)	308	2:30-5:39, 16:44-22:57
genotyping the at least some of the sequence reads by identifying multiple mutations in the at least some of the sequence reads based on the first differences and the second differences	308	2:30-5:39, 21:12-23:5
mapping the at least some of the sequence reads to the reference genome by combining the reference alignment and the sequence read alignments to determine an identity of each of the multiple mutations and its location in the human reference genome	308	2:30-5:39, 21:12-22:44
proximal to one another	308	2:30-5:39, 22:45-23:5
CIGAR strings	308	Fig. 2, 10:41-62, 21:64-22:44
wherein the first plurality of alignment parameters includes a first gap penalty . . . , the second plurality of alignment parameters includes a second gap penalty . . . , and the first gap penalty is greater than the second gap penalty	308	2:30-5:39, 16:44-21:11
RNA	863	2:30-5:39, 5:60-9:35
generating a read-to-reference description by aligning at least	863	2:30-5:39, 16:44-20:48

one of the plurality of contig-to-reference descriptions with a corresponding at least one of the plurality of read-to-contig descriptions, wherein the read-to-reference description maps positional information of the mutations found in at least one of the at least some of the plurality of sequence reads relative to the sequence of the reference genome		
identifying the mutations	863	2:30-5:39, 21:12-23:5
identifying the mutations based on one or more alignments between the contig and the sequence of the reference genome	863	2:30-5:39, 21:12-23:5
wherein the first plurality of alignment parameters includes a first gap penalty and a first substitution probability, the second plurality of alignment parameters includes a second gap penalty and a second substitution probability, and the first gap penalty is greater than the second gap penalty	863	2:30-5:39, 16:44-21:11

Natera's Contentions Based on 35 U.S.C. § 101

Natera's contentions largely recycle its arguments made in its Rule 12(b)(6) motion for all of the Asserted Patents. *See* D.I. 9. The court has found the '799 Patent to be patent eligible under 35 U.S.C. § 101. *See* D.I. 28. For the same reasons, the '308 and '863 Patents are likewise patent eligible. Invitae incorporates by reference and D.I. 13 (Invitae's opposition to Natera's motion to dismiss) and D.I. 28 (memorandum order denying Natera's motion to dismiss).

Invitae further incorporates by reference its responses to Interrogatory Nos. 2 and 13. Invitae further expects to rely on the deposition testimony of Ryan Poplin, Eric Banks, Jared

Maguire, Gregory Porreca, Caleb Kennedy, Nirav Malani, Andrea Velenich, Raheleh Salari, Hsin-Ta Wu, and Joshua Paul. Additional information responsive to this interrogatory is expected from expert discovery.

Dated: April 28, 2023

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IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	C.A. No. 21-669 (GBW)
)	
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	
<hr/>		
LABORATORY CORPORATION OF)	
AMERICA HOLDINGS,)	
)	
Plaintiff,)	C.A. No. 21-1635 (GBW)
)	
v.)	
)	
NATERA, INC.)	
)	
Defendant.)	

PLAINTIFF’S OPPOSITION TO DEFENDANT’S MOTION *IN LIMINE* NO. 1:
PRECLUDE EVIDENCE OR ARGUMENT THAT ANTICIPATION BY A PRIOR ART
SYSTEM CANNOT BE ESTABLISHED USING MULTIPLE DOCUMENTS THAT
DESCRIBE THE SYSTEM

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Dated: August 6, 2025

Natera contends that Labcorp should be precluded from offering evidence or argument that Natera cannot establish anticipation by a prior-art system by relying on multiple references. Whether this is permissible, however, is a pure legal question. If Natera wants a jury instruction on this issue, a motion *in limine* is an inappropriate means to seek such a remedy. Alternatively, if Natera wants summary judgment on this issue, Natera's motion *in limine* is likewise improper. Either way, Natera's motion is improper and should be denied.

I. A MOTION IN LIMINE IS NOT THE APPROPRIATE FORUM FOR THE REMEDY NATERA SEEKS

A “motion *in limine* is appropriate for evidentiary submissions that clearly ought not be presented to the jury because they clearly would be inadmissible for any purpose.” *Hologic, Inc. v. Minerva Surgical, Inc.*, 325 F. Supp. 3d 507, 521 (D. Del. 2018) (internal quotations and citations omitted). But rather than requesting a ruling on an evidentiary issue, Natera improperly seeks findings of law and/or fact as to whether its four references that supposedly pertain to NextGENe may be effectively treated as a single reference that describes the NextGENe system.

If Natera wants a *legal* ruling that more than one reference may be combined to establish anticipation when the alleged prior art is a system, its motion *in limine* is improper. This purely legal issue should be addressed not through an *in limine* motion, but through jury instructions.

On the other hand, if Natera's wants a summary judgment on the factual question of whether its four references—and all relied-upon aspects of these references—all pertain not just to NextGENe but the same version of this system, then its motion *in limine* is an improper summary judgment motion that would demand extensive fact-finding and analysis from the Court. Natera's assertion that it is “too late” for Labcorp to challenge that the references are all directed to the same prior-art system ignores that Natera bears the burden on invalidity and that its motion effectively seeks summary judgment on countless factual questions involving the scope and

content of four different prior art references. *See* Natera’s MIL 1 at 1 n.1. This is not appropriate for a motion *in limine*. *See C R Bard Inc. v. AngioDynamics Inc.*, No. 1:15-cv-218, 2018 WL 3468215, at *4 (D. Del. July 18, 2018) (finding a motion to preclude a plaintiff from attempting to prove an invention date was inappropriate for a motion in limine and is instead a motion for summary judgment); *see also Moon Express, Inc. v. Intuitive Machines, LLC*, No. 16-cv-344-LPS, 2017 WL 6380750, at *2 (D. Del. Dec. 14, 2017) (“Unlike a summary judgment motion, which is designed to eliminate a trial in cases where there are no genuine issues of fact, a motion *in limine* is designed to narrow the evidentiary issues for trial and to eliminate unnecessary trial interruptions.”). In fact, while Natera now moves *in limine*, the eligibility of NextGENe as a prior-art system through multiple references is a topic that has been raised in connection with summary judgment. *See* D.I. 225 at 7; *see also* D.I. 246 at 26; D.I. 266 at 13-14. This confirms that the issue is inappropriate for a motion *in limine*.

II. NATERA HAS FAILED TO SHOW THAT THE REFERENCES ARE DIRECTED TO THE SAME SYSTEM

Even assuming Natera’s motion was the proper subject of a motion *in limine*, it should nonetheless be denied on the merits. A patent challenger must show by “clear and convincing evidence” that a patent is invalid. *Sciele Pharma Inc. v. Lupin Ltd.*, 684 F.3d 1253, 1260 (Fed. Cir. 2012). As part of this burden, Natera must show by clear and convincing evidence that all references it asserts are representative of the NextGENe system as prior art are in fact representative. *See Evolved Wireless, LLC v. Apple, Inc.*, No. 15-cv-543-JFP-SRF, 2019 WL 831112, at *3 (D. Del. Feb. 21, 2019) (“The party challenging the validity of a patent bears the burden of persuasion by clear and convincing evidence on all issues relating to the status of [a reference] as prior art.”) (internal quotations and citations omitted). Natera has failed to meet this burden.

To allegedly show invalidity by anticipation, Natera cites four documents that allegedly show the operation of NextGENe. Natera has failed to show by clear and convincing evidence that these references are representative of the NextGENe software for a number of reasons. *First*, none of the references specify a version of the NextGENe software that is used to perform the described methods. In fact, one reference, U.S. Patent No. 8,271,206 (“Liu”), does not even mention the NextGENe software. Natera has made no showing that any version of the NextGENe software embodies Liu, nor affirmatively shown that the specification of Liu describes any version of the NextGENe software. *Second*, none of the references describe the entire method of operation of the NextGENe software. Natera does not rely on any source code, product manuals, or any other primary reference describing any version of the NextGENe software to support its claims of anticipation by NextGENe. *Third*, Natera’s cited references range in date from September 2008 to April 2009. As software is ever-changing, it is unclear whether these documents are all representative of the same version of NextGENe and Natera has done nothing to provide clarification on this matter. This is far from clear and convincing evidence, and Natera should not be granted a backdoor summary judgment via a motion *in limine*.

In sum, Natera’s attempt to cobble together a myriad of references to allege anticipation by NextGENe is without merit. *See Apple, Inc. v. Samsung Elecs. Co.*, No. 12-cv-00630-LHK, 2012 WL 2576136, at *3 (N.D. Cal. July 3, 2012) (finding that a post-hoc reconstruction “of how a [prior-art system] might have been constructed does not constitute prior art for purposes of anticipation.”). As such, Labcorp should not be precluded from presenting evidence or argument that Natera cannot establish anticipation by a prior-art system through the use of these multiple references.

August 6, 2025

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CERTIFICATE OF SERVICE

I, Brian E. Farnan, hereby certify that on August 6, 2025, a copy of PLAINTIFF'S OPPOSITION TO DEFENDANT'S MOTION *IN LIMINE* NO. 1: PRECLUDE EVIDENCE OR ARGUMENT THAT ANTICIPATION BY A PRIOR ART SYSTEM CANNOT BE ESTABLISHED USING MULTIPLE DOCUMENTS THAT DESCRIBE THE SYSTEM was served on the following as indicated:

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**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

**NATERA’S REPLY IN FURTHER SUPPORT OF ITS MOTION TO
PRECLUDE LABCORP FROM USING, OR PRESENTING
EVIDENCE OR ARGUMENT REGARDING,
THE TESTIMONY AND EXPERT REPORTS OF RYAN SULLIVAN**

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Natera seeks to preclude Labcorp from introducing opinions offered in a different case, *ArcherDX*, by an expert, Ryan Sullivan, Ph.D., who has not been retained and will not testify in this case. Labcorp responds that because 1) its damages expert Mr. Alexander Clemons apparently read some of Dr. Sullivan’s prior testimony, *but did not opine about it*, Labcorp has a blank slate to discuss Dr. Sullivan’s opinions; and 2) that Natera failed to timely object to the admissibility of Dr. Sullivan’s opinions. Labcorp is wrong on both points.

First, Mr. Clemons did not disclose opinions about—or rely on, quote, or even refer to—Dr. Sullivan’s testimony. Labcorp rests its entire argument on the fact that Dr. Sullivan’s *ArcherDX* testimony is on Mr. Clemons’s “documents considered” list. Opp. at 2 (citing Ex. A). If that matters at all, it cuts against Labcorp: it means Mr. Clemons considered Dr. Sullivan’s testimony and then **chose not to** offer an opinion about it. The inclusion of Dr. Sullivan’s *ArcherDX* testimony on Mr. Clemons’s materials considered list does not give Labcorp any basis, much less a blank slate, to introduce and discuss Dr. Sullivan’s prior opinions here. Fed. R. Civ. P. 26(a)(2) requires that experts testifying under FRE 703 disclose “all opinions the witness will express” 90 days before trial. Mr. Clemons disclosed no opinions about Dr. Sullivan in his reports, and Labcorp points to no passages in the body of Mr. Clemons’s reports where he even mentions Dr. Sullivan.

Second, Natera’s objection is timely. Natera objected to the admissibility of Dr. Sullivan’s testimony and reports in a letter filed with the Court on June 23, 2023, **after** Mr. Clemons’s report was served on June 16, 2023. Ex. 1 at 2. (“Dr. Sullivan’s materials would not be admissible at trial in this case.”). At the parties’ July 21, 2023 hearing, the Court deferred ruling on the admissibility of Dr. Sullivan’s opinions. Ex. 2 12:22–13:2 (“whether or not it’s admissible is another question.”). Natera’s timely motion appropriately re-raises this admissibility question.

EXHIBIT 1

IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

INVITAE CORPORATION,)	
)	
Plaintiff,)	
)	
v.)	C.A. No. 21-669 (GBW)
)	
NATERA, INC.,)	HIGHLY CONFIDENTIAL –
)	FILED UNDER SEAL
Defendant.)	
<hr/>		
INVITAE CORPORATION,)	
)	
Plaintiff,)	
)	
v.)	C.A. No. 21-1635 (GBW)
)	
NATERA, INC.,)	
)	
Defendant.)	

**LETTER TO THE HONORABLE GREGORY B. WILLIAMS FROM
DEREK J. FAHNESTOCK REGARDING DISCOVERY DISPUTE**

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Attorneys for Defendant Natera, Inc.

Dear Judge Williams:

Natera respectfully submits this answering letter regarding the pending discovery dispute.

Natera's Position Regarding Production of Altera Sales Data

Invitae first sought “financials relating to sales of” Natera’s Altera product (which is not accused of infringement in this case) in an email on May 5, 2023. Invitae has never served any formal discovery request for these data, which should be reason alone to deny Invitae’s request. Worse, Invitae’s only basis for seeking this information is its mischaracterization of the February 9, 2023 deposition of David Bessette, Natera’s Vice President of Finance. Although Invitae says Mr. Bessette testified that [REDACTED],” D.I. 187 at 1, he actually testified that [REDACTED], Bessette Tr. at 191:16-193:2, that [REDACTED]. Bessette Tr. at 192:21-193:11 (Exhibit A). Nor has Invitae explained why financial information relevant to Altera is remotely relevant to this case, other than to support Invitae’s conveyed-sales argument, which Mr. Bessette’s testimony—[REDACTED]—negates.

Natera's Position Regarding ArcherDX Materials

Natera recognizes that the Court is presiding over the *ArcherDX* action between Natera and Invitae. But that is a separate lawsuit, and Natera’s lead counsel in this case does not represent Natera in that case and is not under the Protective Order in that case. Invitae’s request for *ArcherDX* materials should be denied even without regard to the specific materials themselves.

First, the *ArcherDX* materials Invitae seeks were designated as Highly Confidential—Attorney’s Eyes’ Only pursuant to the Protective Order in that case. *See* C.A. No. 12-125, D.I. 69 (Exhibit B). That Order prohibits the use of such materials for any purpose other than to litigate *that case*. *Id.* at Section 7.1.

The above-captioned actions were filed well after the commencement of the *ArcherDX* case, but there is no cross-use provision in the Protective Order negotiated and entered for this case authorizing the use of information obtained in the *ArcherDX* case, *see* C.A. No. 21-669, D.I. 46, and neither party argued for the consolidation of these cases with the *ArcherDX* case. If Invitae had wanted to treat the cases as the same, it had every opportunity to propose that at the outset to avoid duplicative discovery. Instead, Invitae and its counsel apparently *want* duplicative discovery, to have multiple bites at the apple. That is unfair.

Another issue stemming from the separateness of the actions is that, while counsel for the various Invitae entities (which includes ArcherDX) is the same, Natera’s lead counsel here is not involved in the *ArcherDX* litigation. Invitae’s counsel should not be using in this litigation the confidential information it obtained in the *ArcherDX* litigation under the terms of the protective order in that case. Yet, Invitae is using the contents of those confidential materials from *ArcherDX* in *this case* to argue why they are relevant and discoverable in the present motion. Moreover, Natera’s lead counsel here cannot view in this case the information designated by the Invitae

entities as confidential in the *ArcherDX* case. Invitae would thus be getting disproportionate discovery if its motion were granted—the ability to see, use, and understand the full context of materials while Natera’s lead counsel here would only have access to the portions of those materials that do not contain ArcherDX’s confidential information.

Dr. Sullivan’s Materials from ArcherDX. Invitae’s request for Dr. Sullivan’s materials is an attempt to circumvent the Court’s previous order denying Invitae’s motion to compel production of certain agreements involving Natera. *See* D.I. 177. Invitae protests that it does not seek the “exhibits” to Dr. Sullivan’s materials that overlap with the subject matter of its previous, unsuccessful motion to compel, but Dr. Sullivan’s reports and deposition testimony in the *ArcherDX* case refer to the materials as to which this Court denied Invitae’s prior request. Invitae merely seeks to gain in a different form the discovery this Court already denied.

Moreover, Dr. Sullivan’s materials would not be admissible at trial in this case. He is not an expert in this case and will not be testifying at trial. Although Invitae relies on the *Pernix* case (attached as Exhibit C) to demonstrate why its motion should succeed, *Pernix* actually proves the opposite—that this discovery is not reasonably calculated to lead to the discovery of admissible evidence (a burden of showing that Invitae bears but fails to address in its motion). As discussed below, these materials themselves are not admissible, and fact discovery is closed, so they cannot “lead” to the discovery of admissible evidence. *AgroFresh Inc. v. Essentiv LLC*, C.A. No. 16-662-MN-SRF, 2018 WL 9578196, at *2 (D. Del. Dec. 11, 2018) (“To achieve the policy goals of both Rule 26 and Rule 408, courts within the Third Circuit require the moving party to make a ‘particularized showing’ that the evidence sought is relevant and reasonably calculated to lead to the discovery of admissible evidence.”).

Pernix makes clear that an expert’s reports or opinions cannot be deemed the statements of a party’s agent or employee within the meaning of Fed. R. Evid. 801(d)(2)(C) or (D). *Pernix Ireland v. Alvogen*, 316 F. Supp. 3d 816, 819-23 (D. Del. 2018); *see also Kirk v. Raymark Indus., Inc.*, 61 F.3d 147, 164 (3d Cir. 1995); *VM Techs., LLC v. Intel Corp.*, C. A. No. 15-33-RGA, 2017 WL 1753999, at *2 (D. Del. May 1, 2017) (report of expert not called to testify was inadmissible hearsay). Dr. Sullivan’s opinions and testimony in *ArcherDX* cannot be admissible in this case as the statements of a Natera agent or employee.

Pernix also provides a roadmap, which Invitae ignores, for when an expert’s prior opinions *may* be deemed the adoptive admissions of a party under Fed. R. Evid. 801(d)(2)(B). Specifically, the opinions of an expert retained by a party in a previous case may be deemed adoptive admissions when the party calls the expert to give testimony to prove a particular fact. 316 F. Supp. at 825. But, as *Pernix* makes clear, the expert’s report itself is not evidence of a party’s adoption of those opinions. *See Pernix*, 316 F. Supp. at 825-26. Invitae has made no effort to identify which portions of Dr. Sullivan’s prior reports and deposition testimony would bear indicia of having been adopted by Natera based on Dr. Sullivan’s later trial testimony in *ArcherDX*. Invitae’s request thus seeks discovery that would not lead to admissible evidence as a matter of law.

To the extent Invitae suggests that Dr. Sullivan’s prior reports or deposition testimony could be used to impeach a different expert in this case, *Pernix* also answers that question in the

negative: “[I]f statements by a declarant are inadmissible as hearsay, those statements cannot be used to cross-examine a different witness at trial.” *Id.* at 826.

John Fesko and Solomon Moshkevich’s Deposition Transcripts and Exhibits from ArcherDX. Invitae first requested these materials in March 2023. *After* Invitae made that request, Invitae deposed Messrs. Fesko and Moshkevich in *this case*, in their individual capacities and as Rule 30(b)(6) witnesses. It had a full and fair opportunity to cover any legitimate subject matter.

Invitae’s motion makes no effort to explain what non-duplicative information in their *ArcherDX* depositions would be relevant here and could not have been obtained in their depositions in this case. Invitae has failed to carry its burden to show that the requested information is relevant to “either the claims, defenses, or the subject matter of the litigation” or why its probative value outweighs the costs and burdens producing it would impose on Natera. *See Inventio*, 662 F. Supp. 2d at 380-81 (noting “[a]lthough the scope of discovery is broad, it is not unlimited”); *see also INVISTA N. Am. S.à.r.l. v. M&G USA Corp.*, C.A. No. 11-1007-SLR-CJB, 2013 WL 12171721, at *2 (D. Del. June 25, 2013).

Michael Brophy’s Deposition Transcript and Exhibits from ArcherDX. Natera has not identified Mr. Brophy as a witness in this case and will not be calling him to trial. If Invitae wanted to seek his testimony in *this case*, it should have noticed his deposition. It chose not to do so. It is hard to imagine anything Mr. Brophy might know that Invitae did not cover in its 56 requests for production, 25 interrogatories, 24 requests for admission, and nine deposition notices under Rules 30(b)(1) and 30(b)(6), but if it needed Mr. Brophy, too, it could have sought his deposition. The *ArcherDX* case is not a *de facto* expansion of the deposition limitations and discovery taken in this case. Invitae’s only argument now is that Mr. Brophy is a Natera employee who testified about Signatera and PCM in the *ArcherDX* case. That explains why Invitae might have wanted to depose him, not why it should get to use in this case his deposition from the *ArcherDX* case. That falls well short of demonstrating that the requested information is relevant to the claims.

Respectfully,

/s/ *Derek J. Fahnestock*

Derek J. Fahnestock (#4705)

DJF/rah

Enclosures

cc: All Counsel of Record (via electronic mail)

EXHIBIT 2

1 IN THE UNITED STATES DISTRICT COURT
2 IN AND FOR THE DISTRICT OF DELAWARE

3
4 INVITAE CORPORATION,)
5 Plaintiff,) Civil Action Nos.
6 v.) 21-cv-669-GBW and
7 NATERA, INC.,) 21-cv-1635-GBW
8 Defendant.)

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10 - - - -
11 Wilmington, Delaware
12 Friday, July 21, 2023
13 Teleconference Transcript

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15 BEFORE: HONORABLE GREGORY B. WILLIAMS
16 UNITED STATES DISTRICT COURT JUDGE
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Michele L. Rolfe, RPR, CRR

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11 BY: ELIZA P. STRONG, ESQ.
ERIC ALAN STONE, ESQ.

12 Counsel for Natera, Inc.
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1 MR. WALTER: Good morning, Your Honor. This is
2 Derek Walter. I'll start out with that issue, as you
3 requested.
4 There's, I think, a key point that needs to be
5 stated upfront that might have been implicit in the brief,
6 but might not have been explicit. As the Court knows, we
7 just completed a trial between Invitae and Natera, and the
8 Court might recall that in that trial Natera relied upon the
9 Archer Beacon Dixon agreement through its expert to procure
10 damages, and particularly argued that this agreement
11 warranted a 20 percent royalty for cancer testing products.
12 Well, it is fair play and the key point that the Court
13 should understand is that our expert is now relying upon
14 that very license to seek damages from Natera. The same
15 license that Natera previously relied upon to seek damages
16 with respect to Invitae. And that's why this material is
17 highly relevant.

18 If that wasn't clear from the papers, it should
19 be clear now. We're relying upon that same agreement that
20 they relied upon, that's why this discovery is relevant.

21 Let me go through the arguments they raised.
22 The first argument that they raised is that Natera's lead
23 counsel is not under the protective order from that prior
24 litigation. And that argument, frankly, is a strange
25 argument. Of course, they concede Natera's confidential

3

1 P R O C E E D I N G S

2 (REPORTER'S NOTE: The following teleconference was
3 held beginning at 10:00 a.m.)

4 THE COURT: Good morning. We're here for a
5 discovery conference in Invitae Corp versus Natera Corp.
6 Civil Action Nos. 21-669 and 21-16345.

7 Let's start by having counsel put appearances on
8 the record.

9 MR. FARNAN: Good morning, Your Honor. Brian
10 Farnan on behalf of the plaintiff. And with me is Derek
11 Walter from Weil Gotshal.

12 THE COURT: All right. Good morning.
13 Defendants?

14 MS. JACOBS: Good morning, Your Honor. For
15 Natera this is Karen Jacobs and Derek Fahnestock from Morris
16 Nichols.

17 We have on the line with us and will be arguing
18 today are Eric Stone and Eliza Strong from Groombridge Wu.

19 THE COURT: Okay. Good morning.

20 All right. We have three issues. So let's
21 start with the first issue dealing with the request of
22 plaintiff to compel the expert reports, deposition testimony
23 and corresponding exhibits of Natera's damages expert Ryan
24 Sullivan from the ArcherDX litigation.
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5

1 information, so to the extent the requested information has
2 Natera's information, Natera's counsel can see that; it's
3 odd to contend that they can't. But the strange concern
4 that they seem to have is that they might be prohibited from
5 seeing Invitae's information pursuant to that protective
6 order. Well, it's a strange concern. We're asking them to
7 produce the information.

8 If we thought there was a concern with them
9 seeing the information, we would have said so. Of course
10 Natera's outside counsel can see the information, we want
11 them to produce it to us. So if there's any concern there,
12 let's put that to doubt now; we're granting them permission
13 to see the material so they can produce it to us.

14 They also complain that the protective order
15 prohibits use in another case. Well, that's why we're
16 asking them to produce it. It can't be that you can shield
17 something from forever being used in another case by
18 producing it in a second case, so that's why we're trying to
19 get around this issue. We're asking them to produce it so
20 we can use it in this case.

21 Just picking through their arguments, they cite
22 the *AgroFresch* case, that's a case about production of
23 settlement agreements where there appears to be a heightened
24 standard. That's not what this is. Okay. This is not a
25 settlement agreement situation.

1 admission unless Natera gave that -- called him to give that
2 testimony at trial. And to the extent Natera did so, they
3 have the trial testimony.

4 And after they see the expert report from us
5 today, there is something that they think is inconsistent
6 with his trial court testimony that is in the expert report,
7 they can -- you know, they can ask us. But the notion that
8 they should -- we should have to produce the expert report
9 and deposition testimony of an expert in another case whom
10 we are not calling in this case is exactly what Judge Bryson
11 held in *Pernix* is irrelevant. And it can't lead to the
12 discovery of admissible evidence at this point, fact
13 discovery is over.

14 Let me make one more point because this is a new
15 argument -- forgive me, that I don't think Mr. Walter made
16 in the argument and I don't mean that pergoratively, I just
17 want to make sure I respond to it. The notion that their
18 expert can respond to hearsay because it is hearsay but
19 experts can rely on hearsay, the rule is that experts can
20 rely on hearsay of the type that is usually relied upon by
21 experts in the field. Damages experts can rely on economic
22 analyses, they can rely on the literature. You certainly
23 cannot argue that an expert can rely on another parties'
24 expert report because it is hearsay. The rule is not that
25 experts can use all hearsay of any kind. The rule is that

1 statements or analysis, they are relying effectively upon
2 what other people in the field have said. And the notion
3 that one expert can't rely upon something that another party
4 is saying is an authority in the field, that's erroneous.
5 Of course one expert can rely upon the statements of someone
6 else who the other party has said is an authority in the
7 field; that's precisely the kind of stuff that experts rely
8 upon when they provide their testimony.

9 MR. STONE: Your Honor, I know that the Courts
10 don't ordinarily entertain sur-rebuttal, but I must be doing
11 a very bad job today because neither of those is the
12 argument that I made. So just in the interest of full
13 disclosure, the reason that I pointed out it's a different
14 expert is that if it were the same expert, it would be a
15 prior statement of the expert; we would be having a
16 different conservation.

17 My point is simply it doesn't matter -- the
18 reason that it matters that it's not Dr. Sullivan is that
19 he's not testifying in the case.

20 And on the hearsay point -- on that I'll stop.
21 We simply just --

22 THE COURT: Yeah. On this issue I do think it's
23 fair game for Invitae to have access to that information for
24 discovery purposes; whether or not it's admissible is
25 another question. So I'm going to order the production with

1 experts can use hearsay of the type ordinarily relied upon
2 by experts in the field. That rule has absolutely no
3 applicability here.

4 THE COURT: All right.

5 MR. WALTER: Your Honor, this is Derek Walter.
6 Should i respond briefly to some the points he
7 made?

8 THE COURT: Yes, you can respond.

9 MR. WALTER: All right. So as to the first
10 point that the expert that they plan to rely upon in this
11 case is different from the expert that they relied upon in
12 the first case, that's irrelevant.

13 What matters is Natera would have adopted the
14 statements of their expert and they would have done so in
15 either this trial or the previous trials; it doesn't have to
16 be the same expert. *Pernix* doesn't say that, neither does
17 *Abstracts*. In fact, I think in that *Abstracts* case we cited
18 it was a different expert and that discovery was allowed.
19 So the notion that it has to be the same expert, that's just
20 wrong.

21 And then finally on the last point, the hearsay
22 point, you know that's incorrect, too. It's incorrect that
23 an expert in one field can't rely upon the testimony or the
24 statements or the opinions of someone else in another field.
25 That's what people do when they rely upon publications or

1 respect to the first request.

2 Let's move on to the second request.

3 MR. WALTER: Thank you, Your Honor.

4 The second request, I believe you -- the Natera
5 sales data, that's the one I'm going to take next.

6 I'll just stick to the arguments here. The
7 first thing they do is they complain that there's no
8 document request that relevant to this. That was a
9 surprising argument for us to see in this brief because it
10 was not once mentioned during meet and confer. If they
11 really thought that the lack of a document request was a
12 barrier here, they should have said so and we could have
13 remedied. So I think they've waived that argument. But
14 what's also really telling here is they don't submit the
15 document request we have in this case. And if you look at
16 the document request, which are not before the Court, I can
17 only tell you what's there, I think we probably do have
18 document requests, Request 20 asks for documents relating to
19 identifying somatic sensations. Request 31 asks for things
20 related to the accused product. And to the extent that's
21 sold as a unit, that would be an accused products. Request
22 42 asks for the same sort of things. So the lack of
23 document request was kind of a strange and surprising
24 argument.

25 Also, they make an argument based on the merits.

1 at 10:38 a.m.)

2 I hereby certify the foregoing is a true
3 and accurate transcript from my stenographic notes in the
4 proceeding.

5 /s/ Michele L. Rolfe, RPR, CRR
U.S. District Court

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EXHIBIT 20B

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

**DEFENDANT'S MOTION *IN LIMINE* NO. 2:
PRECLUDE INVITAE FROM USING, OR PRESENTING
EVIDENCE OR ARGUMENT REGARDING,
THE TESTIMONY AND EXPERT REPORTS OF RYAN SULLIVAN**

OF COUNSEL:

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I. INTRODUCTION

Natera respectfully moves to preclude Invitae from using at trial, including presenting evidence or argument regarding, the deposition testimony and expert reports (including supporting materials and exhibits thereto) of Ryan Sullivan, Ph.D. from *Natera, Inc. v. ArcherDX, Inc. et al.*, No. 1:20-cv-125-GBW (D. Del.) (the “*ArcherDX* Case”). Dr. Sullivan’s deposition testimony and reports are not admissible here as a matter of law.

II. BACKGROUND

As the Court may remember, Dr. Sullivan was Natera’s damages expert in the *ArcherDX* Case. But Dr. Sullivan is not Natera’s expert (or anyone’s expert) in this case, and the Natera patents asserted and technologies at issue in the *ArcherDX* Case are unrelated to the Invitae patents asserted and technology at issue here. Dr. Sullivan has not submitted reports or testified in this case, has not offered any opinions relating to the Asserted Patents in this case, and will not testify at trial. On June 21, 2023, Invitae, through its counsel who also represent the defendants in the *ArcherDX* Case, moved to compel here the production of Dr. Sullivan’s expert reports and related materials and his deposition transcript and its exhibits from *ArcherDX* Case. D.I. 187. The Court granted that motion for only “discovery purposes,” noting that “whether or not it’s admissible is another question.” Ex. A at 12:22–25; *see also* D.I. 192.

Invitae now intends to use Dr. Sullivan’s materials at trial in this case, purportedly to impeach Natera’s witnesses and to prove the truth of the matters asserted therein. For the reasons set forth below, such testimony and reports, which concerned different patents and technologies, are irrelevant and prohibited as hearsay under the Federal Rules of Evidence and this District’s and Circuit’s precedents.

III. ARGUMENT

An expert's report and deposition testimony from another litigation are hearsay when offered in a second litigation, in which that expert is not retained or testifying, even if offered against the party that retained that expert in the first case. *Pernix Ireland Pain Dac v. Alvogen Malta Operations Ltd.*, 316 F. Supp. 3d 816, 819 (D. Del. 2018). Yet that is exactly what Invitae proposes to do here: Offer against Natera in this case the expert report and deposition testimony of Natera's former expert, Dr. Sullivan, from the *ArcherDX* Case.

This situation is nearly identical to the facts of *Pernix*, in which the court—after reviewing Delaware and Third Circuit precedents—held that experts' statements from one case could not be used at trial in another case where those experts were not testifying on behalf of the party against whom their statements would be offered. 316 F. Supp. 3d at 828. In *Pernix*, as here, only three exceptions to the hearsay rule were even “arguably pertinent”: Rule 801(d)(2)(B) (adoptive admissions), Rule 801(d)(2)(C) (statements authorized by party); Rule 801(d)(2)(D) (statement by party's agent or employee). *Id.* at 819. The *Pernix* court's reasoning for why none of those three exceptions applied is directly on point here.

Rules 801(d)(2)(C) and (D): While the defendant in *Pernix* had retained these experts in the previous case, their roles were “to serve as independent experts, and there [was] no evidentiary basis from which to conclude that either of them is an agent or employee of [the defendant], such that any statement made by the experts within the scope of their employment or agency should be attributable to the principal.” *Id.* at 823. That holding applies equally to an expert's prior deposition testimony. *See HTC Corp. v. Telefonaktiebolaget LM Ericsson*, 12 F.4th 476, 489–90 (5th Cir. 2021); *Ochoa-Valenzuela v. Ford Motor Co. Inc.*, 685 F. App'x 551, 554 (9th Cir. 2017); *SanDisk Corp. v. Kingston Tech. Co.*, 863 F. Supp. 2d 815, 818–19 (W.D. Wis. 2012); *see also Kirk v. Raymark Indus., Inc.*, 61 F.3d 147, 164 (3d Cir. 1995) (holding expert's prior trial testimony

in unrelated case inadmissible hearsay against different expert in current case). The same is true here: Dr. Sullivan was retained by Natera to serve as an independent expert. His opinions and deposition testimony are not admissions of Natera or statements of its agent or employee, and are not attributable to Natera for purposes of Rule 801(d)(2)(C) or (D).

Rule 801(d)(2)(B): The *Pernix* court held that the experts' reports were not "adoptive admissions" even though—in the prior case—the defendant had "designat[ed] them as experts, serv[ed] reports from them, ma[de] them available for deposition, and designat[ed] them as trial witnesses." 316 F. Supp. 3d at 825–26. None of these actions, however, was "enough" to show that the defendant "adopted any specific statement contained in the expert reports." *Id.* at 825. And this reasoning also applies with equal strength to a former expert's deposition testimony from a different case. *See HTC Corp.*, 12 F.4th at 490; *Ochoa-Valenzuela*, 685 F. App'x at 554; *SanDisk* 863 F. Supp. 2d at 818–19. Accordingly, that Dr. Sullivan served as an expert for Natera in a previous, unrelated case does not render his statements, whether in the form of his expert report or deposition testimony, adopted by Natera for purposes of Rule 801(d)(2)(B).

Use for Impeachment: Finally, the *Pernix* court ruled that because the former experts' statements from the prior case were inadmissible hearsay, they could not be used to impeach a different witness in the later case. 316 F. 3d at 826, 828 (holding that such use would be "contrary to the principle that, if statements by a declarant are inadmissible as hearsay, those statements cannot be used to cross-examine a different witness at trial"); *see* Fed. R. Evid. 613(b) (allowing impeachment only by testifying witness's *own* prior inconsistent statement). That same principle precludes Invitae's intended use of Dr. Sullivan's prior statements here.

EXHIBIT A

1 IN THE UNITED STATES DISTRICT COURT
2 IN AND FOR THE DISTRICT OF DELAWARE

3
4 INVITAE CORPORATION,)
5 Plaintiff,) Civil Action Nos.
6 v.) 21-cv-669-GBW and
7 NATERA, INC.,) 21-cv-1635-GBW
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15 BEFORE: HONORABLE GREGORY B. WILLIAMS
16 UNITED STATES DISTRICT COURT JUDGE
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Michele L. Rolfe, RPR, CRR

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13 Counsel for Natera, Inc.
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1 MR. WALTER: Good morning, Your Honor. This is
2 Derek Walter. I'll start out with that issue, as you
3 requested.
4 There's, I think, a key point that needs to be
5 stated upfront that might have been implicit in the brief,
6 but might not have been explicit. As the Court knows, we
7 just completed a trial between Invitae and Natera, and the
8 Court might recall that in that trial Natera relied upon the
9 Archer Beacon Dixon agreement through its expert to procure
10 damages, and particularly argued that this agreement
11 warranted a 20 percent royalty for cancer testing products.
12 Well, it is fair play and the key point that the Court
13 should understand is that our expert is now relying upon
14 that very license to seek damages from Natera. The same
15 license that Natera previously relied upon to seek damages
16 with respect to Invitae. And that's why this material is
17 highly relevant.
18 If that wasn't clear from the papers, it should
19 be clear now. We're relying upon that same agreement that
20 they relied upon, that's why this discovery is relevant.
21 Let me go through the arguments they raised.
22 The first argument that they raised is that Natera's lead
23 counsel is not under the protective order from that prior
24 litigation. And that argument, frankly, is a strange
25 argument. Of course, they concede Natera's confidential

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3 P R O C E E D I N G S
4 (REPORTER'S NOTE: The following teleconference was
5 held beginning at 10:00 a.m.)
6 THE COURT: Good morning. We're here for a
7 discovery conference in Invitae Corp versus Natera Corp.
8 Civil Action Nos. 21-669 and 21-16345.
9 Let's start by having counsel put appearances on
10 the record.
11 MR. FARNAN: Good morning, Your Honor. Brian
12 Farnan on behalf of the plaintiff. And with me is Derek
13 Walter from Weil Gotshal.
14 THE COURT: All right. Good morning.
15 Defendants?
16 MS. JACOBS: Good morning, Your Honor. For
17 Natera this is Karen Jacobs and Derek Fahnestock from Morris
18 Nichols.
19 We have on the line with us and will be arguing
20 today are Eric Stone and Eliza Strong from Groombridge Wu.
21 THE COURT: Okay. Good morning.
22 All right. We have three issues. So let's
23 start with the first issue dealing with the request of
24 plaintiff to compel the expert reports, deposition testimony
25 and corresponding exhibits of Natera's damages expert Ryan
Sullivan from the ArcherDX litigation.

1 information, so to the extent the requested information has
2 Natera's information, Natera's counsel can see that; it's
3 odd to contend that they can't. But the strange concern
4 that they seem to have is that they might be prohibited from
5 seeing Invitae's information pursuant to that protective
6 order. Well, it's a strange concern. We're asking them to
7 produce the information.
8 If we thought there was a concern with them
9 seeing the information, we would have said so. Of course
10 Natera's outside counsel can see the information, we want
11 them to produce it to us. So if there's any concern there,
12 let's put that to doubt now; we're granting them permission
13 to see the material so they can produce it to us.
14 They also complain that the protective order
15 prohibits use in another case. Well, that's why we're
16 asking them to produce it. It can't be that you can shield
17 something from forever being used in another case by
18 producing it in a second case, so that's why we're trying to
19 get around this issue. We're asking them to produce it so
20 we can use it in this case.
21 Just picking through their arguments, they cite
22 the *AgroFresch* case, that's a case about production of
23 settlement agreements where there appears to be a heightened
24 standard. That's not what this is. Okay. This is not a
25 settlement agreement situation.

1 admission unless Natera gave that -- called him to give that
2 testimony at trial. And to the extent Natera did so, they
3 have the trial testimony.

4 And after they see the expert report from us
5 today, there is something that they think is inconsistent
6 with his trial court testimony that is in the expert report,
7 they can -- you know, they can ask us. But the notion that
8 they should -- we should have to produce the expert report
9 and deposition testimony of an expert in another case whom
10 we are not calling in this case is exactly what Judge Bryson
11 held in *Pernix* is irrelevant. And it can't lead to the
12 discovery of admissible evidence at this point, fact
13 discovery is over.

14 Let me make one more point because this is a new
15 argument -- forgive me, that I don't think Mr. Walter made
16 in the argument and I don't mean that pergoratively, I just
17 want to make sure I respond to it. The notion that their
18 expert can respond to hearsay because it is hearsay but
19 experts can rely on hearsay, the rule is that experts can
20 rely on hearsay of the type that is usually relied upon by
21 experts in the field. Damages experts can rely on economic
22 analyses, they can rely on the literature. You certainly
23 cannot argue that an expert can rely on another parties'
24 expert report because it is hearsay. The rule is not that
25 experts can use all hearsay of any kind. The rule is that

1 statements or analysis, they are relying effectively upon
2 what other people in the field have said. And the notion
3 that one expert can't rely upon something that another party
4 is saying is an authority in the field, that's erroneous.
5 Of course one expert can rely upon the statements of someone
6 else who the other party has said is an authority in the
7 field; that's precisely the kind of stuff that experts rely
8 upon when they provide their testimony.

9 MR. STONE: Your Honor, I know that the Courts
10 don't ordinarily entertain sur-rebuttal, but I must be doing
11 a very bad job today because neither of those is the
12 argument that I made. So just in the interest of full
13 disclosure, the reason that I pointed out it's a different
14 expert is that if it were the same expert, it would be a
15 prior statement of the expert; we would be having a
16 different conservation.

17 My point is simply it doesn't matter -- the
18 reason that it matters that it's not Dr. Sullivan is that
19 he's not testifying in the case.

20 And on the hearsay point -- on that I'll stop.
21 We simply just --

22 THE COURT: Yeah. On this issue I do think it's
23 fair game for Invitae to have access to that information for
24 discovery purposes; whether or not it's admissible is
25 another question. So I'm going to order the production with

1 experts can use hearsay of the type ordinarily relied upon
2 by experts in the field. That rule has absolutely no
3 applicability here.

4 THE COURT: All right.

5 MR. WALTER: Your Honor, this is Derek Walter.
6 Should i respond briefly to some the points he
7 made?

8 THE COURT: Yes, you can respond.

9 MR. WALTER: All right. So as to the first
10 point that the expert that they plan to rely upon in this
11 case is different from the expert that they relied upon in
12 the first case, that's irrelevant.

13 What matters is Natera would have adopted the
14 statements of their expert and they would have done so in
15 either this trial or the previous trials; it doesn't have to
16 be the same expert. *Pernix* doesn't say that, neither does
17 *Abstracts*. In fact, I think in that *Abstracts* case we cited
18 it was a different expert and that discovery was allowed.
19 So the notion that it has to be the same expert, that's just
20 wrong.

21 And then finally on the last point, the hearsay
22 point, you know that's incorrect, too. It's incorrect that
23 an expert in one field can't rely upon the testimony or the
24 statements or the opinions of someone else in another field.
25 That's what people do when they rely upon publications or

1 respect to the first request.

2 Let's move on to the second request.

3 MR. WALTER: Thank you, Your Honor.

4 The second request, I believe you -- the Natera
5 sales data, that's the one I'm going to take next.

6 I'll just stick to the arguments here. The
7 first thing they do is they complain that there's no
8 document request that relevant to this. That was a
9 surprising argument for us to see in this brief because it
10 was not once mentioned during meet and confer. If they
11 really thought that the lack of a document request was a
12 barrier here, they should have said so and we could have
13 remedied. So I think they've waived that argument. But
14 what's also really telling here is they don't submit the
15 document request we have in this case. And if you look at
16 the document request, which are not before the Court, I can
17 only tell you what's there, I think we probably do have
18 document requests, Request 20 asks for documents relating to
19 identifying somatic sensations. Request 31 asks for things
20 related to the accused product. And to the extent that's
21 sold as a unit, that would be an accused products. Request
22 42 asks for the same sort of things. So the lack of
23 document request was kind of a strange and surprising
24 argument.

25 Also, they make an argument based on the merits.

1 at 10:38 a.m.)

2 I hereby certify the foregoing is a true
3 and accurate transcript from my stenographic notes in the
4 proceeding.

5 /s/ Michele L. Rolfe, RPR, CRR
U.S. District Court

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IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.

Defendant.

C.A. No. 21-669 (GBW)

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.

Defendant.

C.A. No. 21-1635 (GBW)

PLAINTIFF'S OPPOSITION TO DEFENDANT'S MOTION *IN LIMINE* NO. 2:
PRECLUDE PLAINTIFF FROM USING, OR PRESENTING EVIDENCE OR
ARGUMENT REGARDING, THE TESTIMONY AND
EXPERT REPORTS OF RYAN SULLIVAN

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Dated: August 6, 2025

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Natera's attempt to exclude Ryan Sullivan's materials rests upon little more than a misunderstanding of law and a mischaracterization of facts. Regarding the law, Natera's lead case, *Pernix*, is not nearly as authoritative as Natera contends. Judge Bryson begins his analysis of the admissibility of prior expert testimony by explaining that "case law on this subject is mixed, however, *with courts reaching different results under a variety of different factual circumstances.*" *Pernix Ireland Pain Dac v. Alvogen Malta Operations Ltd.*, 316 F. Supp. 3d 816, 819 (D. Del. 2018) (emphasis added). In other words, the law calls for a fact-specific inquiry.

Unfortunately for Natera, the facts here, too, are not as it represents. First, Alexander Clemons, Labcorp's damages expert, cited Dr. Sullivan's materials from the *ArcherDX* Case in his opening report, served on **June 16, 2023**. If Natera found this objectionable, it should have said so **eight months** before raising the issue. Second, Nisha Mody, Natera's damages expert in this case, cites testimony from **James Malackowski** in her July 21, 2023 report. Mr. Malackowski, of course, was Dr. Sullivan's counterpart in the *ArcherDX* Case – namely, **ArcherDX's damages expert**. Natera's brief makes no mention of this reciprocal usage. For all of the reasons above, Natera's motion should be denied.

I. DR. SULLIVAN'S MATERIALS ARE ADMISSIBLE

Under Rule 703, an expert may provide an opinion based on inadmissible evidence as long as it is of the type reasonably relied on by experts in the field—such as the testimony of other experts. *See, e.g., Hayes v. Raytheon Co.*, 808 F.Supp.1326, 1329 (N.D. Ill. 1992); *Wilbern v. Culver Franchising System, Inc.*, No. 13-cv-3269, 2015 WL 5722825, at *14 (N.D. Ill. Sept. 29, 2015) ("In general, however, Rule 703 *permits an expert to rely on the opinions of other experts in a related field.*"); *Kovary v. Honeywell Int'l, Inc.*, No. 10-cv-494-GW(CWX), 2014 WL 12564090, at *4 (C.D. Cal. Mar. 17, 2014) ("*Experts are permitted to rely on hearsay, including*

the opinions of other experts, if proper foundation is laid that others in the field would likewise rely on them.”).

Importantly, Rule 703 expressly allows an expert to disclose the inadmissible statements he or she relied on to the jury if its probative value in helping the jury evaluate the opinion substantially outweighs their prejudicial effect. FRE 703 (The “proponent of the opinion may disclose [inadmissible hearsay statements] to the jury only if their probative value in helping the jury evaluate the opinion substantially outweighs their prejudicial effect.”); *see also Hayes v. Raytheon Co.*, 808 F.Supp. at 1329 (“Rule 703 liberalizes the admissibility of expert testimony by permitting experts to base their opinions on hearsay and other evidence not admissible in court.”); *Paddack v. Dave Christensen, Inc.*, 745 F.2d 1254, 1261–62 (9th Cir. 1984) (noting that FRE 703 permits “hearsay, or other inadmissible evidence, upon which an expert properly relies, to be admitted to explain the basis of the expert’s opinion.”).

Here, both parties have proceeded in accordance with these principles. Natera produced Dr. Sullivan’s materials, in his capacity as Natera’s damages expert in the *ArcherDX* Case, to Labcorp, and Labcorp’s damages expert Mr. Clemons duly relied upon them in formulating his report. *See, e.g.*, Ex. A. Natera then proceeded to request Mr. Malackowski’s materials, in *his* capacity as *ArcherDX’s* damages expert in the *ArcherDX* Case, to Natera. Ex. B at 29:10-16. Natera’s damages expert, Dr. Mody, then duly relied upon *Mr. Malackowski’s* materials in formulating *her* report. *See, e.g.*, Ex. C ¶ 198. In summary, both sets of damages expert materials from the *ArcherDX* Case were produced, and both parties’ current damages experts have relied upon the opposite party’s damages expert materials from the *ArcherDX* Case in formulating their current opinions. The parties could not have proceeded in a more reciprocal fashion.

Indeed, from the outset, Natera represented to Labcorp that it viewed the Sullivan and Malackowski reports as equivalent and corresponding, and stated that their use ought to go together. *See, e.g.*, D.I. 187 at 3. Invitae readily agreed to their reciprocal use. *Id.* If Natera is now experiencing buyer's remorse over its approach to production and usage of the Sullivan and Malackowski materials, that is hardly Labcorp's fault.

II. NATERA WAIVED ANY OBJECTIONS TO DR. SULLIVAN'S MATERIALS

In addition to the above, Natera has also waived, at multiple points, its rights to object to Labcorp's usage of Dr. Sullivan's materials.

First, as described above, from the very beginning, both parties understood the production and use of damages expert materials from the *ArcherDX* Case to be reciprocal in nature and made such representations to each other and the Court. Both parties then proceeded to use said materials in the exact same way—namely, by relying upon them in their damages expert reports. If Natera, upon receiving Mr. Clemons' report on June 16, 2023, believed Labcorp's usage of such to be improper, Natera should have said so. Instead, ***over a month later***, Natera served Dr. Mody's rebuttal report, in which Dr. Mody did the exact same thing as Mr. Clemons—rely upon the opposing party's damages expert materials from the *ArcherDX* Case. If Natera no longer feels the need for Mr. Malackowski's materials, it does not need to present them, but it cannot now force Labcorp to divest its own expert reports of Dr. Sullivan's materials.

Second, and relatedly, Natera has been in possession of Mr. Clemons' opening report for ***eight months*** prior to serving the present motion *in limine*. If Natera had an issue with evidence Mr. Clemons relied upon and sought to present, it should have moved to strike in a timely fashion, not delay until the eve of trial.

August 6, 2025

Respectfully submitted,

FARNAN LLP

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CERTIFICATE OF SERVICE

I, Brian E. Farnan, hereby certify that on August 6, 2025, a copy of PLAINTIFF'S OPPOSITION TO DEFENDANT'S MOTION *IN LIMINE* NO. 2: PRECLUDE LABCORP FROM USING, OR PRESENTING EVIDENCE OR ARGUMENT REGARDING, THE TESTIMONY AND EXPERT REPORTS OF RYAN SULLIVAN was served on the following as indicated:

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EXHIBIT A



OCEAN TOMO®

A PART OF  **JS|HELD**

INVITAE CORPORATION

V.

NATERA, INC.

Civil Action Nos. 1:21-cv-00669 & 1:21-cv-01635

United States District Court for the District of Delaware

EXPERT REPORT OF ALEXANDER L. CLEMONS

June 16, 2023



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1 FIRM BACKGROUND AND QUALIFICATIONS

My name is Alexander L. Clemons, and I am a Managing Director at Ocean Tomo, LLC, a part of J.S. Held. Ocean Tomo provides Financial Expert, Management Consulting, and Advisory services related to intellectual property (“IP”) and other intangible assets, corporate accounting investigations, regulatory and reporting obligations, solvency and restructuring, and contractual or competition disputes. Practice offerings address economic damage calculations and testimony, accounting investigations and financial forensics, technology and intangible asset valuation, strategy and risk management consulting, mergers and acquisitions, debt and equity private placement, and IP brokerage. Subsidiaries of Ocean Tomo include Ocean Tomo Investments Group, LLC, a registered broker dealer. With more than 100 offices globally, J.S. Held assists clients—corporations, insurers, law firms, governments, and institutional investors—on complex technical, scientific, and financial matters across all assets and value at risk.

I work in Ocean Tomo’s Intellectual Property Disputes Financial Expert Testimony practice. This practice area quantifies economic damages arising from intellectual property disputes and provides general litigation support. I have extensive experience related to the assessment of economic damages in litigation matters involving intellectual property, breach of contract, and other claims. Outside of a litigation context, I have experience with intellectual property valuation and have provided analytical support to clients engaged in licensing negotiations and other transactions.

I have assisted clients in numerous engagements involving the valuation of intellectual property and the determination of economic damages in commercial suits, including patent infringement, trademark infringement, copyright infringement, trade secret misappropriation, technology misappropriation, and breach of contract litigation. I possess a solid understanding of the financial issues and theories related to the quantification of damages in litigation. While specific issues vary by engagement, most have included evaluation and analysis of financial and strategic data to support or rebut quantification of lost profits, reasonable royalties, price erosion, unjust enrichment, commercial success, and/or business valuation. Various engagements have also included analysis of issues such as of Hatch Waxman Act market exclusivity, business significance of licensing terms including RAND obligations, and equities of a potential injunction. I have supported counsel in all phases of the litigation process from discovery to trial, and my experience spans a wide variety of industries including pharmaceuticals, medical devices, medical diagnostics, laboratory instruments and reagents, healthcare services, healthcare data, telecommunications, semiconductors, consumer electronics, smart phones, software, gaming, VR/AR, e-commerce, consumer goods, food products, dietary supplements, chemical products, automotive, entertainment, financial services, insurance, firearms, military and aviation technologies, airport security, and ventilation products, among others.

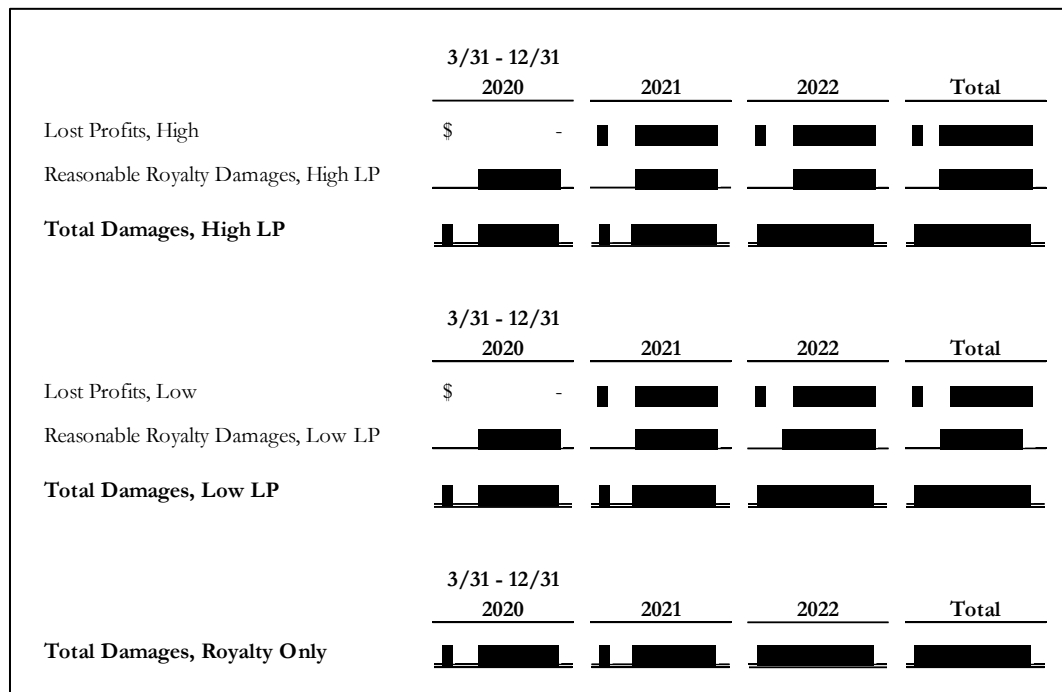
In addition to my role at Ocean Tomo, I have participated in and supported the advanced trial advocacy program at the Notre Dame Law School as a mock expert witness. I am a registered attorney licensed to practice law in the State of Illinois. I graduated with Academic Excellence from the University of Illinois, Urbana-Champaign, with an MBA concentrated in Finance. I graduated cum laude from DePaul University, College of Law, with a JD. I also hold a Bachelor of Arts in Rhetoric from the University of Illinois, Urbana-Champaign.

HIGHLY CONFIDENTIAL – ATTORNEYS’ EYES ONLY



royalties, in addition to or as an alternative to lost profits, I have analyzed quantitative and qualitative valuation metrics, including the *Georgia-Pacific* factors, and have reached a conclusion regarding the appropriate reasonable royalties due to Invitae for Natera's use of the Patents-in-Suit in connection with the Accused Product. As summarized in the figure below, I have calculated total damages, both including and excluding lost profits.

Figure 26: Summary of Damages through 2022⁵¹¹



I reserve the right to update my damages calculations if updated sales information is provided.

16 SIGNATURE

Respectfully submitted,

Alexander L. Clemons

June 16, 2023

Alexander L. Clemons

Date

⁵¹¹ Appendix 3.1.

Invitae Corporation v. Natera, Inc.

DOCUMENTS CONSIDERED

Appendix 2.2

Depositions and Associated Exhibits

Mr. David Bassette, February 9, 2023
Mr. Gregroy Porreca, April 28, 2023
Ms. Hila Moyal, May 17, 2023
Mr. Jim Stuart, April 6, 2023
Mr. John Fesko, May 26, 2023
Mr. Kevin Masukawa, February 28, 2023
Ms. Mary Freivogel, February 24, 2023
Mr. Nirav Malani, March 28, 2023
Mr. Richard Lusk, June 9, 2023
Mr. Solomon Moshkevich, May 23, 2023

Expert Reports

Expert Report of Dan E. Krane, June 16, 2023

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Complaint, Case No. 1:21-cv-00669, May 7, 2021
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Invitae Corporation's First Set of Interrogatories to Natera, Inc. (Nos. 1-5), February 15, 2022
Invitae Corporation's First Supplemental Responses and Objections to Natera, Inc.'s First Set of Interrogatories (Nos. 3 and 7), September 20, 2022
Invitae Corporation's First Supplemental Responses and Objections to Natera, Inc.'s Third Set of Interrogatories (Nos. 10-12), January 18, 2022
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Invitae Corporation's Responses and Objections to Natera, Inc.'s Fifth Set of Interrogatories (Nos. 16-25), March 3, 2023
Invitae Corporation's Responses and Objections to Natera, Inc.'s First Set of Interrogatories (Nos. 1-8), March 25, 2022
Invitae Corporation's Responses and Objections to Natera, Inc.'s Fourth Set of Interrogatories (Nos. 14-15), February 13, 2023
Invitae Corporation's Responses and Objections to Natera, Inc.'s Second Set of Interrogatories (No. 9), June 21, 2022
Invitae Corporation's Responses and Objections to Natera, Inc.'s Third Set of Interrogatories (Nos. 10-13), December 1, 2022
Invitae Corporation's Second Set of Interrogatories to Natera, Inc. (Nos. 6-15), January 16, 2023
Invitae Corporation's Second Supplemental Responses and Objections to Natera, Inc.'s First Set of Interrogatories (Nos. 3 and 7), September 23, 2022
Invitae Corporation's Supplemental Responses and Objections to Natera, Inc.'s Fifth Set of Interrogatories (Nos. 16-25), April 28, 2023
Invitae Corporation's Supplemental Responses and Objections to Natera, Inc.'s Fifth Set of Interrogatories (Nos. 17-22), June 5, 2023
Invitae Corporation's Supplemental Responses and Objections to Natera, Inc.'s First Set of Interrogatories (Nos. 1 and 5), June 5, 2023
Invitae Corporation's Supplemental Responses and Objections to Natera, Inc.'s First Set of Interrogatories (Nos. 1-8), April 28, 2023
Invitae Corporation's Supplemental Responses and Objections to Natera, Inc.'s First Set of Interrogatories (Nos. 2 and 7), February 15, 2023
Invitae Corporation's Supplemental Responses and Objections to Natera, Inc.'s Fourth Set of Interrogatories (Nos. 14-15), April 28, 2023
Invitae Corporation's Supplemental Responses and Objections to Natera, Inc.'s Interrogatories (No. 15), March 24, 2023
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Invitae Corporation's Third Supplemental Responses and Objections to Natera, Inc.'s First Set of Interrogatories (No. 3), September 30, 2022
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Invitae Corporation v. Natera, Inc.

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Appendix 2.2

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Natera, Inc.'s Fifth Set of Interrogatories to Invitae Corporation, (Nos. 16-25), February 1, 2023
Natera, Inc.'s First Set of Interrogatories to Invitae Corporation, (Nos. 1-7), February 23, 2022
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Invitae Corporation v. Natera, Inc.

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Appendix 2.2

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EXHIBIT B

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IN THE UNITED STATES DISTRICT COURT
IN AND FOR THE DISTRICT OF DELAWARE

INVITAE CORPORATION,
Plaintiff,
v.
NATERA, INC.,
Defendant.

)
)
) Civil Action Nos.
) 21-cv-669-GBW and
) 21-cv-1635-GBW
)
)
)

- - - -
Wilmington, Delaware
Friday, July 21, 2023
Teleconference Transcript
- - - -

BEFORE: HONORABLE GREGORY B. WILLIAMS
UNITED STATES DISTRICT COURT JUDGE
- - - -

Michele L. Rolfe, RPR, CRR

1 APPEARANCES:

2
3 FARNAN, LLP
4 BY: MICHAEL J. FARNAN, ESQ.

5 -and-

6 WEIL GOTSHAL & MANGES, LLP
7 BY: DEREK WALTER, ESQ.
8 Counsel on behalf of Invitae Corporation

9 MORRIS NICHOLS ARSHT & TUNNELL, LLP
10 BY: DEREK JAMES FAHNESTOCK, ESQ.

11 -and-

12 GROOMBRIDGE WU
13 BY: ELIZA P. STRONG, ESQ.
14 ERIC ALAN STONE, ESQ.

15 Counsel for Natera, Inc.
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1 them, in that they are entitled to this Brophy transcript,
2 even though they didn't depose him, and they are entitled to
3 the Moshkevich and Fesko transcript, even though they didn't
4 depose them. And, you know, it seems to me that what they
5 are looking for here is improper with respect to Mr. Brophy,
6 they could have deposed him. And what they are looking to
7 do with the Fesko and Moshkevich testimony is give them more
8 hours than what the rule would apply by deposing them here,
9 deposing them there and using all of it and I respectfully
10 submit that that's inappropriate.

11 Thank you, Your Honor.

12 MR. WALTER: Your Honor, real quickly, if the
13 rule is going forward I can't have someone else's prior
14 deposition transcript in another cases unless I do a
15 deposition -- and going forward I'm going to make sure I
16 take every possible deposition out of everybody else in
17 every case because I'm not going to ever get any relevant
18 discovery regarding what they might have said; if that's the
19 rule, it would be good to know.

20 THE COURT: All right. So here on this issue
21 I'm going to separate Brophy from Fesko and Moshkevich.

22 With respect to the request for Brophy, it's
23 denied.

24 With respect to the request of Fesko and
25 Moshkevich, it's granted.

1 MR. WALTER: Thank you, Your Honor.

2 MR. STONE: Thank you.

3 THE COURT: All right. The parties should
4 follow the protective order with respect to this information
5 that's being produced.

6 So that's all I have on the agenda for today.

7 MR. STONE: Your Honor, just one thing I want to
8 put on the record, it's in the letter, but I want to make
9 clear.

10 [REDACTED]
11 [REDACTED]
12 [REDACTED]
13 [REDACTED]
14 [REDACTED]
15 [REDACTED]
16 [REDACTED]

17 And with that, nothing further from Natera and
18 thank you, Your Honor.

19 THE COURT: All right. So Invitae represented
20 that you would produce your damages expert report, so Natera
21 expects to get that. So the Court will expect that to be
22 produced as well.

23 So with that, we'll adjourn.

24 Everybody have a good day.

25 (Whereupon, the following proceeding concluded

1 at 10:38 a.m.)

2 I hereby certify the foregoing is a true
3 and accurate transcript from my stenographic notes in the
4 proceeding.

5 /s/ Michele L. Rolfe, RPR, CRR
6 U.S. District Court
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EXHIBIT C

HIGHLY CONFIDENTIAL – ATTORNEYS’ EYES ONLY



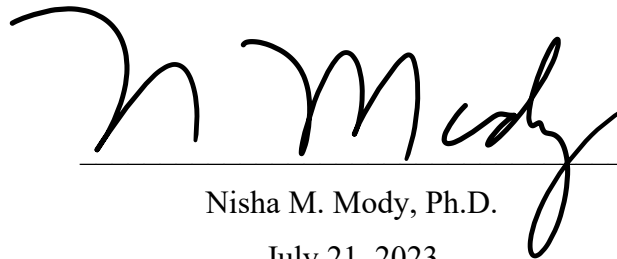
UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

Invitae Corporation

v.

Natera, Inc.

Civil Actions:
1:21-cv-00669 &
1:21-cv-01635



Nisha M. Mody, Ph.D.
July 21, 2023

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1. Qualifications, Assignment and Compensation

1.1. Qualifications

- (1) I am a Managing Director at Intensity LLC, a consulting firm specializing in litigation damages and financial valuation. I work primarily on economic and financial issues that arise from complex litigation, including patent litigation. In December 2019, I co-founded Eurekaonomics LLC with my partner, Evan Schulz. Prior to that, I was a partner at OSKR LLC from 2010 to 2019. For some of the time while I was at OSKR, I also co-taught a course on the economics and finance of intellectual property at Santa Clara University School of Law. I have more than twenty years' experience as a consultant and expert of economic analysis.
- (2) I have analyzed numerous issues including damages, valuations, licensing practices, prejudgment interest, economic domestic industry, public interest, irreparable harm, trade secret monetary remedies, competitive markets, and antitrust harm. I continue to give lectures to fellow economists, businesspeople, and attorneys. I provide a list of publications I have authored in my Appendix A. Appendix A also contains my CV and at least the last six years of my testifying experience.

1.2. Assignment

- (3) I have been retained by Groombridge, Wu, Baughman and Stone LLP, counsel for Natera, Inc. ("Natera") to consider the opinions of Mr. Alexander L. Clemons provided in his Expert Report dated June 16, 2023 and to offer an alternative rebuttal damages opinion in the event liability is found and Invitae Corporation ("Invitae") is entitled to damages.

1.3. Scope of Work

- (4) Intensity is being compensated at a rate of \$985 per hour for my work on this matter and at lower rates for time spent by others on my team. The compensation of Intensity is not dependent on the substance of my testimony or the outcome of this matter.
- (5) This report is a statement of opinions I currently expect to express in this matter and the bases and reasons for those opinions. In forming the opinions expressed in this report, I relied upon my education, experience, and knowledge of the subjects discussed. I have also considered documents and other materials, which are cited herein and/or listed in Appendix B. I have also relied on discussions with Dr. Michael Metzker and Mr. John Fesko, Mr. David Bessette, Dr. Raheleh Salari, and Dr. Hsin-Ta Wu and I have reviewed the reports of the technical experts, Dr. Michael Metzker, Dr. Dan Edward Krane and Dr. Joshua P. Earl that were provided along with the Expert

5.11. *Georgia-Pacific* No. 11: The extent to which the infringer has made use of the invention, and any evidence probative of the value of that use.

(196) Dr. Salari explains that [REDACTED]
[REDACTED].³⁹³ [REDACTED]
[REDACTED]. As such, I assume Natera has made use of the invention and this would suggest that a rate closer to \$2.33 million or more may be appropriate given what has been discussed in this report.


5.12. *Georgia-Pacific* No. 12: The portion of the profit or of the selling price that may be customary in the business or in comparable businesses to allow for the use of the invention or analogous inventions.

(197) This factor has no effect on the starting royalty as I have seen no relevant information for this factor.

5.13. *Georgia-Pacific* No. 13: The portion of the realizable profit that should be credited to the invention as distinguished from non-patented elements, the manufacturing process, business risks, or significant features or improvements added by the infringer.

(198) I have discussed all of the business risks Natera has incurred by creating a novel product and creating demand for this novel product and I incorporate those discussions by reference here. [REDACTED]
[REDACTED]:

³⁹³ Raheleh Salari, May 2, 2023, Dep. Tr. at 68:9-70:14 (“Q Okay. As of this time in 2017 when you were conceptualizing the workflow, were GATK and Sentieon considered the most accurate variant calling software? MR. STONE: Object to the form. THE WITNESS: [REDACTED]
[REDACTED]”); Expert Report of Michael Metzker, Ph.D., June 16, 2023, at 80.



Mr. Michael Brophy, Natera CFO, identified factors important to customers, including:

Sales and Marketing:
Q. How does the effectiveness of sales and marketing efforts affect the competitiveness of Signatera?
A. Well, I think are sales reps that -- for example, that are attentive to the customer will have an impact, kind of a self-evident impact on -- on demand for the product.
Brophy Depo. Tr. at 59:21-60:3

Turnaround Time:
A. My best understanding is that the test turnaround time is -- is one variable amongst several that's important to physicians.
Brophy Depo. Tr. at 61:22-24

Reputation and New Products:
A. Yeah. Like I said, I'm not capable of providing an exhaustive list, you know, on a topic that I didn't prepare for. There's -- there's a list of bullets here that drive -- that reference the competitive factors. ... probably not exhaustive, but...
Q. I mean, other than test turnaround time and performance, are there any other factors that are important to physicians when choosing to order a Signatera test?
A. Yeah, I think reputation among patients and providers for development and introduction of new innovative products is another indicative example of something important to physicians and patients.
Brophy Depo. Tr. at 63:11-64:3

These factors drive demand for Natera and Archer products but are unrelated to the Asserted Patents

Rebuttal Expert Report of James E. Malackowski, October 22, 2021, pp. 19-22; Deposition testimony of Mr. Michael Brophy, August 23, 2021, pp. 59-64

DDX-4.26

(199) As one can see, non-patent related expenses and risks have been taken by Natera. Natera created the market for MRD testing, and the MRD market exists now because of commercial risks Natera embraced since at least 2019.³⁹⁴ Before Signatera, notes Kevin Masukawa, VP of Oncology Marketing at Natera, [REDACTED] [REDACTED].³⁹⁵ To date,

³⁹⁴ Kevin Masukawa, Feb. 28, 2023, Dep. Tr. at 82:11-85:5 (“Q And in your LinkedIn profile, you said you drove adoption of MRD testing in solid tumors to oncologists, surgeons, biopharms. What do you mean -- what did you do to drive the adoption? A [REDACTED]

[REDACTED] Q And do you consider your efforts as successful? A [REDACTED]. Q Why is that? A [REDACTED]

[REDACTED] Q When you say you created markets -- (A discussion was held off the written record.) MR. STONE: You may want to withdraw that question and start it again. Q When you said -- what do you mean by “we created a market”? A [REDACTED]

[REDACTED] Q So are you saying Natera also created the market, the MRD market, for Guardant Health? MR. STONE: Object to the form of the question. A [REDACTED]

[REDACTED] Q Which year do you think Natera has created this MRD market? A [REDACTED]

[REDACTED]”).
³⁹⁵ Kevin Masukawa, Feb. 28, 2023, Dep. Tr. at 82:11-84:17 (“Q And in your LinkedIn profile, you said you drove adoption of MRD testing in solid tumors to oncologists, surgeons, biopharms. What do you mean -- what did you do to drive the adoption? A [REDACTED]

[REDACTED] Q And do you consider your efforts as successful? A [REDACTED]. Q Why is that? A [REDACTED]

[REDACTED] Q When you say you created markets -- (A discussion was held off the written record.) MR. STONE: You may want to withdraw that question and start it again. When you said -- what do you mean by “we created a market”? A [REDACTED]

[REDACTED] Q So are you saying Natera also created the market, the MRD market, for Guardant Health? MR. STONE: Object to the form of the question. A [REDACTED]

[REDACTED] Q Which year do you think Natera has created this MRD market? A [REDACTED].

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE**

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-669-GBW

LABORATORY CORPORATION OF
AMERICA HOLDINGS,

Plaintiff,

v.

NATERA, INC.,

Defendant.

C.A. No. 21-cv-1635-GBW

**NATERA’S REPLY IN FURTHER SUPPORT OF ITS MOTION TO
PRECLUDE LABCORP FROM USING, OR PRESENTING
EVIDENCE OR ARGUMENT REGARDING,
THE TESTIMONY AND EXPERT REPORTS OF RYAN SULLIVAN**

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Natera seeks to preclude Labcorp from introducing opinions offered in a different case, *ArcherDX*, by an expert, Ryan Sullivan, Ph.D., who has not been retained and will not testify in this case. Labcorp responds that because 1) its damages expert Mr. Alexander Clemons apparently read some of Dr. Sullivan's prior testimony, *but did not opine about it*, Labcorp has a blank slate to discuss Dr. Sullivan's opinions; and 2) that Natera failed to timely object to the admissibility of Dr. Sullivan's opinions. Labcorp is wrong on both points.

First, Mr. Clemons did not disclose opinions about—or rely on, quote, or even refer to—Dr. Sullivan's testimony. Labcorp rests its entire argument on the fact that Dr. Sullivan's *ArcherDX* testimony is on Mr. Clemons's "documents considered" list. Opp. at 2 (citing Ex. A). If that matters at all, it cuts against Labcorp: it means Mr. Clemons considered Dr. Sullivan's testimony and then **chose not to** offer an opinion about it. The inclusion of Dr. Sullivan's *ArcherDX* testimony on Mr. Clemons's materials considered list does not give Labcorp any basis, much less a blank slate, to introduce and discuss Dr. Sullivan's prior opinions here. Fed. R. Civ. P. 26(a)(2) requires that experts testifying under FRE 703 disclose "all opinions the witness will express" 90 days before trial. Mr. Clemons disclosed no opinions about Dr. Sullivan in his reports, and Labcorp points to no passages in the body of Mr. Clemons's reports where he even mentions Dr. Sullivan.

Second, Natera's objection is timely. Natera objected to the admissibility of Dr. Sullivan's testimony and reports in a letter filed with the Court on June 23, 2023, **after** Mr. Clemons's report was served on June 16, 2023. Ex. 1 at 2. ("Dr. Sullivan's materials would not be admissible at trial in this case."). At the parties' July 21, 2023 hearing, the Court deferred ruling on the admissibility of Dr. Sullivan's opinions. Ex. 2 12:22–13:2 ("whether or not it's admissible is another question."). Natera's timely motion appropriately re-raises this admissibility question.

EXHIBIT 1

IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

INVITAE CORPORATION,)	
)	
Plaintiff,)	
)	
v.)	C.A. No. 21-669 (GBW)
)	
NATERA, INC.,)	HIGHLY CONFIDENTIAL –
)	FILED UNDER SEAL
Defendant.)	
<hr/>		
INVITAE CORPORATION,)	
)	
Plaintiff,)	
)	
v.)	C.A. No. 21-1635 (GBW)
)	
NATERA, INC.,)	
)	
Defendant.)	

**LETTER TO THE HONORABLE GREGORY B. WILLIAMS FROM
DEREK J. FAHNESTOCK REGARDING DISCOVERY DISPUTE**

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Attorneys for Defendant Natera, Inc.

Dear Judge Williams:

Natera respectfully submits this answering letter regarding the pending discovery dispute.

Natera's Position Regarding Production of Altera Sales Data

Invitae first sought “financials relating to sales of” Natera’s Altera product (which is not accused of infringement in this case) in an email on May 5, 2023. Invitae has never served any formal discovery request for these data, which should be reason alone to deny Invitae’s request. Worse, Invitae’s only basis for seeking this information is its mischaracterization of the February 9, 2023 deposition of David Bessette, Natera’s Vice President of Finance. Although Invitae says Mr. Bessette testified that [REDACTED],” D.I. 187 at 1, he actually testified that [REDACTED], Bessette Tr. at 191:16-193:2, that [REDACTED], and that [REDACTED]. Bessette Tr. at 192:21-193:11 (Exhibit A). Nor has Invitae explained why financial information relevant to Altera is remotely relevant to this case, other than to support Invitae’s convoked-sales argument, which Mr. Bessette’s [REDACTED]—negates.

Natera's Position Regarding ArcherDX Materials

Natera recognizes that the Court is presiding over the *ArcherDX* action between Natera and Invitae. But that is a separate lawsuit, and Natera’s lead counsel in this case does not represent Natera in that case and is not under the Protective Order in that case. Invitae’s request for *ArcherDX* materials should be denied even without regard to the specific materials themselves.

First, the *ArcherDX* materials Invitae seeks were designated as Highly Confidential—Attorney’s Eyes’ Only pursuant to the Protective Order in that case. *See* C.A. No. 12-125, D.I. 69 (Exhibit B). That Order prohibits the use of such materials for any purpose other than to litigate *that case*. *Id.* at Section 7.1.

The above-captioned actions were filed well after the commencement of the *ArcherDX* case, but there is no cross-use provision in the Protective Order negotiated and entered for this case authorizing the use of information obtained in the *ArcherDX* case, *see* C.A. No. 21-669, D.I. 46, and neither party argued for the consolidation of these cases with the *ArcherDX* case. If Invitae had wanted to treat the cases as the same, it had every opportunity to propose that at the outset to avoid duplicative discovery. Instead, Invitae and its counsel apparently *want* duplicative discovery, to have multiple bites at the apple. That is unfair.

Another issue stemming from the separateness of the actions is that, while counsel for the various Invitae entities (which includes ArcherDX) is the same, Natera’s lead counsel here is not involved in the *ArcherDX* litigation. Invitae’s counsel should not be using in this litigation the confidential information it obtained in the *ArcherDX* litigation under the terms of the protective order in that case. Yet, Invitae is using the contents of those confidential materials from *ArcherDX* in *this case* to argue why they are relevant and discoverable in the present motion. Moreover, Natera’s lead counsel here cannot view in this case the information designated by the Invitae

entities as confidential in the *ArcherDX* case. Invitae would thus be getting disproportionate discovery if its motion were granted—the ability to see, use, and understand the full context of materials while Natera’s lead counsel here would only have access to the portions of those materials that do not contain ArcherDX’s confidential information.

Dr. Sullivan’s Materials from ArcherDX. Invitae’s request for Dr. Sullivan’s materials is an attempt to circumvent the Court’s previous order denying Invitae’s motion to compel production of certain agreements involving Natera. *See* D.I. 177. Invitae protests that it does not seek the “exhibits” to Dr. Sullivan’s materials that overlap with the subject matter of its previous, unsuccessful motion to compel, but Dr. Sullivan’s reports and deposition testimony in the *ArcherDX* case refer to the materials as to which this Court denied Invitae’s prior request. Invitae merely seeks to gain in a different form the discovery this Court already denied.

Moreover, Dr. Sullivan’s materials would not be admissible at trial in this case. He is not an expert in this case and will not be testifying at trial. Although Invitae relies on the *Pernix* case (attached as Exhibit C) to demonstrate why its motion should succeed, *Pernix* actually proves the opposite—that this discovery is not reasonably calculated to lead to the discovery of admissible evidence (a burden of showing that Invitae bears but fails to address in its motion). As discussed below, these materials themselves are not admissible, and fact discovery is closed, so they cannot “lead” to the discovery of admissible evidence. *AgroFresh Inc. v. Essentiv LLC*, C.A. No. 16-662-MN-SRF, 2018 WL 9578196, at *2 (D. Del. Dec. 11, 2018) (“To achieve the policy goals of both Rule 26 and Rule 408, courts within the Third Circuit require the moving party to make a ‘particularized showing’ that the evidence sought is relevant and reasonably calculated to lead to the discovery of admissible evidence.”).

Pernix makes clear that an expert’s reports or opinions cannot be deemed the statements of a party’s agent or employee within the meaning of Fed. R. Evid. 801(d)(2)(C) or (D). *Pernix Ireland v. Alvogen*, 316 F. Supp. 3d 816, 819-23 (D. Del. 2018); *see also Kirk v. Raymark Indus., Inc.*, 61 F.3d 147, 164 (3d Cir. 1995); *VM Techs., LLC v. Intel Corp.*, C. A. No. 15-33-RGA, 2017 WL 1753999, at *2 (D. Del. May 1, 2017) (report of expert not called to testify was inadmissible hearsay). Dr. Sullivan’s opinions and testimony in *ArcherDX* cannot be admissible in this case as the statements of a Natera agent or employee.

Pernix also provides a roadmap, which Invitae ignores, for when an expert’s prior opinions *may* be deemed the adoptive admissions of a party under Fed. R. Evid. 801(d)(2)(B). Specifically, the opinions of an expert retained by a party in a previous case may be deemed adoptive admissions when the party calls the expert to give testimony to prove a particular fact. 316 F. Supp. at 825. But, as *Pernix* makes clear, the expert’s report itself is not evidence of a party’s adoption of those opinions. *See Pernix*, 316 F. Supp. at 825-26. Invitae has made no effort to identify which portions of Dr. Sullivan’s prior reports and deposition testimony would bear indicia of having been adopted by Natera based on Dr. Sullivan’s later trial testimony in *ArcherDX*. Invitae’s request thus seeks discovery that would not lead to admissible evidence as a matter of law.

To the extent Invitae suggests that Dr. Sullivan’s prior reports or deposition testimony could be used to impeach a different expert in this case, *Pernix* also answers that question in the

negative: “[I]f statements by a declarant are inadmissible as hearsay, those statements cannot be used to cross-examine a different witness at trial.” *Id.* at 826.

John Fesko and Solomon Moshkevich’s Deposition Transcripts and Exhibits from ArcherDX. Invitae first requested these materials in March 2023. *After* Invitae made that request, Invitae deposed Messrs. Fesko and Moshkevich in *this case*, in their individual capacities and as Rule 30(b)(6) witnesses. It had a full and fair opportunity to cover any legitimate subject matter.

Invitae’s motion makes no effort to explain what non-duplicative information in their *ArcherDX* depositions would be relevant here and could not have been obtained in their depositions in this case. Invitae has failed to carry its burden to show that the requested information is relevant to “either the claims, defenses, or the subject matter of the litigation” or why its probative value outweighs the costs and burdens producing it would impose on Natera. *See Inventio*, 662 F. Supp. 2d at 380-81 (noting “[a]lthough the scope of discovery is broad, it is not unlimited”); *see also INVISTA N. Am. S.à.r.l. v. M&G USA Corp.*, C.A. No. 11-1007-SLR-CJB, 2013 WL 12171721, at *2 (D. Del. June 25, 2013).

Michael Brophy’s Deposition Transcript and Exhibits from ArcherDX. Natera has not identified Mr. Brophy as a witness in this case and will not be calling him to trial. If Invitae wanted to seek his testimony in *this case*, it should have noticed his deposition. It chose not to do so. It is hard to imagine anything Mr. Brophy might know that Invitae did not cover in its 56 requests for production, 25 interrogatories, 24 requests for admission, and nine deposition notices under Rules 30(b)(1) and 30(b)(6), but if it needed Mr. Brophy, too, it could have sought his deposition. The *ArcherDX* case is not a *de facto* expansion of the deposition limitations and discovery taken in this case. Invitae’s only argument now is that Mr. Brophy is a Natera employee who testified about Signatera and PCM in the *ArcherDX* case. That explains why Invitae might have wanted to depose him, not why it should get to use in this case his deposition from the *ArcherDX* case. That falls well short of demonstrating that the requested information is relevant to the claims.

Respectfully,

/s/ *Derek J. Fahnestock*

Derek J. Fahnestock (#4705)

DJF/rah

Enclosures

cc: All Counsel of Record (via electronic mail)

EXHIBIT 2

1 IN THE UNITED STATES DISTRICT COURT
2 IN AND FOR THE DISTRICT OF DELAWARE

3
4 INVITAE CORPORATION,)
5 Plaintiff,) Civil Action Nos.
6 v.) 21-cv-669-GBW and
7 NATERA, INC.,) 21-cv-1635-GBW
8 Defendant.)

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10 - - - -
11 Wilmington, Delaware
12 Friday, July 21, 2023
13 Teleconference Transcript

14 - - - -
15 BEFORE: HONORABLE GREGORY B. WILLIAMS
16 UNITED STATES DISTRICT COURT JUDGE
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Michele L. Rolfe, RPR, CRR

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1 MR. WALTER: Good morning, Your Honor. This is
2 Derek Walter. I'll start out with that issue, as you
3 requested.
4 There's, I think, a key point that needs to be
5 stated upfront that might have been implicit in the brief,
6 but might not have been explicit. As the Court knows, we
7 just completed a trial between Invitae and Natera, and the
8 Court might recall that in that trial Natera relied upon the
9 Archer Beacon Dixon agreement through its expert to procure
10 damages, and particularly argued that this agreement
11 warranted a 20 percent royalty for cancer testing products.
12 Well, it is fair play and the key point that the Court
13 should understand is that our expert is now relying upon
14 that very license to seek damages from Natera. The same
15 license that Natera previously relied upon to seek damages
16 with respect to Invitae. And that's why this material is
17 highly relevant.
18 If that wasn't clear from the papers, it should
19 be clear now. We're relying upon that same agreement that
20 they relied upon, that's why this discovery is relevant.
21 Let me go through the arguments they raised.
22 The first argument that they raised is that Natera's lead
23 counsel is not under the protective order from that prior
24 litigation. And that argument, frankly, is a strange
25 argument. Of course, they concede Natera's confidential

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2
3 P R O C E E D I N G S
4 (REPORTER'S NOTE: The following teleconference was
5 held beginning at 10:00 a.m.)
6 THE COURT: Good morning. We're here for a
7 discovery conference in Invitae Corp versus Natera Corp.
8 Civil Action Nos. 21-669 and 21-16345.
9 Let's start by having counsel put appearances on
10 the record.
11 MR. FARNAN: Good morning, Your Honor. Brian
12 Farnan on behalf of the plaintiff. And with me is Derek
13 Walter from Weil Gotshal.
14 THE COURT: All right. Good morning.
15 Defendants?
16 MS. JACOBS: Good morning, Your Honor. For
17 Natera this is Karen Jacobs and Derek Fahnestock from Morris
18 Nichols.
19 We have on the line with us and will be arguing
20 today are Eric Stone and Eliza Strong from Groombridge Wu.
21 THE COURT: Okay. Good morning.
22 All right. We have three issues. So let's
23 start with the first issue dealing with the request of
24 plaintiff to compel the expert reports, deposition testimony
25 and corresponding exhibits of Natera's damages expert Ryan
Sullivan from the ArcherDX litigation.

1 information, so to the extent the requested information has
2 Natera's information, Natera's counsel can see that; it's
3 odd to contend that they can't. But the strange concern
4 that they seem to have is that they might be prohibited from
5 seeing Invitae's information pursuant to that protective
6 order. Well, it's a strange concern. We're asking them to
7 produce the information.
8 If we thought there was a concern with them
9 seeing the information, we would have said so. Of course
10 Natera's outside counsel can see the information, we want
11 them to produce it to us. So if there's any concern there,
12 let's put that to doubt now; we're granting them permission
13 to see the material so they can produce it to us.
14 They also complain that the protective order
15 prohibits use in another case. Well, that's why we're
16 asking them to produce it. It can't be that you can shield
17 something from forever being used in another case by
18 producing it in a second case, so that's why we're trying to
19 get around this issue. We're asking them to produce it so
20 we can use it in this case.
21 Just picking through their arguments, they cite
22 the *AgroFresch* case, that's a case about production of
23 settlement agreements where there appears to be a heightened
24 standard. That's not what this is. Okay. This is not a
25 settlement agreement situation.

1 admission unless Natera gave that -- called him to give that
2 testimony at trial. And to the extent Natera did so, they
3 have the trial testimony.

4 And after they see the expert report from us
5 today, there is something that they think is inconsistent
6 with his trial court testimony that is in the expert report,
7 they can -- you know, they can ask us. But the notion that
8 they should -- we should have to produce the expert report
9 and deposition testimony of an expert in another case whom
10 we are not calling in this case is exactly what Judge Bryson
11 held in *Pernix* is irrelevant. And it can't lead to the
12 discovery of admissible evidence at this point, fact
13 discovery is over.

14 Let me make one more point because this is a new
15 argument -- forgive me, that I don't think Mr. Walter made
16 in the argument and I don't mean that pergoratively, I just
17 want to make sure I respond to it. The notion that their
18 expert can respond to hearsay because it is hearsay but
19 experts can rely on hearsay, the rule is that experts can
20 rely on hearsay of the type that is usually relied upon by
21 experts in the field. Damages experts can rely on economic
22 analyses, they can rely on the literature. You certainly
23 cannot argue that an expert can rely on another parties'
24 expert report because it is hearsay. The rule is not that
25 experts can use all hearsay of any kind. The rule is that

1 statements or analysis, they are relying effectively upon
2 what other people in the field have said. And the notion
3 that one expert can't rely upon something that another party
4 is saying is an authority in the field, that's erroneous.
5 Of course one expert can rely upon the statements of someone
6 else who the other party has said is an authority in the
7 field; that's precisely the kind of stuff that experts rely
8 upon when they provide their testimony.

9 MR. STONE: Your Honor, I know that the Courts
10 don't ordinarily entertain sur-rebuttal, but I must be doing
11 a very bad job today because neither of those is the
12 argument that I made. So just in the interest of full
13 disclosure, the reason that I pointed out it's a different
14 expert is that if it were the same expert, it would be a
15 prior statement of the expert; we would be having a
16 different conservation.

17 My point is simply it doesn't matter -- the
18 reason that it matters that it's not Dr. Sullivan is that
19 he's not testifying in the case.

20 And on the hearsay point -- on that I'll stop.
21 We simply just --

22 THE COURT: Yeah. On this issue I do think it's
23 fair game for Invitae to have access to that information for
24 discovery purposes; whether or not it's admissible is
25 another question. So I'm going to order the production with

1 experts can use hearsay of the type ordinarily relied upon
2 by experts in the field. That rule has absolutely no
3 applicability here.

4 THE COURT: All right.

5 MR. WALTER: Your Honor, this is Derek Walter.
6 Should i respond briefly to some the points he
7 made?

8 THE COURT: Yes, you can respond.

9 MR. WALTER: All right. So as to the first
10 point that the expert that they plan to rely upon in this
11 case is different from the expert that they relied upon in
12 the first case, that's irrelevant.

13 What matters is Natera would have adopted the
14 statements of their expert and they would have done so in
15 either this trial or the previous trials; it doesn't have to
16 be the same expert. *Pernix* doesn't say that, neither does
17 *Abstracts*. In fact, I think in that *Abstracts* case we cited
18 it was a different expert and that discovery was allowed.
19 So the notion that it has to be the same expert, that's just
20 wrong.

21 And then finally on the last point, the hearsay
22 point, you know that's incorrect, too. It's incorrect that
23 an expert in one field can't rely upon the testimony or the
24 statements or the opinions of someone else in another field.
25 That's what people do when they rely upon publications or

1 respect to the first request.

2 Let's move on to the second request.

3 MR. WALTER: Thank you, Your Honor.

4 The second request, I believe you -- the Natera
5 sales data, that's the one I'm going to take next.

6 I'll just stick to the arguments here. The
7 first thing they do is they complain that there's no
8 document request that relevant to this. That was a
9 surprising argument for us to see in this brief because it
10 was not once mentioned during meet and confer. If they
11 really thought that the lack of a document request was a
12 barrier here, they should have said so and we could have
13 remedied. So I think they've waived that argument. But
14 what's also really telling here is they don't submit the
15 document request we have in this case. And if you look at
16 the document request, which are not before the Court, I can
17 only tell you what's there, I think we probably do have
18 document requests, Request 20 asks for documents relating to
19 identifying somatic sensations. Request 31 asks for things
20 related to the accused product. And to the extent that's
21 sold as a unit, that would be an accused products. Request
22 42 asks for the same sort of things. So the lack of
23 document request was kind of a strange and surprising
24 argument.

25 Also, they make an argument based on the merits.

1 at 10:38 a.m.)

2 I hereby certify the foregoing is a true
3 and accurate transcript from my stenographic notes in the
4 proceeding.

5 /s/ Michele L. Rolfe, RPR, CRR
U.S. District Court

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